

52552

**From:** Chan, Christina  
**Sent:** Tuesday, October 09, 2001 12:52 PM  
**To:** Davis, Minh-Tam; STIC-Biotech/ChemLib  
**Subject:** RE: Rush search request for 09/580523

**Please rush. Thanks Chris**

-----Original Message-----

**From:** Davis, Minh-Tam  
**Sent:** Tuesday, October 09, 2001 12:37 PM  
**T :** Chan, Christina  
**Subject:** Rush search request for 09/580523

*priority date 05/99  
2000*

Please search in commercial data base and issued patent file:

- 1) SEQ ID NO:1
- 2) SEQ ID NO:1, without Serine, or glycine or alanine at amino acid position 118.
- 3) SEQ ID NO:1 having alanine at amino acid position 118.
- 4) Amino acid sequence 103-123 of SEQ ID NO:1.
- 5) An amino acid sequence comprising the amino acid sequence 143-168 of SEQ ID NO:1, but no serine at amino acid position 118.
- 6) Please search SEQ ID NO:1 against the parent case 60/136783 for priority date.

Thank you  
MINH TAM DAVIS  
ART UNIT 1642, ROOM 8A01, MB 8E12  
305-2008

**Point of Contact:**  
Jan Delavel  
Librarian-Physical Sciences  
CM1 1E01 Tel: 308-4498

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**SEARCH REQUEST FORM**

Scientific and Technical Information Center

Requester's Full Name: \_\_\_\_\_ Examiner #: \_\_\_\_\_ Date: \_\_\_\_\_  
Art Unit: \_\_\_\_\_ Phone Number 30 \_\_\_\_\_ Serial Number: \_\_\_\_\_  
Mail Box and Bldg/Room Location: \_\_\_\_\_ Results Format Preferred (circle): PAPER DISK E-MAIL

**If more than one search is submitted, please prioritize searches in order of need.**

\*\*\*\*\*

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: \_\_\_\_\_

Inventors (please provide full names): \_\_\_\_\_

Earliest Priority Filing Date: \_\_\_\_\_

*\*For Sequence Searches Only\* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

Point of Contact:  
Jan Delaval  
Librarian-Physical Sciences  
CM1 1E01 Tel: 308-4498

**STAFF USE ONLY**

Searcher Jan  
Searcher Phone # 4498  
Searcher Location \_\_\_\_\_  
Date Searcher Picked Up 10/9  
Date Completed 10/9  
Searcher Prep & Review Time \_\_\_\_\_  
Clencal Prep Time 20  
Online Time 30

**Type of Search**

NA Sequence (#) \_\_\_\_\_  
AA Sequence (#) 5  
Structure (#) \_\_\_\_\_  
Bibliographic \_\_\_\_\_  
Litigation \_\_\_\_\_  
Fulltext \_\_\_\_\_  
Patent Family \_\_\_\_\_  
Other \_\_\_\_\_

**Vendors and cost where applicable**

STN \_\_\_\_\_  
Dialog \_\_\_\_\_  
Questel/Orbit \_\_\_\_\_  
Dr Link \_\_\_\_\_  
Lexis/Nexis \_\_\_\_\_  
Sequence Systems ☒  
WWW/Internet \_\_\_\_\_  
Other (specify) \_\_\_\_\_

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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 9, 2001, 15:52:36 ; Search time 25.99 Seconds  
(without alignments)  
20.598 Million cell updates/sec

Title: US-09-580-523-l\_copy\_143\_168

Perfect score: 145

Sequence: 1 QSSSWTRVFSQWMDNLGRGSSAPSQ 26

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 197339 seqs, 20590346 residues

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents\_AA.\*

- 1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep.\*
- 2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep.\*
- 3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep.\*
- 4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep.\*
- 5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep.\*
- 6: /cgn2\_6/ptodata/2/iaa/backfiles!.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	145	100.0	168	2	US-08-717-123-2
2	145	100.0	168	3	US-08-985-335-1
3	145	100.0	168	3	US-08-985-335-7
4	139	95.9	166	1	US-08-665-617-2
5	120	82.8	204	1	US-08-333-565-2
6	120	82.8	204	2	US-08-661-479-2
7	120	82.8	204	2	US-08-733-505A-1
8	120	82.8	204	2	US-08-733-505A-12
9	120	82.8	204	2	US-08-733-505A-13
10	120	82.8	204	2	US-08-733-505A-14
11	120	82.8	204	2	US-08-717-123-3
12	84	57.9	16	1	US-08-333-565-17
13	84	57.9	16	2	US-08-661-479-17
14	81	55.9	16	1	US-08-333-565-28
15	81	55.9	16	2	US-08-661-479-28
16	55	37.9	9	2	US-08-733-505A-44
17	50	34.5	138	2	US-07-857-224B-112
18	50	34.5	151	1	US-08-614-935-28
19	50	34.5	151	3	US-09-130-287-28
20	50	34.5	1170	1	US-08-313-288B-20
21	49	33.8	137	2	US-07-857-224B-110
22	47	32.4	492	4	US-09-342-749-2
23	46	31.7	18	1	US-08-029-333-16
24	46	31.7	30	1	US-08-029-333-15
25	46	31.7	30	1	US-08-347-000-8
26	46	31.7	219	2	US-08-796-676-1
27	46	31.7	855	2	US-08-482-090-12

28 46 31.7 856 2 US-08-481-700B-8 Sequence 8, Appli  
29 46 31.7 856 2 US-09-007-383-16 Sequence 16, Appli  
30 45 31.0 863 1 US-08-325-547-4 Sequence 4, Appli  
31 45 31.0 869 1 US-08-188-582-32 Sequence 32, Appli  
32 45 31.0 869 1 US-08-646-715-32 Sequence 32, Appli  
33 44 30.3 9 2 US-08-706-741B-79 Sequence 79, Appli  
34 44 30.3 9 2 US-08-924-695A-79 Sequence 111, Appl  
35 44 30.3 137 2 US-07-857-224B-111 Sequence 29, Appl  
36 44 30.3 150 1 US-08-614-935-29 Sequence 29, Appl  
37 44 30.3 150 3 US-09-130-287-29 Sequence 29, Appl  
38 44 30.3 390 2 US-08-614-156B-1 Sequence 1, Appli  
39 43 29.7 162 1 US-08-087-016-4 Sequence 4, Appli  
40 43 29.7 890 1 US-08-145-006C-5 Sequence 5, Appli  
41 43 29.7 890 5 PCT-US94-00545-5 Sequence 5, Appli  
42 43 29.7 1091 6 5516630-2 Patent No. 5516630  
43 43 29.7 1528 1 US-08-463-092B-6 Sequence 6, Appli  
44 43 29.7 1528 2 US-08-462-109A-6 Sequence 6, Appli  
45 43 29.7 1528 2 US-08-460-907B-6 Sequence 6, Appli

ALIGNMENTS

RESULT 1  
US-08-717-123-2  
; Sequence 2, Application US/08717123  
; Patent No. 5965703  
; GENERAL INFORMATION:  
; APPLICANT: Horne, William A.  
; ATTORNEY/AGENT INFORMATION: Oltersdorf, Tilman  
; TITLE OF INVENTION: Human BAD Polypeptides, Encoding Nucleic  
; TITLE OF INVENTION: Acids and Methods of Use  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Campbell and Flores  
; STREET: 4370 La Jolla Village Drive, Suite 700  
; CITY: San Diego  
; STATE: California  
; COUNTRY: United States  
; ZIP: 92122  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/717,123  
; FILING DATE: 20-SEP-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Campbell, Cathryn A.  
; REGISTRATION NUMBER: 31,815  
; REFERENCE/DOCKET NUMBER: P-ID 1929  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 535-9001  
; TELEFAX: (619) 535-8949  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 168 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-717-123-2

Query Match 100.0%; Score 145; DB 2; Length 168;  
Best Local Similarity 100.0%; Pred. No. 3.6e-14;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QSSSWTRVFSQWMDNLGRGSSAPSQ 26

DB 143 QSSSWTRVFSQWMDNLGRGSSAPSQ 168

```

CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,335
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0421 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 168 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 1683637
US-08-985-335-7

Query Match 100.0%; Score 145; DB 3; Length 168;
Best Local Similarity 100.0%; Pred. No. 3 6e-14;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QSSSWTRVFQSWWDRNLGRGSSAPSQ 26
|||||
DB 143 QSSSWTRVFQSWWDRNLGRGSSAPSQ 168

RESULT 4
US-08-665-617-2
; Sequence 2, Application US/08665617
; Patent No. 5663316
; GENERAL INFORMATION:
; APPLICANT: Xudong, Yin
; TITLE OF INVENTION: Gene and Protein for Regulation of Cell Death
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/665,617
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794

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REFERENCE/DOCKET NUMBER: CL-8  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (352) 375-8100  
TELEFAX: (352) 372-5800  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 166 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-665-617-2

Query Match 95.9%; Score 139; DB 1; Length 166;  
Best Local Similarity 92.3%; Pred. No. 2.7e-13;  
Matches 24; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QSSWTRVFQSWDRNLGRGSSAPSQ 26  
Db 141 QSSWTRVFQSWDRNLGRGTAAPSQ 166

RESULT 5  
US-08-333-565-2  
Sequence 2, Application US/083333565  
Patent No. 5622852  
GENERAL INFORMATION:  
APPLICANT: KORSMEYER, Stanley J.  
TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH  
TITLE OF INVENTION: REGULATOR  
NUMBER OF SEQUENCES: 59  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Kourie and Crew  
STREET: 379 Lytton Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: US  
ZIP: 94301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/333,565  
FILING DATE: 31-OCT-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 15726A-000700  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 326-2422  
TELEFAX: (415) 326-2422  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 204 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..204  
OTHER INFORMATION: /note= "Deduced amino acid sequence  
of mouse BAD."  
US-08-333-565-2

Query Match 82.8%; Score 120; DB 1; Length 204;  
Best Local Similarity 73.1%; Pred. No. 2.1e-10;  
Matches 19; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 QSSWTRVFQSWDRNLGRGSSAPSQ 26  
Db 179 QSAGWTRIIQSWDRNLKGGSTPSQ 204

RESULT 6  
US-08-661-479-2  
Sequence 2, Application US/08661479  
Patent No. 5834209  
GENERAL INFORMATION:  
APPLICANT: KORSMEYER, Stanley J.  
TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH  
TITLE OF INVENTION: REGULATOR  
NUMBER OF SEQUENCES: 59  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Kourie and Crew  
STREET: 379 Lytton Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: US  
ZIP: 94301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/661,479  
FILING DATE: 11-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/333,565  
FILING DATE: 31-OCT-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 15726A-000700  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 326-2422  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 204 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FEATURE:  
NAME/KEY: protein  
LOCATION: 1..204  
OTHER INFORMATION: /note= "Deduced amino acid sequence  
of mouse BAD."  
US-08-661-479-2

Query Match 82.8%; Score 120; DB 2; Length 204;  
Best Local Similarity 73.1%; Pred. No. 2.1e-10;  
Matches 19; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 QSSWTRVFQSWDRNLGRGSSAPSQ 26  
Db 179 QSAGWTRIIQSWDRNLKGGSTPSQ 204

RESULT 7  
US-08-733-505A-1  
Sequence 1, Application US/08733505A  
Patent No. 5856445  
GENERAL INFORMATION:  
APPLICANT: KORSMEYER, STANLEY J.  
TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF  
TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR

```

; TELEPHONE: (314) 727-5188
; TELEFAX: (314) 727-6092
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 204 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-733-505A-12

Query Match 82.8%; Score 120; DB 2; Length 204;
Best Local Similarity 73.1%; Pred. No. 2.1e-10;
Matches 19; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 QSSWTRVFQSWDRNLGRGSSAPSQ 26
||: |||: |||||: |||
Db 179 QSAGWTRIIQSWDRNLGRGGSTPSQ 204

RESULT 9
US-08-733-505A-13
; Sequence 13, Application US/08733505A
; Patent No. 5856445
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, STANLEY J.
; TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
; TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWELL, & HAFFERKAMP, I. C.

```

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? CITY: ST. LOUIS
? STATE: MISSOURI
? COUNTRY: USA
? ZIP: 63105
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS

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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/733,505A
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 965458
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 204 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-733-505A-13

Query Match 82.8%; Score 120; DB 2; Length 204;
Best Local Similarity 73.1%; Pred. No. 2.1e-10;
Matches 19; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 QSSSWTRVFQSWWDRNLGSGSAPSQ 26
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Db 179 QSNAGWTRIIQSWWDRNLGKGSTPSQ 204

RESULT 10

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RESULT 11
US-08-717-123-3
; Sequence 3, Application US/08717123
; Patent No. 5965703
; GENERAL INFORMATION:
; APPLICANT: Horne, William A.
; APPLICANT: Oltersdorf, Tilman
; TITLE OF INVENTION: Human BAD Polypeptides, Encoding Nucleic
; TITLE OF INVENTION: Acids and Methods of Use
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

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Query Match 57.9%; Score 84; DB 1; Length 16;  
Best Local Similarity 80.0%; Pred. NO. 2.1e-06;  
Matches 12; Conservative 2; Mismatches 1; Indels

QY 5 WTRVFQSWDRNLGR 19  
| | | : | | | | | | | |  
Db 2 WTRIQSWDRNLGK 16

RESULT 13  
US-08-661-479-17  
; Sequence 17, Application US/08661479  
; Patent No. 5834209  
; GENERAL INFORMATION:  
; APPLICANT: KORSMEYER, Stanley J.  
; TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH  
; TITLE OF INVENTION: REGULATOR  
; NUMBER OF SEQUENCES: 59  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend Kourie and Crew  
; STREET: 379 Lytton Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: US  
; ZIP: 94301  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/661,479  
; FILING DATE: 11-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/333,565  
; FILING DATE: 31-OCT-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 15726A-000700  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 326-2400  
; TELEFAX: (415) 326-2422  
; INFORMATION FOR SEQ ID NO: 17:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 16 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-661-479-17

Query Match 57.9%; Score 84; DB 2; Length 16;  
Best Local Similarity 80.0%; Pred. No. 2.1e-06;  
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 WTRVFQSWDRNLGR 19  
| | | : | | | | | | | |  
Db 2 WTRIQSWDRNLGK 16

RESULT 14  
US-08-333-565-28  
; Sequence 28, Application US/08333565  
; Patent No. 5622852  
; GENERAL INFORMATION:  
; APPLICANT: KORSMEYER, Stanley J.  
; TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH  
; TITLE OF INVENTION: REGULATOR  
; NUMBER OF SEQUENCES: 59  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend Kourie and Crew  
; STREET: 379 Lytton Avenue  
; CITY: Palo Alto  
; STATE: California

; COUNTRY: US  
; ZIP: 94301  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/333,565  
; FILING DATE: 31-OCT-1994  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 15726A-000700  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 326-2400  
; TELEFAX: (415) 326-2422  
; INFORMATION FOR SEQ ID NO: 28:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 16 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-333-565-28

Query Match 55.9%; Score 81; DB 1; Length 16;  
Best Local Similarity 75.0%; Pred. No. 5.9e-06;  
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 SSSWTRVFQSWDRNL 17  
| : | | | : | | | | | | | |  
Db 1 SAGWTRIQSWDRNL 16

RESULT 15  
US-08-661-479-28  
; Sequence 28, Application US/08661479  
; Patent No. 5834209  
; GENERAL INFORMATION:  
; APPLICANT: KORSMEYER, Stanley J.  
; TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH  
; TITLE OF INVENTION: REGULATOR  
; NUMBER OF SEQUENCES: 59  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend Kourie and Crew  
; STREET: 379 Lytton Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: US  
; ZIP: 94301  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/661,479  
; FILING DATE: 11-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/333,565  
; FILING DATE: 31-OCT-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 15726A-000700  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 326-2400  
; TELEFAX: (415) 326-2422  
; INFORMATION FOR SEQ ID NO: 28:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 16 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-333-565-28

```

; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-661-479-28

```

```

Query Match          55.9%; Score 81; DB 2; Length 16;
Best Local Similarity 75.0%; Pred. No. 5.9e-06;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

```

```

QY 2 SSSWTRVFQSWDRNL 17
   I: |||||
Db 1 SAGWTRIIQSWDRNL 16

```

```

Search completed: October 9, 2001, 15:52:36
Job time: 151 sec

```

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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 9, 2001, 16:08:31 ; Search time 36.31 Seconds  
(without alignments)  
33.961 Million cell updates/sec

Title: US-09-580-523-1-copy\_143\_168

Perfect score: 145

Sequence: 1 QSSSWTRVFQSWDRNLGRGSSAPSQ 26

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 311045 seqs, 47428042 residues

Total number of hits satisfying chosen parameters: 311045

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Pending\_Patents\_AA\_New.\*

1: /cgn2\_6/ptodata/2/paa/PCT\_NEW\_COMB.pcp.\*

2: /cgn2\_6/ptodata/2/paa/US06\_NEW\_COMB.pcp.\*

3: /cgn2\_6/ptodata/2/paa/US07\_NEW\_COMB.pcp.\*

4: /cgn2\_6/ptodata/2/paa/US08\_NEW\_COMB.pcp.\*

5: /cgn2\_6/ptodata/2/paa/US09\_NEW\_COMB.pcp.\*

6: /cgn2\_6/ptodata/2/paa/US60\_NEW\_COMB.pcp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	145	100.0	168	5	US-09-922-378-2	Sequence 2, Appli
2	120	82.8	204	5	US-09-922-378-3	Sequence 3, Appli
3	115	79.3	201	1	PCT-US01-18569-2762	Sequence 2762, Ap
4	52	35.9	66	1	PCT-US01-08631-56706	Sequence 56706, A
5	52	35.9	103	5	US-09-617-681A-7103	Sequence 7103, Ap
6	50	34.5	97	1	PCT-US01-08631-58580	Sequence 58580, A
7	50	34.5	140	5	US-09-758-446-1130	Sequence 1130, Ap
8	50	34.5	257	1	PCT-US01-08631-37015	Sequence 37015, A
9	50	34.5	1170	5	US-09-784-356-114	Sequence 114, App
10	50	34.5	1223	5	US-09-758-447-658	Sequence 658, App
11	49	33.8	37	5	US-09-764-905-10865	Sequence 10865, A
12	49	33.8	168	1	PCT-US01-08631-37014	Sequence 37014, A
13	49	33.8	458	1	PCT-US01-14827-9450	Sequence 9450, Ap
14	49	33.8	1189	1	PCT-US01-08656-8991	Sequence 8991, Ap
15	48.5	33.4	209	1	PCT-US01-08656-7468	Sequence 7468, Ap
16	48.5	33.4	241	5	US-09-803-110-12532	Sequence 12532, A
17	48	33.1	93	1	PCT-US01-08631-47656	Sequence 47656, A
18	48	33.1	127	5	US-09-649-866A-1103	Sequence 1103, Ap
19	48	33.1	139	5	US-09-649-866A-1102	Sequence 1102, Ap
20	48	33.1	140	5	US-09-758-471-2894	Sequence 2894, Ap
21	48	33.1	445	1	PCT-US01-08631-45047	Sequence 45047, A
22	47.5	32.8	96	5	US-09-764-905-15545	Sequence 15545, A
23	47	32.4	209	5	US-09-895-793-897	Sequence 897, App
24	47	32.4	209	5	US-09-895-814-897	Sequence 814, App
25	47	32.4	393	5	US-09-895-793-934	Sequence 934, App
26	47	32.4	393	5	US-09-895-814-934	Sequence 934, App
27	47	32.4	492	5	US-09-895-793-895	Sequence 895, App

ALIGNMENTS

RESULT 1

US-09-922-378-2

; Sequence 2, Application US/099222378

; GENERAL INFORMATION:

; APPLICANT: Horne, William A.

; APPLICANT: Oltersdorf, Tilman

; TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC

; FILE OF INVENTION: ACIDS AND METHODS OF USE

; FILE REFERENCE: 480140.428D3

; CURRENT APPLICATION NUMBER: US/09/922,378

; CURRENT FILING DATE: 2001-08-03

; NUMBER OF SEQ ID NOS: 15

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 2

; LENGTH: 168

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-922-378-2

Query Match

Best Local Similarity 100.0%; Score 145; DB 5; Length 168;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QSSSWTRVFQSWDRNLGRGSSAPSQ 26

Db 143 QSSSWTRVFQSWDRNLGRGSSAPSQ 168

RESULT 2

US-09-922-378-3

; Sequence 3, Application US/099222378

; GENERAL INFORMATION:

; APPLICANT: Horne, William A.

; APPLICANT: Oltersdorf, Tilman

; TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC

; FILE OF INVENTION: ACIDS AND METHODS OF USE

; FILE REFERENCE: 480140.428D3

; CURRENT APPLICATION NUMBER: US/09/922,378

; CURRENT FILING DATE: 2001-08-03

; NUMBER OF SEQ ID NOS: 15

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 3

; LENGTH: 204

; TYPE: PRT

; ORGANISM: Mus musculus

US-09-922-378-3

Query Match

Best Local Similarity 82.8%; Score 120; DB 5; Length 204;

```

2 SSNIRVFQSWNRLGSSAPS 23
||:| | | | | | | |
Db 13 SSAAKRFSEQW--GLSLGSSAPS 34

RESULT 5
US-09-617-681A-7103
; Sequence 7103, Application US/09617681A
; GENERAL INFORMATION:
; APPLICANT: N. ALEXANDROV et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptid
; TITLE OF INVENTION: Thereby
; FILE REFERENCE: 2750-1084P
; CURRENT APPLICATION NUMBER: US/09/617,681A
; CURRENT FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 9311
; SEQ ID NO 7103
; LENGTH: 103
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..103
; OTHER INFORMATION: Ceres Seq. ID 1437722
; NAME/KEY: misc_feature
; LOCATION: 1..103
; OTHER INFORMATION: Xaa is any amino acid
US-09-617-681A-7103

```

```

> GENERAL INFORMATION:
> APPLICANT: Hyseq, Inc
> TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
> FILE REFERENCE: 21272-049
> CURRENT APPLICATION NUMBER: PCT/US01/086331
> CURRENT FILING DATE: 2001-03-30
> PRIOR APPLICATION NUMBER: 09/540,217
> PRIOR FILING DATE: 2000-03-31
> PRIOR APPLICATION NUMBER: 09/649,167
> PRIOR FILING DATE: 2000-08-23
> NUMBER OF SEQ ID NOS: 60736
> SOFTWARE: Custom
> SEQ ID NO 58580
> LENGTH: 97
> TYPE: PRT
> ORGANISM: Homo sapiens
> FEATURE:
> NAME/KEY: DOMAIN
> LOCATION: (53)..(67)
> OTHER INFORMATION: Extracellular proteins
> OTHER INFORMATION: identified by eMATRIX, accession num
> OTHER INFORMATION: 12, raw score of 10.54
> NAME/KEY: DOMAIN
> LOCATION: (20)..(75)
>

```

```

; LOCATION: (35)...(37)
; OTHER INFORMATION: Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 proteins domain
; OTHER INFORMATION: identified by eMATTRX, accession number BL01009C, p-value=1.78
; OTHER INFORMATION: 12, raw score of 10.54
; NAME/KEY: DOMAIN
; LOCATION: (20)...(75)

```



```
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: SITE
/ LOCATION: (461)
/ OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
US-09-758-447-658

Query Match          34.5%; Score 50; DB 5; Length 1223;
Best Local Similarity 50.0%; Pred. No. 1e+02;
Matches 11; Conservative 2; Mismatches 3; Indels 6; Gaps 1;

QY 1 QSSS-----WTRVFQSWDRN 16
    |||| I : I I I I I
Db 1083 QSSRRFVVMMKQVTSYWDN 1104

RESULT 11
US-09-764-905-10865
/ Sequence 10865, Application US/09764905
/ GENERAL INFORMATION:
/ APPLICANT: Rosen et al.
/ TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
/ FILE REFERENCE: PC004
/ CURRENT APPLICATION NUMBER: US/09/764,905
/ CURRENT FILING DATE: 2001-01-17
/ PRIOR APPLICATION NUMBER: 60/179,065
/ PRIOR FILING DATE: 2000-01-31
/ PRIOR APPLICATION NUMBER: 60/180,628
/ PRIOR FILING DATE: 2000-02-04
/ PRIOR APPLICATION NUMBER: 60/214,886
/ PRIOR FILING DATE: 2000-06-28
/ PRIOR APPLICATION NUMBER: 60/217,487
/ PRIOR FILING DATE: 2000-07-11
/ PRIOR APPLICATION NUMBER: 60/225,758
/ PRIOR FILING DATE: 2000-08-14
/ PRIOR APPLICATION NUMBER: 60/220,963
/ PRIOR FILING DATE: 2000-07-26
/ PRIOR APPLICATION NUMBER: 60/217,496
/ PRIOR FILING DATE: 2000-07-11
/ PRIOR APPLICATION NUMBER: 60/225,447
/ PRIOR FILING DATE: 2000-08-14
/ PRIOR APPLICATION NUMBER: 60/218,290
/ PRIOR FILING DATE: 2000-07-14
/ PRIOR APPLICATION NUMBER: 60/225,757
/ PRIOR FILING DATE: 2000-08-14
/ PRIOR APPLICATION NUMBER: 60/226,868
/ PRIOR FILING DATE: 2000-08-22
/ PRIOR APPLICATION NUMBER: 60/216,647
/ PRIOR FILING DATE: 2000-07-07
/ PRIOR APPLICATION NUMBER: 60/225,267
/ PRIOR FILING DATE: 2000-08-14
/ PRIOR APPLICATION NUMBER: 60/216,880
/ PRIOR FILING DATE: 2000-07-07
/ PRIOR APPLICATION NUMBER: 60/225,270
/ PRIOR FILING DATE: 2000-08-14
/ PRIOR APPLICATION NUMBER: 60/251,869
/ PRIOR FILING DATE: 2000-12-08
/ PRIOR APPLICATION NUMBER: 60/235,834
/ PRIOR FILING DATE: 2000-09-27
/ PRIOR APPLICATION NUMBER: 60/234,274
/ PRIOR FILING DATE: 2000-09-21
/ PRIOR APPLICATION NUMBER: 60/234,223
/ PRIOR FILING DATE: 2000-09-21
/ PRIOR APPLICATION NUMBER: 60/228,924
/ PRIOR FILING DATE: 2000-08-30
/ PRIOR APPLICATION NUMBER: 60/224,518
/ PRIOR FILING DATE: 2000-08-14
/ PRIOR APPLICATION NUMBER: 60/236,369
/ PRIOR FILING DATE: 2000-09-29
/ PRIOR APPLICATION NUMBER: 60/224,519
/ PRIOR FILING DATE: 2000-08-14
/ PRIOR APPLICATION NUMBER: 60/227,182
/ PRIOR FILING DATE: 2000-07-26
/ PRIOR APPLICATION NUMBER: 60/241,809
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: 60/249,299
/ PRIOR FILING DATE: 2000-11-17
/ PRIOR APPLICATION NUMBER: 60/236,327
/ PRIOR FILING DATE: 2000-09-29
/ PRIOR APPLICATION NUMBER: 60/241,785
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: 60/244,617
/ PRIOR FILING DATE: 2000-11-01
/ PRIOR APPLICATION NUMBER: 60/225,268
/ PRIOR FILING DATE: 2000-08-14
/ PRIOR APPLICATION NUMBER: 60/236,368
/ PRIOR FILING DATE: 2000-09-29
/ PRIOR APPLICATION NUMBER: 60/251,856
/ PRIOR FILING DATE: 2000-12-08
/ PRIOR APPLICATION NUMBER: 60/251,868
/ PRIOR FILING DATE: 2000-12-08
/ PRIOR APPLICATION NUMBER: 60/229,344
/ PRIOR FILING DATE: 2000-09-01
/ PRIOR APPLICATION NUMBER: 60/234,997
/ PRIOR FILING DATE: 2000-09-25
/ PRIOR APPLICATION NUMBER: 60/229,343
/ PRIOR FILING DATE: 2000-09-01
/ PRIOR APPLICATION NUMBER: 60/229,345
/ PRIOR FILING DATE: 2000-09-01
/ PRIOR APPLICATION NUMBER: 60/229,287
/ PRIOR FILING DATE: 2000-09-01
/ PRIOR APPLICATION NUMBER: 60/229,513
/ PRIOR FILING DATE: 2000-09-05
/ PRIOR APPLICATION NUMBER: 60/231,413
/ PRIOR FILING DATE: 2000-09-08
/ PRIOR APPLICATION NUMBER: 60/229,509
/ PRIOR FILING DATE: 2000-09-05
/ PRIOR APPLICATION NUMBER: 60/236,367
/ PRIOR FILING DATE: 2000-09-29
/ PRIOR APPLICATION NUMBER: 60/237,039
/ PRIOR FILING DATE: 2000-10-02
/ PRIOR APPLICATION NUMBER: 60/237,038
/ PRIOR FILING DATE: 2000-10-02
/ PRIOR APPLICATION NUMBER: 60/236,370
/ PRIOR FILING DATE: 2000-09-29
/ PRIOR APPLICATION NUMBER: 60/236,802
/ PRIOR FILING DATE: 2000-10-02
/ PRIOR APPLICATION NUMBER: 60/237,037
/ PRIOR FILING DATE: 2000-10-02
/ PRIOR APPLICATION NUMBER: 60/237,040
/ PRIOR FILING DATE: 2000-10-02
/ PRIOR APPLICATION NUMBER: 60/240,960
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: 60/239,935
/ PRIOR FILING DATE: 2000-10-13
/ PRIOR APPLICATION NUMBER: 60/239,937
/ PRIOR FILING DATE: 2000-10-13
/ PRIOR APPLICATION NUMBER: 60/241,787
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: 60/246,474
/ PRIOR FILING DATE: 2000-11-08
/ PRIOR APPLICATION NUMBER: 60/246,532
/ PRIOR FILING DATE: 2000-11-08
/ PRIOR APPLICATION NUMBER: 60/249,216
/ PRIOR FILING DATE: 2000-11-17
/ PRIOR APPLICATION NUMBER: 60/249,210
/ PRIOR FILING DATE: 2000-11-17
/ PRIOR APPLICATION NUMBER: 60/226,681
/ PRIOR FILING DATE: 2000-08-22
/ PRIOR APPLICATION NUMBER: 60/225,759
/ PRIOR FILING DATE: 2000-08-14
/ PRIOR APPLICATION NUMBER: 60/225,213
/ PRIOR FILING DATE: 2000-08-14
/ PRIOR APPLICATION NUMBER: 60/227,182
```



```

; SEQ ID NO 7468
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo
; FEATURE:
; NAME/KEY: mi
; LOCATION: (1
; OTHER INFORM
PCT-US01-08656-7

```

```

Query Match          33.4%; Score 48.5; DB 1; Length 209;
Best Local Similarity 40.6%; Pred. No. 32;
Matches 13; Conservative 5; Mismatches 7; Indels 7; Gaps 2;

y      2 SSSWTVFOS-----WWDRLNLR-GSSAPSQ 26
      |||::||| ||| ||| |||
b      81 SSSFSRISFSVSGICPMWDSRDSRGVGTTFPSQ 112

```

Search completed: October 9, 2001, 16:08:32  
Job time: 382 sec

Query Match 33.8%; Score 49; DB 1; Length 1189;  
Best Local Similarity 50.0%; Pred. No. 1.4e+02;  
Matches 9; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

```

RESULT 15
PCT-US01-08656-7468
; Sequence 7468, Application PC/TUS0108656
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-066
; CURRENT APPLICATION NUMBER: PCT/US01/08656
; CURRENT FILING DATE: 2001-04-16
; PRIOR APPLICATION NUMBER: 09/522,929
; PRIOR FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: 09/770,160
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 10994
; SOFTWARE: Custom

```



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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 9, 2001, 15:53:27 ; Search time 44.37 Seconds  
(without alignments)  
35.525 Million cell updates/sec

Title: US-09-580-523-1\_COPY\_143\_168

Perfect score: 145

Sequence: 1 OSSSWTRVFQSWDRNLGRGSSAPSQ 26

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A\_Geneseq\_0601.\*  
1: /SIDS8/gcgdata/geneseq/geneseq/AA1980.DAT.\*  
2: /SIDS8/gcgdata/geneseq/geneseq/AA1981.DAT.\*  
3: /SIDS8/gcgdata/geneseq/geneseq/AA1982.DAT.\*  
4: /SIDS8/gcgdata/geneseq/geneseq/AA1983.DAT.\*  
5: /SIDS8/gcgdata/geneseq/geneseq/AA1984.DAT.\*  
6: /SIDS8/gcgdata/geneseq/geneseq/AA1985.DAT.\*  
7: /SIDS8/gcgdata/geneseq/geneseq/AA1986.DAT.\*  
8: /SIDS8/gcgdata/geneseq/geneseq/AA1987.DAT.\*  
9: /SIDS8/gcgdata/geneseq/geneseq/AA1988.DAT.\*  
10: /SIDS8/gcgdata/geneseq/geneseq/AA1989.DAT.\*  
11: /SIDS8/gcgdata/geneseq/geneseq/AA1990.DAT.\*  
12: /SIDS8/gcgdata/geneseq/geneseq/AA1991.DAT.\*  
13: /SIDS8/gcgdata/geneseq/geneseq/AA1992.DAT.\*  
14: /SIDS8/gcgdata/geneseq/geneseq/AA1993.DAT.\*  
15: /SIDS8/gcgdata/geneseq/geneseq/AA1994.DAT.\*  
16: /SIDS8/gcgdata/geneseq/geneseq/AA1995.DAT.\*  
17: /SIDS8/gcgdata/geneseq/geneseq/AA1996.DAT.\*  
18: /SIDS8/gcgdata/geneseq/geneseq/AA1997.DAT.\*  
19: /SIDS8/gcgdata/geneseq/geneseq/AA1998.DAT.\*  
20: /SIDS8/gcgdata/geneseq/geneseq/AA1999.DAT.\*  
21: /SIDS8/gcgdata/geneseq/geneseq/AA2000.DAT.\*  
22: /SIDS8/gcgdata/geneseq/geneseq/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	145	100.0	168	19	AAW55779 Human Bcl-xL/Bcl-2
2	145	100.0	168	21	AA13512 Human cell prolif
3	145	100.0	168	22	AA13512 Human cell prolif
4	145	100.0	168	22	AA13512 Human cell prolif
5	139	95.9	166	18	AA13512 Human cell prolif
6	120	82.8	162	22	AA13512 Human cell prolif
7	120	82.8	204	17	AA13512 Human cell prolif
8	120	82.8	204	19	AA13512 Human cell prolif
9	120	82.8	204	19	AA13512 Human cell prolif
10	120	82.8	204	19	AA13512 Human cell prolif
11	120	82.8	204	19	AA13512 Human cell prolif

12	120	82.8	204	19	AAW58832	Murine BAD protein
13	120	82.8	204	22	AAW70369	Longer murine BAD
14	84	57.9	16	17	AA13512	bcl-x(L)/bcl-2 ass
15	81	55.9	16	17	AA13512	bcl-x(L)/bcl-2 ass
16	51	35.2	247	22	AA13512	Human secreted pro
17	51	35.2	855	13	AA13512	Env polypeptide of
18	51	35.2	855	15	AA13512	FIV JAPAN2 envel
19	50	34.5	138	20	AA13512	Human testis speci
20	50	34.5	158	15	AA13512	FIV UK5 envelope p
21	50	34.5	1152	21	AA13512	Human thrombospond
22	50	34.5	1170	22	AA13512	Human variant thro
23	49	33.8	137	20	AA13512	Rat sperm coating
24	49	33.8	155	22	AA13512	Human prostate can
25	49	33.8	225	22	AA13512	Human prostate can
26	49	33.8	242	15	AA13512	FIV ITALYM4 envelo
27	49	33.8	646	22	AA13512	Human prostate can
28	49	33.8	1148	20	AA13512	Renal cancer assoc
29	48.5	33.4	350	21	AA13512	Streptomyces nogal
30	48	33.1	241	15	AA13512	FIV UK14 envelope
31	48	33.1	3054	14	AA13512	Translation of TEV
32	47	32.4	492	21	AA13512	Human TMPSR22 prot
33	47	32.4	492	21	AA13512	HrPca6/7 polypepti
34	47	32.4	492	21	AA13512	Ovrl15 homolog pro
35	47	32.4	492	21	AA13512	Human tumour suppr
36	47	32.4	492	21	AA13512	Human 20p1F12-GTC2
37	46.5	32.1	695	22	AA13512	Mouse Dishevelled-
38	46.5	32.1	708	21	AA13512	Mouse PAMP protein
39	46	31.7	18	16	AA13512	Subpeptide 4N of t
40	46	31.7	30	16	AA13512	Thrombospondin 1 (
41	46	31.7	30	17	AA13512	Cell binding domai
42	46	31.7	111	21	AA13512	Human ORFX ORF1286
43	46	31.7	219	19	AA13512	Human LEA-motif de
44	46	31.7	240	15	AA13512	FIV DUTCH6 envelop
45	46	31.7	373	14	AA13512	Grass pollen aller

#### ALIGNMENTS

#### RESULT 1

AAW55779  
ID AAW55779 standard; Protein; 168 AA.

XX  
AC AAW55779;

XX  
DT 17-JUL-1998 (first entry)

XX  
DE Human Bcl-xL/Bcl-2 associated death promoting polypeptide.

XX  
DE Human; Bcl-xL/Bcl-2 associated death promoting polypeptide; Bad;

XX  
KW programmed cell death; apoptosis.

XX  
OS Homo sapiens.

XX  
PN WO9812328-A2.

XX  
PD 26-MAR-1998.

XX  
PF 18-SEP-1997; 97WO-US16991.

XX  
PR 20-SEP-1996; 96US-0717123.

XX  
PA (IDUN-) IDUN PHARM INC.

XX  
PI Horne WA, Oltersdorf T;

XX  
DR WPI; 1998-217267/19.

XX  
DR N-PSDB; AAV25877.

XX  
PT Bad gene mediating apoptosis - used to develop products for treating e.g. neurodegenerative disease, cancers or autoimmune disease

XX  
PS Claim 8; Fig 1; 4lpp; English.

XX The present sequence is the human Bcl-xL/Bcl-2 associated  
CC death promoting polypeptide, Bad, the binding of which to Bcl-XL  
CC results in the induction of programmed cell death, i.e. apoptosis.  
CC Bad can be used in screening assays for compounds to treat or  
CC prevent diseases characterised by apoptotic cell death, such as  
CC neurodegenerative disorders, e.g. Alzheimer's and Parkinson's  
CC disease, amyotrophic lateral sclerosis, retinitis pigmentosa and  
CC cerebellar degeneration, and myelodysplastic syndromes, e.g.  
CC aplastic anaemia and ischaemic injury including myocardial  
CC infarction, stroke and reperfusion injury. Assays can also be  
CC used to obtain apoptosis enhancing compounds to treat or prevent  
CC diseases characterised by the loss of apoptotic cell death, such as  
CC cancers, e.g. lymphoma and hormone dependent tumours, autoimmune  
CC diseases, e.g. systemic lupus erythematosus and immune-mediated  
CC glomerulonephritis and viral infections, e.g. herpesvirus,  
CC poxvirus or adenovirus infection. Bad can also be used for  
CC detection and diagnosis.  
XX  
XX  
SQ Sequence 168 AA;

Query Match 100.0%; Score 145; DB 19; Length 168;  
Best Local Similarity 100.0%; Pred. No. 1.1e-13;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QSSWTRVFQSWMDNRLGRGSSAPSO 26  
Db 143 qsswtrvfqswmdnrlgrgssapseq 168  
|||||

RESULT 2  
AAB13512 ID AAB13512 standard; protein; 168 AA.  
XX AAB13512;  
XX  
XX 02-NOV-2000 (first entry)  
XX Human cell proliferation protein APOP-1.  
XX  
XX Human; cell proliferation; APOP-1; cancer; inflammation; infection;  
KW trauma; neurodegenerative disease; ischaemic injury; wasting disease.  
XX  
XX Homo sapiens.  
XX  
XX US6080847-A.  
XX  
XX 27-JUN-2000.  
XX  
XX 04-DEC-1997; 97US-0985335.  
XX  
XX 04-DEC-1997; 97US-0985335.  
XX  
XX (INCY-) INCYTE PHARM INC.  
XX  
XX Corley NC, Hillman JL, Yue H, Lal P, Shah P;  
XX  
XX WPI; 2000-451230/39.  
XX  
XX N-PSDB; AAA63332.  
XX  
XX  
XX Novel polynucleotide and polypeptide sequences of proteins associated  
PT with cell proliferation for diagnosis, prevention and treatment of e.g.  
PT cancer, acquired immunodeficiency syndrome, and Parkinson's disease -  
XX  
XX Example 8; Fig 1; 58pp; English.

XX The present sequence is the human APOP-1 protein. This protein, which  
CC shares structural and chemical homology with Bcl-2, is involved in cell  
CC proliferation. Its coding sequence was isolated by screening a synovial  
CC tissue cDNA library using a computer search for amino acid sequence  
CC alignments. The gene and protein can be used in the treatment of various  
CC cancers, disorders with associated inflammation such as Addison's  
XX

disease, adult respiratory distress syndrome, allergies, anaemia, asthma,  
atherosclerosis, Crohn's disease, ulcerative colitis, diabetes mellitus,  
emphysema, glomerulonephritis, gout, Graves' disease, irritable bowel  
syndrome, lupus erythematosus, multiple sclerosis, myasthenia gravis,  
myocardial or pericardial inflammation, osteoporosis, rheumatoid  
arthritis, Sjogren's syndrome and autoimmune thyroiditis, complications  
of cancer, haemodialysis and extracorporeal circulation, infections,  
trauma, disorders with associated apoptosis including AIDS and other  
infectious and genetic immunodeficiencies, neurodegenerative diseases  
such as Alzheimer's disease and Parkinson's disease, ischaemic injuries  
such as myocardial infarction, and wasting diseases including cachexia.

Sequence 168 AA;

Query Match 100.0%; Score 145; DB 21; Length 169;  
Best Local Similarity 100.0%; Pred. No. 1.1e-13;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 OSSWTRVFQSWDNLGRGSSAPSQ 26  
| | | | | | | | | | | | | | | | | | | |  
Db 143 qssswtrvfqswdrnlgrgssapsq 168

RESULT 3  
AAB70368  
ID AAB70368 standard; protein; 168 AA.  
AC AAB70368;  
XX  
DT 02-MAY-2001 (first entry)  
XX  
DE Human BAD mutant amino acid sequence SEQ ID NO:1.  
XX  
KW Bcl-XL/Bcl-2 associated cell death regulator; BAD; mutant; apoptosis;  
immunostimulant; neuroprotective; nontoxic; antiischaemic; vulnery;  
cystatic; antiviral; antiarthritic; antiinflammatory; wound healing;  
immunosuppressive; apoptosis inducer; apoptosis inhibitor; cancer;  
immunodeficiency disease; neurodegenerative disease; viral infection;  
ischaemic cell death; reperfusion cell death; arthritis; infertility;  
lymphoproliferative condition; inflammation; autoimmune disease.  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO200110888-A1.  
XX  
PD 15-FEB-2001.  
XX  
PF 30-MAY-2000; 2000WO-US11864.  
XX  
PR 28-MAY-1999; 99US-0136783.  
XX  
PA (APOP-) APOPTOSIS TECHNOLOGY INC.  
XX  
PI Zhou X;  
XX  
DR WPI; 2001-138734/14.  
XX  
PT New mutant Bcl-XL/Bcl-2 Associated Cell Death Regulator polypeptide,  
useful for screening for candidate compounds which induce or inhibit  
apoptosis, comprises amino acid substitutions at Ser118, Ser155 or  
Ser113 -  
XX  
XX Claim 1; Page 147; 157pp; English.  
XX  
CC The present invention describes an isolated or synthetic polypeptide  
(I) comprising a less than full length amino acid sequence of a mutant  
Bcl-XL/Bcl-2 associated cell death regulator polypeptide (BAD) or its  
fragment, which contains amino acid substitutions at Ser118 of a human  
BAD, Ser155 of a murine BAD (longer murine BAD) or Ser113 of a murine  
BAD (shorter murine BAD). (I) has immunostimulant, neuroprotective,  
nontoxic, antiischaemic, vulnery, cytostatic, antiviral  
properties.

antiarthritic, antiinflammatory and immunosuppressive activities, and can be used as an apoptosis inducer or inhibitor. BAD polypeptides and polynucleotides can be used for screening candidate compounds and drugs for activity that promote cell survival or apoptosis. Other uses include inducing or inhibiting apoptosis in a cell. Candidate compounds identified and (mutant) BAD polypeptides are useful in treating immunodeficiency diseases, neurodegenerative diseases, ischaemic cell death, reperfusion cell death, wound healing, cancer, viral infections, lymphoproliferative conditions, arthritis, infertility, inflammation and autoimmune diseases. The present sequence represents a specifically claimed human BAD mutant amino acid sequence from the present invention.

Sequence 168 AA:

```
Query Match      100.0%; Score 145; DB 22; Length 168;
Best Local Similarity 100.0%; Pred. NO. 1.1e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Qy	1	QSSWTRVFQSWDRNLGRGSSAPSQ	26
Db	143	qssswtrvfqswdrnlgrqssapsq	168

RESULT 4  
AAB48287  
ID AAB48287 standard; protein; 168 AA.

AC AAB48287;

XX	
DT	02-APR-2001 (first entry)
XX	
DE	Human Bad protein.

AA  
KW S-phase kinase associated protein; SKP1; SKP2; SKP2-like protein; ZF;  
KW CUL-1; cullin; CDC53; p27; cyclin E; Max; Mad; c-Myc; MDM2; p53; Bax;  
KW Bad; Bcl-2; tumour; cytostatic.

OS Homo sapiens.

XX PN WO2000075184-A1

XX  
14-DEC-2000XX  
RE 05 - TUN - 2000. 2000070 - 0515440

XX XX

XX

XX

[illegible]

DR N-PSDB; AAC84599.

Modulating polypeptides

PT involves altering levels of proteins such as S-phase kinase associated proteins 1, 2 and cullin/CDC53 proteins -

XX  
DS  
Claim 5. Page 102-103. 16300. English

xx The invention relates to methods of altering the polypeptide levels in a cell, using proteins selected from S-phase kinase associated proteins 1 and 2 (SKP1, SKP2), SKP2-like proteins (ZF) and CUL-1 (a member of the cullin/CD523 family of proteins). The method is useful for altering the level of p27, cyclin E, Max, Mad, c-Myc, MDM2, p53, Bax, Bad or Bcl-2 polypeptide in a cell. SKP2 and SKP2-like protein levels are useful for detecting tumours, and in monitoring tumor treatment in a mammal. Agents that modulate interactions between SKP and target proteins are useful for treating tumours.

AA	Sequence	168 AA:
SO		

```
Query Match      100.0%; Score 145; DB 22; Length 168;
Best Local Similarity 100.0%; Pred. No. 1.1e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 QSSWTRVFQSWDRNLGRGSSAPSQ 26
    |||||
Db 143 qssswtrvfgswdrnlgrgssapsq 168
```

RESULT 5  
AAW32476  
ID AAW32476 standard; Protein; 166 AA.

AC AAW32476;

15-JAN-1998 (first entry)

DE: BBC6 protein for regulating cell death.

XX  
KW  
BRC6 gene: cell death; cell cycle; Bcl2; human

XX Homo sapiens

XX 11056633501 4-316633501

7  
C  
C  
7  
C  
C  
C  
C

XX

XX

XX

[illegible]

XX

XX

DR N-PSDB; AAT91561.

Isolated BBC6 gene - encodes a protein that regulates cell death through interaction with Bcl-2

PS Claim 1: Column 11-12: 7pp: English

The present sequence represents a protein of 166 amino acids. The sequence is disclosed as being a protein called BBC6 which regulates cell death through interaction with Bcl-2. The DNA may be used for the production of the recombinant protein, which can be used in unspecified therapeutic or diagnostic procedures, as a molecular weight marker, and to raise antibodies that can be used in unspecified diagnostic or therapeutic applications and to reduce or eliminate the biological activity of the BBC6 protein in vivo.

AX	Sequence	166 AA:
SQ		

Query Match 95.9%; Score 139; DB 18; Length 166;  
Best Local Similarity 92.3%; Pred. No. 7.8e-13;  
Matches 24: Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```
Qy 1 QSSWTRVFQSWDRNLGRGSSAPSQ 26
    |||
Db 141 qssswtrvfqswdrnlgrqtaapsq 166
```

RESULT 6  
AAB70370  
ID AAB70370 standard: protein: 162 AA.

XX  
AC AAB70370:

XX DT 02-MAY-2001 (first entry)

XX

DE Shorter murine BAD mutant amino acid sequence SEQ ID NO:3.

XX Bcl-XL/Bcl-2 associated cell death regulator; BAD; mutant; apoptosis;  
 KW immunostimulant; neuroprotective; nootropic; antiischaemic; vulnerary;  
 KW cytoskeletal; antiviral; antiarthritic; antiinflammatory; wound healing;  
 KW immunosuppressive; apoptosis inducer; apoptosis inhibitor; cancer;  
 KW immunodeficiency disease; neurodegenerative disease; viral infection;  
 KW ischaemic cell death; reperfusion cell death; arthritis; infertility;  
 KW lymphoproliferative condition; inflammation; autoimmune disease.

OS Mus musculus.  
 OS Synthetic.

XX WO200110888-A1.

XX PD 15-FEB-2001.

XX PF 30-MAY-2000; 2000WO-US11864.

XX PR 28-MAY-1999; 99US-0136783.

XX PA (APOB-) APOPTOSIS TECHNOLOGY INC.

XX PI Zhou X;

XX WI: 2001-138734/14.

XX New mutant Bcl-XL/Bcl-2 Associated Cell Death Regulator polypeptide,  
 PT useful for screening for candidate compounds which induce or inhibit  
 PT apoptosis, comprises amino acid substitutions at Ser118, Ser155 or  
 PT Ser113 -

XX Claim 7; Page 148-149; 157pp; English.

PS The present invention describes an isolated or synthetic polypeptide  
 CC (I) comprising a less than full length amino acid sequence of a mutant  
 CC Bcl-XL/Bcl-2 associated cell death regulator polypeptide (BAD) or its  
 CC fragment, which contains amino acid substitutions at Ser118 of a human  
 CC BAD, Ser155 of a murine BAD (longer murine BAD) or Ser113 of a murine  
 CC BAD (shorter murine BAD). (I) has immunostimulant, neuroprotective,  
 CC nootropic, antiischaemic, vulnerary, cytoskeletal, antiviral,  
 CC antiarthritic, antiinflammatory and immunosuppressive activities, and  
 CC can be used as an apoptosis inducer or inhibitor. BAD polypeptides and  
 CC polynucleotides can be used for screening candidate compounds and drugs  
 CC for activity that promote cell survival or apoptosis. Other uses include  
 CC inducing or inhibiting apoptosis in a cell. Candidate compounds  
 CC identified and (mutant) BAD polypeptides are useful in treating  
 CC immunodeficiency diseases, neurodegenerative diseases, ischaemic cell  
 CC death, reperfusion cell death, wound healing, cancer, viral infections,  
 CC lymphoproliferative conditions, arthritis, infertility, inflammation and  
 CC autoimmune diseases. The present sequence represents a specifically  
 CC claimed shorter murine BAD mutant amino acid sequence from the present  
 CC invention.

XX Sequence 162 AA;

Query Match 82.8%; Score 120; DB 22; Length 162;  
 Best Local Similarity 73.1%; Pred. No. 4.5e-10;  
 Matches 19; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 QSSSWTRVFQSWDRNLGRGSSAPSQ 26

Db 137 qsagwtrliqswdrnlkggstpsq 162

RESULT 7

AAR95168

ID AAR95168 standard; Protein; 204 AA.

XX AAR95168;

AC AAR95168;

XX 06-JAN-1997 (first entry)

XX bcl-x(L)/bcl-2 associated death promoter protein.

DE Epitope; murine; bcl-x(L)/bcl-2 associated death promoter; Bad; stroke;  
 KW polypeptide; bcl-x; cell death; regulate; BH1; BH2; apoptotic cell death;  
 KW cytokine deprivation; IL-3 dependent cell line; immunodeficiency; AIDS;  
 KW neurodegenerative disease; senescence; ischaemia; neoplasia.

XX Mus musculus.

XX Key Location/Qualifiers  
 FT Region 147..149

FT /note= "BH1 conserved amino acids"

FT Region 191..192

FT /note= "BH2 conserved amino acids"

FT Domain 38..61

FT /note= "PEST sequence"

FT Domain 111..130

FT /note= "PEST sequence"

XX WO9613614-A1.

XX PD 09-MAY-1996.

XX PF 31-OCT-1995; 95WO-US14246.

XX PR 31-OCT-1994; 94US-0333565.

XX PA (UNIW ) UNIV WASHINGTON.

XX PI Korsmeyer SJ;

XX WI: 1996-251465/25.

XX N-PSDB; AAT29479.

XX Polynucleotide encoding bcl-x(L)/bcl-2 associated death promoter -  
 PT useful to treat neoplasia and apoptosis and to identify agents  
 PT inhibiting its binding to bcl-2 or bcl-x(L) to form heteromultimers  
 XX Claim 3; Fig 1; 130pp; English.

XX This sequence represents the murine bcl-x(L)/bcl-2 associated death  
 CC promoter (Bad) gene. Bad is a 22.1 kb protein which interacts with  
 CC bcl-2 and bcl-x proteins and regulates cell death. It has homology  
 CC to the bcl-2-related family clustered in the BH1 and BH2 domain. Bad  
 CC has been found to hybridize to bcl-x(L) and bcl-2 in yeast two-hybrid  
 CC assays and in vivo in mammalian cells. Overexpressed Bad counters the  
 CC death inhibitory activity of bcl-x(L), but is much less effective at  
 CC countering the death inhibitory activity of bcl-2. Bad expression can  
 CC accelerate apoptotic cell death induced by cytokine deprivation in an  
 CC IL-3 dependent cell line expressing bcl-x(L), and its also counters the  
 CC death repressor activity of bcl-x(L). Bad competes with Bax for binding  
 CC to bcl-x(L). Bad may be used to identify agents which inhibit its  
 CC binding to bcl-2 or bcl-x(L) to form heterodimers. Such agents may be  
 CC used to treat neurodegenerative diseases, immunodeficiency diseases,  
 CC e.g. AIDS, senescence or ischaemia.

XX Sequence 204 AA;

Query Match 82.8%; Score 120; DB 17; Length 204;  
 Best Local Similarity 73.1%; Pred. No. 5.8e-10;  
 Matches 19; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 QSSSWTRVFQSWDRNLGRGSSAPSQ 26

Db 179 qsagwtrliqswdrnlkggstpsq 204

RESULT 8

AAW61315

ID AAW61315 standard; Protein; 204 AA.

XX

AC AAW61315;  
XX  
DT 07-OCT-1998 (first entry)  
XX  
DE Murine BCL-XL/BCL-2 associated cell death regulator.  
XX  
XX Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein;  
KW serine substituted mutant; apoptosis; cancer; viral infection.  
XX  
OS Mus sp.  
XX  
XX WO9817682-A1.  
PN  
PD 30-APR-1998.  
XX  
XX 17-OCT-1997; 97WO-US19175.  
PF  
XX 18-OCT-1996; 96US-0733505.  
PR  
XX (UNIW ) UNIV WASHINGTON.  
PA  
XX Korsmeyer SJ;  
PI  
XX WPI; 1998-261422/23.  
DR N-PSDB; AAV27833.  
XX  
PT New mutant BAD polypeptide with phosphorylatable serine replaced -  
PT useful for, e.g. treating reduced apoptosis such as in cancer or  
PT viral infection  
XX  
PS Claim 1; Fig 10; 95pp; English.  
XX  
CC The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell  
CC death regulator) proteins, having an amino acid other than Ser at  
CC position 112 and/or 136, relative to the murine BAD 204 aa sequence. The  
CC present sequence is the murine BAD protein. Also described are: (1)  
CC fragments of mutant BAD protein able to decrease cell viability; (2)  
CC fusion proteins of mutant BAD with a heterologous polypeptide that  
CC increases intracellular delivery. Mutant BAD proteins are used to treat  
CC or prevent diseases associated with reduced apoptosis, e.g. cancer,  
CC viral infection, lymphoproliferation, arthritis, infertility,  
CC inflammation and autoimmune disease. Polynucleotide sequences encoding  
CC mutant BAD proteins can be used similarly by gene therapy or to produce  
CC transgenic animals for use as disease models or in drug screening. BAD  
CC proteins phosphorylated at specified Ser are used to screen for enhancers  
CC and inhibitors of serine-phosphatase. Inhibitors are potentially useful  
CC in treatment of excessive apoptosis such as AIDS, neurodegeneration,  
CC aging or ischemic cell death. The apoptotic status of cells is  
CC determined by measuring relative amounts of phosphorylated and non-  
CC phosphorylated BAD, by usual immunoassays. Mutant BAD proteins have  
CC greater death-promoting activity than wild-type BAD which can become  
CC phosphorylated on the specified Ser, forming a product that does not  
CC heterodimerise with BCL-2 or BCL-XL but instead binds to 14-3-3 family  
CC proteins in the cytosol, thus promoting cell survival. The mutants with  
CC Ser substituted cannot bind 14-3-3.  
XX  
SQ Sequence 204 AA;

Query Match 82.8%; Score 120; DB 19; Length 204;  
Best Local Similarity 73.1%; Pred. No. 5.8e-10;  
Matches 19; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 QSSWTRVFQSWDRNLGRGSSAPSQ 26  
||: |||: |||||: |||  
Db 179 qsgwttriiqswdrnlkggstpsq 204

RESULT 9  
AAW61316  
ID AAW61316 standard; Protein: 204 AA.  
XX  
AC AAW61316;

XX  
DT 07-OCT-1998 (first entry)  
XX  
DE Mutant BCL-XL/BCL-2 associated cell death regulator #1.  
XX  
KW Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein;  
KW serine substituted mutant; apoptosis; cancer; viral infection.  
XX  
OS Mus sp.  
XX  
XX WO9817682-A1.  
PN  
PD 30-APR-1998.  
XX  
XX 17-OCT-1997; 97WO-US19175.  
PF  
XX 18-OCT-1996; 96US-0733505.  
PR  
XX (UNIW ) UNIV WASHINGTON.  
PA  
XX Korsmeyer SJ;  
PI  
XX WPI; 1998-261422/23.  
DR N-PSDB; AAV27834.  
XX  
PT New mutant BAD polypeptide with phosphorylatable serine replaced -  
PT useful for, e.g. treating reduced apoptosis such as in cancer or  
PT viral infection  
XX  
PS Claim 7; Page 59; 95pp; English.  
XX  
CC The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell  
CC death regulator) proteins, having an amino acid other than Ser at  
CC position 112 and/or 136, relative to the murine BAD 204 aa sequence. The  
CC present sequence represents a mutant BAD protein. Also described are: (1)  
CC fragments of mutant BAD protein able to decrease cell viability; (2)  
CC fusion proteins of mutant BAD with a heterologous polypeptide that  
CC increases intracellular delivery. Mutant BAD proteins are used to treat  
CC or prevent diseases associated with reduced apoptosis, e.g. cancer,  
CC viral infection, lymphoproliferation, arthritis, infertility,  
CC inflammation and autoimmune disease. Polynucleotide sequences encoding  
CC mutant BAD proteins can be used similarly by gene therapy or to produce  
CC transgenic animals for use as disease models or in drug screening. BAD  
CC proteins phosphorylated at specified Ser are used to screen for enhancers  
CC and inhibitors of serine-phosphatase. Inhibitors are potentially useful  
CC in treatment of excessive apoptosis such as AIDS, neurodegeneration,  
CC aging or ischemic cell death. The apoptotic status of cells is  
CC determined by measuring relative amounts of phosphorylated and non-  
CC phosphorylated BAD, by usual immunoassays. Mutant BAD proteins have  
CC greater death-promoting activity than wild-type BAD which can become  
CC phosphorylated on the specified Ser, forming a product that does not  
CC heterodimerise with BCL-2 or BCL-XL but instead binds to 14-3-3 family  
CC proteins in the cytosol, thus promoting cell survival. The mutants with  
CC Ser substituted cannot bind 14-3-3.  
XX  
SQ Sequence 204 AA;

Query Match 82.8%; Score 120; DB 19; Length 204;  
Best Local Similarity 73.1%; Pred. No. 5.8e-10;  
Matches 19; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 QSSWTRVFQSWDRNLGRGSSAPSQ 26  
||: |||: |||||: |||  
Db 179 qsgwttriiqswdrnlkggstpsq 204

RESULT 10  
AAW61317  
ID AAW61317 standard; Protein: 204 AA.  
XX  
AC AAW61317;

```

XX 07-OCT-1998 (first entry)
DT
XX
DE Mutant BCL-XL/BCL-2 associated cell death regulator #2.
XX
KW Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein;
KW serine substituted mutant; apoptosis; cancer; viral infection.
XX
OS Mus sp.
OS Synthetic.
XX W09817682-A1.
XX
XX 30-APR-1998.
XX
XX 17-OCT-1997; 97WO-US19175.
XX
XX 18-OCT-1996; 96US-0733505.
XX
XX (UNIW ) UNIV WASHINGTON.
XX
XX Korsmeyer SJ;
XX
XX WPI; 1998-261422/23.
DR N-PSDB; AAV27835.
XX
XX New mutant BAD polypeptide with phosphorylatable serine replaced -
PT useful for, e.g. treating reduced apoptosis such as in cancer or
PT viral infection
XX
XX Claim 7; Page 60; 95pp; English.
XX
XX The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell
CC death regulator) proteins, having an amino acid other than Ser at
CC position 112 and/or 136, relative to the murine BAD 204 aa sequence. The
CC present sequence represents a mutant BAD protein. Also described are: (1)
CC fragments of mutant BAD protein able to decrease cell viability; (2)
CC fusion proteins of mutant BAD with a heterologous polypeptide that
CC increases intracellular delivery. Mutant BAD proteins are used to treat
CC or prevent diseases associated with reduced apoptosis, e.g. cancer,
CC viral infection, lymphoproliferation, arthritis, infertility,
CC inflammation and autoimmune disease. Polynucleotide sequences encoding
CC mutant BAD proteins can be used similarly by gene therapy or to produce
CC transgenic animals for use as disease models or in drug screening. BAD
CC proteins phosphorylated at specified Ser are used to screen for enhancers
CC and inhibitors of serine-phosphatase. Inhibitors are potentially useful
CC in treatment of excessive apoptosis such as AIDS, neurodegeneration,
CC aging or ischaemic cell death. The apoptotic status of cells is
CC determined by measuring relative amounts of phosphorylated and non-
CC phosphorylated BAD, by usual immunoassays. Mutant BAD proteins have
CC greater death-promoting activity than wild-type BAD which can become
CC phosphorylated on the specified Ser, forming a product that does not
CC heterodimerise with BCL-2 or BCL-XL but instead binds to 14-3-3 family
CC proteins in the cytosol, thus promoting cell survival. The mutants with
CC Ser substituted cannot bind 14-3-3.
XX
XX Sequence 204 AA;
SQ

```

Query Match 82.8%; Score 120; DB 19; Length 204;  
 Best Local Similarity 73.1%; Pred. NO. 5.8e-10;  
 Matches 19; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

```

QY 1 QSSWTRVFQSWDRNLGRGSSAPSQ 26
   ||: |||: ||||| ||| |||
Db 179 qsagwtrilqswdrnlkggstpsq 204

```

```

RESULT 11
AAW61318
ID PAAW61318 standard; Protein; 204 AA.
XX
XX AAW61318;
AC

```

```

XX 07-OCT-1998 (first entry)
DT
XX
DE Mutant BCL-XL/BCL-2 associated cell death regulator #3.
XX
KW Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein;
KW serine substituted mutant; apoptosis; cancer; viral infection.
XX
OS Mus sp.
OS Synthetic.
XX W09817682-A1.
XX
XX 30-APR-1998.
XX
XX 17-OCT-1997; 97WO-US19175.
XX
XX 18-OCT-1996; 96US-0733505.
XX
XX (UNIW ) UNIV WASHINGTON.
XX
XX Korsmeyer SJ;
XX
XX WPI; 1998-261422/23.
DR N-PSDB; AAV27836.
XX
XX New mutant BAD polypeptide with phosphorylatable serine replaced -
PT useful for, e.g. treating reduced apoptosis such as in cancer or
PT viral infection
XX
XX Claim 7; Page 60-61; 95pp; English.
XX
XX The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell
CC death regulator) proteins, having an amino acid other than Ser at
CC position 112 and/or 136, relative to the murine BAD 204 aa sequence. The
CC present sequence represents a mutant BAD protein. Also described are: (1)
CC fragments of mutant BAD protein able to decrease cell viability; (2)
CC fusion proteins of mutant BAD with a heterologous polypeptide that
CC increases intracellular delivery. Mutant BAD proteins are used to treat
CC or prevent diseases associated with reduced apoptosis, e.g. cancer,
CC viral infection, lymphoproliferation, arthritis, infertility,
CC inflammation and autoimmune disease. Polynucleotide sequences encoding
CC mutant BAD proteins can be used similarly by gene therapy or to produce
CC transgenic animals for use as disease models or in drug screening. BAD
CC proteins phosphorylated at specified Ser are used to screen for enhancers
CC and inhibitors of serine-phosphatase. Inhibitors are potentially useful
CC in treatment of excessive apoptosis such as AIDS, neurodegeneration,
CC aging or ischaemic cell death. The apoptotic status of cells is
CC determined by measuring relative amounts of phosphorylated and non-
CC phosphorylated BAD, by usual immunoassays. Mutant BAD proteins have
CC greater death-promoting activity than wild-type BAD which can become
CC phosphorylated on the specified Ser, forming a product that does not
CC heterodimerise with BCL-2 or BCL-XL but instead binds to 14-3-3 family
CC proteins in the cytosol, thus promoting cell survival. The mutants with
CC Ser substituted cannot bind 14-3-3.
XX
XX Sequence 204 AA;
SQ

```

Query Match 82.8%; Score 120; DB 19; Length 204;  
 Best Local Similarity 73.1%; Pred. NO. 5.8e-10;  
 Matches 19; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

```

QY 1 QSSWTRVFQSWDRNLGRGSSAPSQ 26
   ||: |||: ||||| ||| |||
Db 179 qsagwtrilqswdrnlkggstpsq 204

```

```

RESULT 12
AAW58832
ID AAW58832 standard; protein; 204 AA.
XX
XX AAW58832;
AC

```

XX 23-JUL-1998 (first entry)  
 XX Murine BAD protein.  
 DE  
 XX BAD protein; Bcl-XL/Bcl-2 associated cell death regulator; 14-3-3;  
 KW serine phosphorylation; post-translational modification; apoptosis;  
 KW signal transduction regulator; phosphoserine phosphatase; senescence;  
 KW immunodeficiency disease; neurodegenerative disease; infertility;  
 KW cancer, viral infection; lymphoproliferative condition; arthritis;  
 KW inflammation; autoimmune diseases.  
 XX  
 OS Mus sp.  
 XX  
 PN WO9809643-A1.  
 XX  
 PD 12-MAR-1998.  
 XX  
 XX 09-SEP-1997; 97WO-US15871.  
 PF  
 XX 09-SEP-1996; 96US-0707868.  
 PR  
 XX (UNITW ) UNIV WASHINGTON.  
 PA  
 XX Korsmeyer SJ;  
 PI  
 XX WPI; 1998-207049/18.  
 DR  
 XX Serine-phosphorylated Bcl-X-L/Bcl-2 Associated cell Death regulator  
 PT polypeptide - useful for modulation of apoptosis associated with,  
 PT e.g. cancer and immunodeficiency diseases  
 XX  
 PS Claim 3; Fig 8; 61pp; English.  
 XX  
 CC This sequence represents a novel serine-phosphorylated protein, BAD  
 CC (Bcl-XL/Bcl-2 associated cell death regulator). The serine residue is  
 CC phosphorylated in a post-translational modification and allows binding  
 CC to the 14-3-3 protein which is a signal transduction regulator.  
 CC Modulators of phosphorylated BAD, which act through inhibition/activation  
 CC of a phosphoserine phosphatase, are useful for preventing/treating  
 CC increased/decreased apoptosis in a cell. The increased apoptosis may  
 CC result from immunodeficiency diseases, senescence, neurodegenerative  
 CC disease, ischaemic cell death, reperfusion cell death, infertility and  
 CC wound-healing. Decreased apoptosis may result from cancer, viral  
 CC infection, lymphoproliferative conditions, arthritis, infertility,  
 CC inflammation and autoimmune diseases. Measuring the amount of  
 CC phosphorylated compared to unphosphorylated BAD polypeptide and/or total  
 CC BAD in a cell is useful for determining the apoptotic state of a cell.  
 XX  
 SQ Sequence 204 AA;

Query Match 82.8%; Score 120; DB 19; Length 204;  
 Best Local Similarity 73.1%; Pred. No. 5.8e-10;  
 Matches 19; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 QSSWTRVFQSWWDRNLGRGSSAPSQ 26  
 ||: |||: ||||| |||: | |||  
 Db 179 qsgawtrliqswdrnlqg9gstpsq 204

RESULT 13  
 AAB70369  
 ID AAB70369 standard; protein; 204 AA.  
 XX  
 AC AAB70369;  
 XX  
 DT 02-MAY-2001 (first entry)  
 XX  
 DE Longer murine BAD mutant amino acid sequence SEQ ID NO:2.  
 XX  
 KW Bcl-XL/Bcl-2 associated cell death regulator; BAD; mutant; apoptosis;  
 KW immunostimulant; neuroprotective; neutrotropic; antiischaemic; vulnerary;

KW cytostatic; antiviral; antiarthritic; antiinflammatory; wound healing;  
 KW immunosuppressive; apoptosis inducer; apoptosis inhibitor; cancer;  
 KW immunodeficiency disease; neurodegenerative disease; viral infection;  
 KW ischaemic cell death; reperfusion cell death; arthritis; infertility;  
 KW lymphoproliferative condition; inflammation; autoimmune disease.  
 XX  
 OS Mus musculus.  
 OS Synthetic.  
 PN WO200110888-A1.  
 XX  
 PD 15-FEB-2001.  
 XX  
 XX 30-MAY-2000; 2000WO-US11864.  
 PF  
 XX 28-MAY-1999; 99US-0136783.  
 PR  
 XX (APOP-) APOPTOSIS TECHNOLOGY INC.  
 PA  
 XX Zhou X;  
 PI  
 XX WPI; 2001-138734/14.  
 DR  
 XX New mutant Bcl-XL/Bcl-2 Associated Cell Death Regulator polypeptide,  
 PT useful for screening for candidate compounds which induce or inhibit  
 PT apoptosis, comprises amino acid substitutions at Ser118, Ser155 or  
 PT Ser113 -  
 PT  
 XX Claim 4; Page 148; 157pp; English.  
 PS  
 XX The present invention describes an isolated or synthetic polypeptide  
 CC comprising a less than full length amino acid sequence of a mutant  
 CC Bcl-XL/Bcl-2 associated cell death regulator polypeptide (BAD) or its  
 CC fragment, which contains amino acid substitutions at Ser118 of a human  
 CC BAD, Ser155 of a murine BAD (longer murine BAD) or Ser113 of a murine  
 CC BAD (shorter murine BAD). (I) has immunostimulant, neuroprotective,  
 CC antiarthritic, antiischaemic, vulnerary, cytostatic, antiviral,  
 CC neutrotropic, antiinflammatory and immunosuppressive activities, and  
 CC can be used as an apoptosis inducer or inhibitor. BAD polypeptides and  
 CC polynucleotides can be used for screening candidate compounds and drugs  
 CC for activity that promote cell survival or apoptosis. Other uses include  
 CC inducing or inhibiting apoptosis in a cell. Candidate compounds  
 CC identified and (mutant) BAD polypeptides are useful in treating  
 CC immunodeficiency diseases, neurodegenerative diseases, ischaemic cell  
 CC death, reperfusion cell death, wound healing, cancer, viral infections,  
 CC lymphoproliferative conditions, arthritis, infertility, inflammation and  
 CC autoimmune diseases. The present sequence represents a specifically  
 CC claimed longer murine BAD mutant amino acid sequence from the present  
 CC invention.  
 XX  
 SQ Sequence 204 AA;

Query Match 82.8%; Score 120; DB 22; Length 204;  
 Best Local Similarity 73.1%; Pred. No. 5.8e-10;  
 Matches 19; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 QSSWTRVFQSWWDRNLGRGSSAPSQ 26  
 ||: |||: ||||| |||: | |||  
 Db 179 qsgawtrliqswdrnlqg9gstpsq 204

RESULT 14  
 AAR95167  
 ID AAR95167 standard; peptide; 16 AA.  
 XX  
 AC AAR95167;  
 XX  
 DT 03-JAN-1997 (first entry)  
 XX  
 DE bcl-x(L)/bcl-2 associated death promoter epitope, residues 182-197.  
 XX  
 KW Epitope; murine; bcl-x(L)/bcl-2 associated death promoter; Bad; stroke;

KW polypeptide; bcl-x; cell death; regulate; BH1; BH2; apoptotic cell death;  
 KW cytokine deprivation; IL-3 dependent cell line; immunodeficiency; AIDS;  
 KW neurodegenerative disease; senescence; ischaemia; neoplasia.

OS Mus musculus.

XX WO9613614-A1.

XX 09-MAY-1996.

XX 31-OCT-1995; 95WO-US14246.

XX 31-OCT-1994; 94US-0333565.

XX (UNIW ) UNIV WASHINGTON.

XX Korsmeyer SJ;

XX WPI; 1996-251465/25.

XX Polynucleotide encoding bcl-x(L)/bcl-2 associated death promoter -  
 PT useful to treat neoplasia and apoptosis and to identify agents  
 PT inhibiting its binding to bcl-2 or bcl-x(L) to form heteromultimers

PS Claim 2; Page 103; 130pp; English.

XX The sequences given in AAR95155-67 represent epitopes derived from the  
 CC murine bcl-x(L)/bcl-2 associated death promoter (Bad) polypeptide (see  
 CC also AAR95168). Bad is a 22.1 kD protein which interacts with bcl-2 and  
 CC bcl-x proteins and regulates cell death. It has homology to the bcl-2-  
 CC related family clustered in the BH1 and BH2 domain. Bad has been found  
 CC to hybridise to bcl-x(L) and bcl-2 in yeast two-hybrid assays and in  
 CC vivo in mammalian cells. Overexpressed Bad counters the death  
 CC inhibitory activity of bcl-x(L), but is much less effective at countering  
 CC the death inhibitory activity of bcl-2. Bad expression can accelerate  
 CC apoptotic cell death induced by cytokine deprivation in an IL-3 dependent  
 CC cell line expressing bcl-x(L), and its also counters the death repressor  
 CC activity of bcl-x(L). Bad competes with Bax for binding to bcl-x(L).  
 CC Bad may be used to identify agents which inhibit its binding to bcl-2  
 CC or bcl-x(L) to form heterodimers. Such agents may be used to treat  
 CC neurodegenerative diseases, immunodeficiency diseases, e.g. AIDS,  
 CC senescence or ischaemia.

XX Sequence 16 AA;

Query Match 57.9%; Score 84; DB 17; Length 16;  
 Best Local Similarity 80.0%; Pred. No. 6.1e-06;  
 Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 WTRVFQSWDRNLGR 19  
 Db |||: |||||  
 2 wtrlgswdrnlgr 16

RESULT 15

ID AAR95165  
 AC AAR95165 standard; peptide; 16 AA.

XX AAR95165;

XX 03-JAN-1997 (first entry)

XX bcl-x(L)/bcl-2 associated death promoter epitope, residues 180-195.

DE Epitope: murine; bcl-x(L)/bcl-2 associated death promoter; Bad; stroke;  
 KW polypeptide; bcl-x; cell death; regulate; BH1; BH2; apoptotic cell death;  
 KW cytokine deprivation; IL-3 dependent cell line; immunodeficiency; AIDS;  
 KW neurodegenerative disease; senescence; ischaemia; neoplasia.

XX Mus musculus.

XX WO9613614-A1.

XX 09-MAY-1996.

XX 31-OCT-1995; 95WO-US14246.

XX 31-OCT-1994; 94US-0333565.

XX (UNIW ) UNIV WASHINGTON.

XX Korsmeyer SJ;

XX WPI; 1996-251465/25.

XX Polynucleotide encoding bcl-x(L)/bcl-2 associated death promoter -  
 PT useful to treat neoplasia and apoptosis and to identify agents  
 PT inhibiting its binding to bcl-2 or bcl-x(L) to form heteromultimers

PS Claim 2; Page 103; 130pp; English.

XX The sequences given in AAR95155-67 represent epitopes derived from the  
 CC murine bcl-x(L)/bcl-2 associated death promoter (Bad) polypeptide (see  
 CC also AAR95168). Bad is a 22.1 kD protein which interacts with bcl-2 and  
 CC bcl-x proteins and regulates cell death. It has homology to the bcl-2-  
 CC related family clustered in the BH1 and BH2 domain. Bad has been found  
 CC to hybridise to bcl-x(L) and bcl-2 in yeast two-hybrid assays and in  
 CC vivo in mammalian cells. Overexpressed Bad counters the death  
 CC inhibitory activity of bcl-x(L), but is much less effective at countering  
 CC the death inhibitory activity of bcl-2. Bad expression can accelerate  
 CC apoptotic cell death induced by cytokine deprivation in an IL-3 dependent  
 CC cell line expressing bcl-x(L), and its also counters the death repressor  
 CC activity of bcl-x(L). Bad competes with Bax for binding to bcl-x(L).  
 CC Bad may be used to identify agents which inhibit its binding to bcl-2  
 CC or bcl-x(L) to form heterodimers. Such agents may be used to treat  
 CC neurodegenerative diseases, immunodeficiency diseases, e.g. AIDS,  
 CC senescence or ischaemia.

XX Sequence 16 AA;

Query Match 55.9%; Score 81; DB 17; Length 16;  
 Best Local Similarity 75.0%; Pred. No. 1.7e-05;  
 Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 SSSWTRVFQSWDRNL 17  
 Db |||: |||||  
 1 sagwtrlgswdrnl 16

Search completed: October 9, 2001, 15:53:28  
 Job time: 204 sec





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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: October 9, 2001, 15:55:21 ; Search time 17.79 seconds  
(without alignments)  
50.064 Million cell updates/sec

Title: US-09-580-523-1\_COPY\_143\_168

Perfect score: 145

Sequence: 1 QSSSWTRVFQSWDRNLGRGSSAPSQ 26

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	145	100.0	168	1 BAD_HUMAN	Q92934 homo sapien
2	120	82.8	204	1 BAD_MOUSE	Q61337 mus musculus
3	65	44.8	419	1 NOEE_RHISN	P55472 rhizobium s
4	57	39.3	245	1 CRS3_HUMAN	P54108 homo sapien
5	57	39.3	3068	1 POLG_PEMVC	Q01500 p genome po
6	54	37.2	1632	1 CTPL_MYCTU	Q10900 mycobacteri
7	54	37.2	3164	1 POLG_TUNVJ	P89509 t genome po
8	53	36.6	3163	1 POLG_TUNVQ	Q02597 t genome po
9	51	35.2	855	1 ENV_FIVT2	Q02282 feline immu
10	50	34.5	243	1 TPX1_HUMAN	P16562 homo sapien
11	50	34.5	1170	1 TSPI_BOVIN	Q28178 bos taurus
12	50	34.5	1170	1 TSPI_HUMAN	P07996 homo sapien
13	50	34.5	1170	1 TSPI_MOUSE	P35441 mus musculu
14	50	34.5	3061	1 POLG_PVTHU	Q02963 p genome po
15	50	34.5	3063	1 POLG_PVYN	P18247 p genome po
16	49.5	34.1	335	1 NAUG_METME	Q50233 methylophil
17	49.5	34.1	361	1 VAL1_TMOV	Q06657 tomato mott
18	49	33.8	246	1 AEG_RAT	P12020 rattus norv
19	48	33.1	3054	1 POLG_TEV	P04517 t genome po
20	48	33.1	3066	1 POLG_BCMVN	Q65399 b genome po
21	48	33.1	3255	1 POLG_LMYO	P13199 l genome po
22	48	33.1	3255	1 POLG_LMYE	P89876 l genome po
23	47.5	32.8	3082	1 POLG_ZYMVS	Q36979 z genome po
24	47	32.4	462	1 MPBB_YEAST	P10507 saccharomyc
25	47	32.4	432	1 TMS2_HUMAN	Q15393 homo sapien
26	47	32.4	1926	1 LPH_RABIT	P09849 oryctolagus
27	46.5	32.1	695	1 DVLI_MOUSE	P51141 mus musculu
28	46.5	32.1	695	1 DVLI_RAT	Q9wvb9 rattus norv
29	46.5	32.1	708	1 NICA_MOUSE	P57716 mus musculu
30	46	31.7	244	1 TPX1_CAVPO	Q60477 cavia porce
31	46	31.7	260	1 MTM2_MORBO	P23192 moraxella b
32	46	31.7	314	1 YMA3_BACST	Q45633 bacillus st
33	46	31.7	373	1 MP91_POAPR	P22284 poa pratens

34	46	31.7	441	1 SECY_MYCTU	P94926 mycobacteri
35	46	31.7	854	1 ENV_FIVWO	Q05312 feline immu
36	45.5	31.4	431	1 PHOR_ECOLI	P08400 escherichia
37	45.5	31.4	431	1 PHOR_KLEPN	P45608 klebsiella
38	45.5	31.4	431	1 PHOR_SHIDY	P45609 shigella dy
39	45.5	31.4	518	1 VG47_HSV11	Q00139 ictaluriid h
40	45.5	31.4	3083	1 POLG_ZYMVR	Q89330 z genome po
41	45	31.0	353	1 VAL1_BGMV	P05175 bean golden
42	45	31.0	394	1 PEPA_ASPAW	P17946 aspergillus
43	45	31.0	856	1 ENV_FIVPE	P16090 feline immu
44	45	31.0	1146	1 MMLC_MYCTU	Q50585 mycobacteri
45	44.5	30.7	953	1 YM8G_YEAST	Q03516 saccharomyc

## ALIGNMENTS

RESULT 1					
BAD_HUMAN					
ID	BAD_HUMAN	STANDARD;	PRT;	168 AA.	
AC	Q92934;				
DT	01-NOV-1997 (Rel. 35, Created)				
DT	01-NOV-1997 (Rel. 35, Last sequence update)				
DE	01-OCT-2000 (Rel. 40, Last annotation update)				
DE	BAD PROTEIN (BCL-2 BINDING COMPONENT 6).				
GN	BAD OR BBC6 OR BCL2L8.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	Yin D.X., Li Z., Huang B., Chen S., Zhou H.;				
RL	Submitted (NOV-1996) to the EMBL/GenBank/DBSJ databases.				
CC	-!- FUNCTION: PROMOTES CELL DEATH. SUCCESSFULLY COMPETES FOR THE				
CC	BINDING TO BCL-X(L) AND BCL-2, THEREBY AFFECTING THE LEVEL				
CC	OF HETERODIMERIZATION OF BOTH THESE PROTEINS WITH BAX. CAN REVERSE				
CC	THE DEATH REPRESSOR ACTIVITY OF BCL-X(L), BUT NOT THAT OF BCL-2				
CC	(BY SIMILARITY).				
CC	-!- SUBUNIT: FORMS HETERODIMERS WITH BCL-X(L) AND BCL-2, BUT NOT WITH				
CC	BAX, MCL-1, A1, OR BCL-X(S) (BY SIMILARITY).				
CC	-!- TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES.				
CC	-!- SIMILARITY: CONTAINS A BCL-2 HOMOLOG DOMAIN 1 (BH1).				
CC	-!- SIMILARITY: CONTAINS A BCL-2 HOMOLOG DOMAIN 2 (BH2).				
CC	-!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.				
CC	-----				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration				
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CC	use by non-profit institutions as long as its content is in no way				
CC	modified and this statement is not removed. Usage by and for commercial				
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/				
CC	or send an email to license@isb-sib.ch).				
CC	-----				
CC	EMBL; U66879; AAB36516.1; -				
DR	MIM; 603167; -				
DR	KW Apoptosis.				
FT	DOMAIN 101 121 BH1.				
FT	DOMAIN 146 163 BH2.				
SQ	SEQUENCE 168 AA; 18408 MW; BDF3D9959587C222BE CRC64;				

Query Match 100.0%; Score 145; DB 1; Length 168;  
Best Local Similarity 100.0%; Pred. No. 7.7e-14;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QSSSWTRVFQSWDRNLGRGSSAPSQ 26

Db 143 QSSSWTRVFQSWDRNLGRGSSAPSQ 168

RESULT 2

BAD\_MOUSE

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ID BAD_MOUSE STANDARD; PRT; 204 AA.
AC Q61337;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE BAD PROTEIN (BCL-2 BINDING COMPONENT 6).
GN BAD OR BBC6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Brain, and Thymus;
RX MEDLINE=951136361; PubMed=7834748;
RA Yang E., Zha J., Jockel J., Boile L.H., Thompson C.B., Korsmeyer S.J.;
RT *Bad, a heterodimeric partner for Bcl-XL and Bcl-2, displaces Bax and
promotes cell death.*;
RL Cell 80:285-291(1995).
CC -!- FUNCTION: PROMOTES CELL DEATH. SUCCESSFULLY COMPETES FOR THE
BINDING TO BCL-X(L) AND BCL-2, THEREBY AFFECTING THE LEVEL
HETERODIMERIZATION OF BOTH THESE PROTEINS WITH BAX. CAN REVERSE
THE DEATH REPRESSOR ACTIVITY OF BCL-X(L), BUT NOT THAT OF BCL-2.
CC -!- SUBUNIT: FORMS HETERODIMERS WITH BCL-X(L) AND BCL-2, BUT NOT WITH
BAX, MCL-1, AL, OR BCL-X(S).
CC -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 1 (BH1).
CC -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 2 (BH2).
CC -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC
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or send an email to license@isb-sib.ch).
CC -----
DR EMBL; L37296; AAA64465.1; -
DR MGD; MGI:1096330; Bad.
KW Apoptosis.
FT DOMAIN 138 158 BH1.
FT DOMAIN 182 199 BH2.
FT SEQUENCE 204 AA; 22080 MW; 6C2BA910205053F7 CRC64;
SQ
Query Match 82.8%; Score 120; DB 1; Length 204;
Best Local Similarity 73.1%; Pred. No. 3.3e-10;
Matches 19; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 1 QSSSWTRVFQSWDRNLGRGSSAPSQ 26
II: |||: |||||: |||: |||
DB 179 QSAGWTRIIQSWDRNLGRGSGTPSQ 204
RESULT 3
NOEE_RHISN STANDARD; PRT; 419 AA.
AC P55472; P72326;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE NODULATION PROTEIN NOEE (EC 2.8.2.-).
GN NOEE OR Y4HB.
OS Rhizobium sp. (strain NGR234).
OG Plasmid sym pNGR234a.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Rhizobium.
OX NCBI_TaxID=394;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97361801; PubMed=9218762;
RA Hanlin M., Jabbouri S., Quesada-Vincens S., Freiberg C., Perret X.,
Broughton W.J., Fellay R.;

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RT *Sulphation of Rhizobium sp. NGR234 Nod factors is dependent on noe,
a new host-specificity gene.*;
RL Mol. Microbiol. 24:1119-1129(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97305956; PubMed=9163424;
RA Freiberg C.A., Fellay R., Bairoch A., Broughton W.J., Rosenthal A.,
Perret X.;
RT *Molecular basis of symbiosis between Rhizobium and legumes.*;
RL Nature 387:394-401(1997).
CC -!- FUNCTION: REQUIRED FOR THE FORMATION OF SULFATED NOD FACTOR.
PROPOSED TO TRANSFER ACTIVATED SULFATE (PAPS) TO THE FUCOSE
OF THE NOD FACTOR.
CC -!- SIMILARITY: LIMITED TO NODH AND TO C.ELEGANS F42G9.8.
CC
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CC -----
DR EMBL; Y09415; CAA70569.1; -
DR EMBL; AE000076; AAB91690.1; -
KW Nodulation; Transferase; Plasmid.
SQ SEQUENCE 419 AA; 46569 MW; 848C48E0416AAALF CRC64;
Query Match 44.8%; Score 65; DB 1; Length 419;
Best Local Similarity 47.6%; Pred. No. 0.044;
Matches 10; Conservative 3; Mismatches 8; Indels 0; Gaps 0;
QY 5 WTRVFQSWDRNLGRGSSAPS 25
II: ||||: |||: |||: |||
DB 308 YRRVFTWMDLRGEGGIPA 328
RESULT 4
CRS3_HUMAN STANDARD; PRT; 245 AA.
ID CRS3_HUMAN
AC P54108; Q15512;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE CYSTEINE-RICH SECRETORY PROTEIN-3 PRECURSOR (CRISP-3) (SGP28 PROTEIN).
GN CRISP3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96270732; PubMed=8665901;
RA Kraetzschmar J., Haendler B., Eberspaecher U., Roostermann D.,
Donner P., Schleuning W.-D.;
RT *The human cysteine-rich secretory protein (CRISP) family. Primary
structure and tissue distribution of CRISP-1, CRISP-2 and CRISP-3.*;
RL Eur. J. Biochem. 236:827-836(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96186934; PubMed=8601434;
RA Kjeldsen L., Cowland J.B., Johnson A.H., Borregaard N.;
RT *SGP28, a novel matrix glycoprotein in specific granules of human
neutrophils with similarity to a human testis-specific gene product
and a rodent sperm-coating glycoprotein.*;
RL FEBS Lett. 380:246-250(1996).
CC -!- SUBCELLULAR LOCATION: SECRETED; IN NEUTROPHILS, LOCALIZED IN
SPECIFIC GRANULES.
CC -!- TISSUE SPECIFICITY: SALIVARY GLAND, PANCREAS AND PROSTATE >
EPIDIDYMIS, OVARY, THYMUS AND COLON.
CC -!- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;
INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
CC

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CC EMBL; X95240; CAA64527.1; -  
CC EMBL; X94323; CAA63984.1; -  
CC HSSP; P04284; ICFE.  
CC InterPro; IPR001283; -  
CC Pfam; PF00188; SCP; 1.  
CC PRINTS; PR00837; V5TPXLIKE.  
CC PROSITE; PS01009; SCP\_AG5\_PRL\_SC7.1; 1.  
CC PROSITE; PS01010; SCP\_AG5\_PRL\_SC7.2; 1.  
CC Glycoprotein; Signal; Multigene family.  
FT SIGNAL 1 20 POTENTIAL.  
FT CHAIN 21 245  
FT CARBOHYD 239 239 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CONFLICT 106 106 S -> P (IN REF. 2).  
SQ SEQUENCE 245 AA; 27630 MW; B4DD79CB7AE9E5F9 CRC64;

Query Match 39.3%; Score 57; DB 1; Length 245;  
Best Local Similarity 39.3%; Pred. No. 0.35;  
Matches 11; Conservative 5; Mismatches 8; Indels 4; Gaps 1;

Qy 2 SSSWTRVFQSWWDR-----NLGRGSSAPS 25  
||||: |||:| :| | |

Db 106 SSSWSQAIQSWFDEYNDFDVGVPKTPN 133  
||||: |||:| :| | |

## RESULT 5

ID POLG\_PEMVC STANDARD; PRT; 3068 AA.  
AC Q01500;  
DT 01-OCT-1993 (Rel. 27, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DE GENOME POLYPROTEIN [CONTAINS: N-TERMINAL PROTEIN (P1); HELPER  
COMPONENT PROTEINASE (EC 3.4.22.-) (HC-PRO); PROTEIN P3; 6 KDA PROTEIN  
1 (6K1); CYTOPLASMIC INCLUSION PROTEIN (CI); 6 KDA PROTEIN 2 (6K2);  
GENOME-LINKED PROTEIN (VPG); NUCLEAR INCLUSION PROTEIN A (NI-A) (NIA)  
(EC 3.4.22.-) (49 KDA PROTEINASE) (49 KDA-PRO); NUCLEAR INCLUSION  
PROTEIN B (NI-B) (NIB) (RNA-DIRECTED RNA POLYMERASE) (EC 2.7.7.48);  
COAT PROTEIN (CP)].  
OS Pepper mottle virus (California isolate) (PeMV) (PepMoV C).  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;  
OC Potyvirus.  
OX NCBI\_TaxID=31737;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA MEDLINE=93033110; PubMed=14113501;  
RX Vance V.B., Moore D., Turpen T.H., Bracker A., Hollowell V.C.;  
RT "The complete nucleotide sequence of pepper mottle virus genomic RNA:  
comparison of the encoded polyprotein with those of other sequenced  
potyviruses";  
RL Virology 191:19-30(1992).  
CC -1- FUNCTION: HELPER COMPONENT-PROTEINASE IS REQUIRED FOR APHID  
TRANSMISSION AND ALSO HAS PROTEOLYTIC ACTIVITY.  
CC -1- FUNCTION: CYTOPLASMIC INCLUSION PROTEIN HAS HELICASE ACTIVITY. IT  
MAY BE INVOLVED IN REPLICATION.  
CC -1- FUNCTION: NUCLEAR INCLUSION PROTEIN A HAS PROTEOLYTIC ACTIVITY.  
CC -1- P1M: VPG IS COVALENTLY LINKED TO THE GENOMIC RNA.  
CC -1- P1M: THE VIRAL RNA OF POTYVIRUSES IS EXPRESSED AS A SINGLE  
POLYPROTEIN WHICH UNDERGOES POSTTRANSLATIONAL PROTEOLYTIC  
PROCESSING RESULTING IN THE PRODUCTION OF AT LEAST EIGHT  
INDIVIDUAL PROTEINS.  
CC -1- SIMILARITY: HC PROTEINASE BELONGS TO PEPTIDASE FAMILY C6.  
CC -1- SIMILARITY: NI-A PROTEINASE BELONGS TO PEPTIDASE FAMILY C4.  
CC -1- SIMILARITY: BELONGS TO THE POTYVIRUSES POLYPROTEIN FAMILY.

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CC EMBL; M96425; AAA46903.1; -  
CC PIR; A44062; A44062.  
CC MEROPS; C04.001; -  
CC MEROPS; C06.001; -  
CC MEROPS; S30.001; -  
CC InterPro; IPR001205; -  
CC InterPro; IPR001410; -  
CC InterPro; IPR001456; -  
CC InterPro; IPR001592; -  
CC InterPro; IPR001650; -  
CC InterPro; IPR001730; -  
CC InterPro; IPR002540; -  
CC Pfam; PF00270; DEAD; 1.  
CC Pfam; PF00663; Peptidase\_C4; 1.  
CC Pfam; PF00851; Peptidase\_C6; 1.  
CC Pfam; PF01577; Poty\_P1; 1.  
CC Pfam; PF00767; Poty\_Coat; 1.  
CC Pfam; PF00680; RNA\_dep\_RNA\_pol; 1.  
CC Pfam; PF00271; helicase\_C; 1.  
CC PRINTS; PR00966; NIAPOTYPTASE.  
KW Hydrolase; Transferase; Thiol protease; RNA-directed RNA polymerase;  
KW Coat protein; Polyprotein; Covalent protein-RNA linkage; Helicase;  
KW ATP-binding.

FT CHAIN 1 287 N-TERMINAL PROTEIN.  
FT CHAIN 288 743 HELPER COMPONENT PROTEINASE.  
FT CHAIN 744 ? PROTEIN P3.  
FT CHAIN ? 1156 6 KDA PROTEIN 1.  
FT CHAIN 1157 1790 CYTOPLASMIC INCLUSION PROTEIN.  
FT CHAIN 1791 1842 6 KDA PROTEIN 2.  
FT CHAIN 1843 ? GENOME-LINKED PROTEIN.  
FT CHAIN ? 2276 NUCLEAR INCLUSION PROTEIN A.  
FT CHAIN 2277 2795 NUCLEAR INCLUSION PROTEIN B.  
FT CHAIN 2796 3068 COAT PROTEIN.  
FT BINDING 1906 1906 COVALENT LINKAGE OF VIRAL RNA  
(BY SIMILARITY).  
FT NP\_BIND 1241 1248 ATP (POTENTIAL).  
SQ SEQUENCE 3068 AA; 348651 MW; FD3458B837FDA7C2 CRC64;

Query Match 39.3%; Score 57; DB 1; Length 3068;  
Best Local Similarity 50.0%; Pred. No. 4.4;  
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 9 FQSWWDRNLGRGSSAP 24  
|:||||:| | |

Db 1191 FESWWDQVARGFTIP 1206  
|:||||:| | |

## RESULT 6

ID CTPI\_MYCTU STANDARD; PRT; 1632 AA.  
AC Q10900;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 15-JUL-1999 (Rel. 38, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE PROBABLE CATION-TRANSPORTING APPASE I (EC 3.6.1.-).  
GN CTPI OR RV0107C OR MTCY251.26C.  
OS Mycobacterium tuberculosis.  
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
OC Actinomycetales; Corynebacterineae; Mycobacterium.  
OX NCBI\_TaxID=1773;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=H37RV;

```

RX MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E.,
RA Taylor K., Whitehead S., Barrell B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence.";
RL Nature 393:537-544(1998).
CC -|- CATALYTIC ACTIVITY: ATP + H(2O) = ADP + ORTHOPHOSPHATE.
CC -|- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
CC -|- SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY
CC (E1-E2 ATPASES). STRONGEST SIMILARITY TO EUKARYOTIC CALCIUM-
CC ATPASE TRANSPORT SYSTEMS.
CC -----
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CC -----
CC EMBL; 274410; CAA98940.1; -
CC TubercuList; RV0107C; -
CC InterPro: IPR000695; -
CC InterPro: IPR001757; -
CC InterPro: IPR001899; -
CC Pfam; PF00122; E1-E2_ATPase; 1.
CC PRINTS; PR00119; CATATPASE.
CC PRINTS; PR00120; HATPASE.
CC PROSITE; PS00154; ATPASE_E1_E2; 1.
KW Hydrolase; Transmembrane; Phosphorylation; ATP-binding.
FT TRANSMEM 30 50 POTENTIAL.
FT TRANSMEM 148 168 POTENTIAL.
FT TRANSMEM 177 197 POTENTIAL.
FT TRANSMEM 315 335 POTENTIAL.
FT TRANSMEM 358 378 POTENTIAL.
FT TRANSMEM 637 657 POTENTIAL.
FT TRANSMEM 673 693 POTENTIAL.
FT TRANSMEM 778 798 POTENTIAL.
FT TRANSMEM 921 941 POTENTIAL.
FT TRANSMEM 969 989 POTENTIAL.
FT TRANSMEM 997 1017 POTENTIAL.
FT TRANSMEM 1401 1421 POTENTIAL.
FT TRANSMEM 1432 1452 POTENTIAL.
FT TRANSMEM 1547 1567 POTENTIAL.
FT MOD_RES 1053 1053 PHOSPHORYLATION (BY SIMILARITY).
FT SEQUENCE 1632 AA; 169606 MW; A29F651A55EF7F8 CRC64;

Query Match 37.2%; Score 54; DB 1; Length 1632;
Best Local Similarity 71.4%; Pred. No. 6.2;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 13 WDRNLGRGSSAPSQ 26
Db 1576 WDRSPGRASSAPRQ 1589
|||||
RESULT 7
POLG_TUMVJ STANDARD; PRT; 3164 AA.
ID POLG_TUMVJ
AC P89509;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE GENOME POLYPROTEIN [CONTAINS: N-TERMINAL PROTEIN (P1); HELPER
DE COMPONENT PROTEINASE (EC 3.4.22.-) (HC-PRO); PROTEIN P3; 6 KDA PROTEIN
DE 1 (6K1); CYTOPLASMIC INCLUSION PROTEIN (CI); 6 KDA PROTEIN 2 (6K2);

DE GENOME-LINKED PROTEIN (VPG); NUCLEAR INCLUSION PROTEIN A (NI-A) (NIA)
DE (EC 3.4.22.-) (49 KDA PROTEINASE) (49 KDA-PRO); NUCLEAR INCLUSION
DE PROTEIN B (NI-B) (NIB) (RNA-DIRECTED RNA POLYMERASE) (EC 2.7.7.48);
DE COAT PROTEIN (CP)].
DE Turnip mosaic virus (strain Japanese) (TUMV).
OS Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
OC Potyvirus.
OX NCBI_TaxID=12230;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97079098; PubMed=8920830;
RA Ohshima K., Tanaka M., Sako N.;
RT "The complete nucleotide sequence of turnip mosaic virus RNA Japanese
RT strain.";
RL Arch. Virol. 141:1991-1997(1996).
CC -|- FUNCTION: CYTOPLASMIC INCLUSION PROTEIN HAS HELICASE ACTIVITY. IT
CC MAY BE INVOLVED IN REPLICATION.
CC -|- FUNCTION: NUCLEAR INCLUSION PROTEIN A HAS PROTEOLYTIC ACTIVITY.
CC -|- PTM: VPG IS COVALENTLY LINKED TO THE GENOMIC RNA.
CC -|- PTM: THE VIRAL RNA OF POTYVIRUSES IS EXPRESSED AS A SINGLE
CC POLYPROTEIN WHICH UNDERGOES POSTTRANSLATIONAL PROTEOLYTIC
CC PROCESSING RESULTING IN THE PRODUCTION OF AT LEAST EIGHT
CC INDIVIDUAL PROTEINS.
CC -|- SIMILARITY: HC PROTEINASE BELONGS TO PEPTIDASE FAMILY C6.
CC -|- SIMILARITY: NI-A PROTEINASE BELONGS TO PEPTIDASE FAMILY C4.
CC -|- SIMILARITY: BELONGS TO THE POTYVIRUSES POLYPROTEIN FAMILY.
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; D83184; BAA11836.1; -
CC InterPro: IPR001205; -
CC InterPro: IPR001410; -
CC InterPro: IPR001456; -
CC InterPro: IPR001592; -
CC InterPro: IPR001650; -
CC InterPro: IPR001730; -
CC InterPro: IPR002540; -
CC Pfam; PF00270; DEAD; 1.
CC Pfam; PF00863; Peptidase_C4; 1.
CC Pfam; PF00851; Peptidase_C6; 1.
CC Pfam; PF01577; Poly_P1; 1.
CC Pfam; PF00767; Poly_coat; 1.
CC Pfam; PF00680; RNA_dep_RNA_pol; 1.
CC Pfam; PF00271; helicase_C; 1.
CC PRINTS; PR00966; NIAPOTYPASE.
KW Hydrolase; Transferase; Thiol protease; RNA-directed RNA polymerase;
KW Coat protein; Polyprotein; Covalent protein-RNA linkage; Helicase;
KW ATP-binding.
FT CHAIN 1 362 N-TERMINAL PROTEIN.
FT CHAIN 363 820 HELPER COMPONENT PROTEINASE.
FT CHAIN 821 1175 PROTEIN P3.
FT CHAIN 1176 1227 6 KDA PROTEIN 1.
FT CHAIN 1228 1871 CYTOPLASMIC INCLUSION PROTEIN.
FT CHAIN 1872 1924 6 KDA PROTEIN 2.
FT CHAIN 1925 2116 GENOME-LINKED PROTEIN.
FT CHAIN 2117 2359 NUCLEAR INCLUSION PROTEIN A.
FT CHAIN 2360 2876 NUCLEAR INCLUSION PROTEIN B.
FT CHAIN 2877 3164 COAT PROTEIN.
FT BINDING 1987 1987 COVALENT LINKAGE OF VIRAL RNA (BY
FT SIMILARITY).
FT NP_BIND 1313 1320 ATP (POTENTIAL).
FT SEQUENCE 3164 AA; 357731 MW; 0DFC735CB3A5231F CRC64;

Query Match 37.2%; Score 54; DB 1; Length 3164;
Best Local Similarity 44.4%; Pred. No. 12;
Matches 8; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
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Qy 7 RVFOSWMDRNLGRGSSAP 24
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Db 1261 KTFASWNHQLSRGFTIP 1278

RESULT 8
POLG_TUMVQ
ID POLG_TUMVQ STANDARD; PRT; 3163 AA.
AC Q02597;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE GENOME POLYPROTEIN [CONTAINS: N-TERMINAL PROTEIN (P1); HELPER
DE COMPONENT PROTEINASE (EC 3.4.22.-) (HC-PRO); PROTEIN P3; 6 KDA PROTEIN
DE 1 (6K1); CYTOPLASMIC INCLUSION PROTEIN (C1); 6 KDA PROTEIN 2 (6K2);
DE GENOME-LINKED PROTEIN (VPG); NUCLEAR INCLUSION PROTEIN A (NI-A) (NIA)
DE (EC 3.4.22.-) (49 KDA PROTEINASE) (49 KDA-PRO); NUCLEAR INCLUSION
DE PROTEIN B (NI-B) (NIB) (RNA-DIRECTED RNA POLYMERASE) (EC 2.7.7.48);
DE COAT PROTEIN (CP)].
OS Turnip mosaic virus (strain Quebec) (TUMV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
OC Potyvirus
OC NCBI_TaxID=36396;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93057350; PubMed=1431807;
RA Nicolas O., Laliberte J.F.;
RT "The complete nucleotide sequence of turnip mosaic potyvirus RNA.";
RL J. Gen. Virol. 73:2785-2793(1992).
RN [2]
RP SEQUENCE OF 1534-3163 FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=91073142; PubMed=2254757;
RA Tremblay M.F., Nicolas O., Sinha R., Lazure C., Laliberte J.F.;
RT "Sequence of the 3'-terminal region of turnip mosaic virus RNA and
RT the capsid protein gene.";
RL J. Gen. Virol. 71:2769-2772(1990).
CC -!- FUNCTION: CYTOPLASMIC INCLUSION PROTEIN HAS HELICASE ACTIVITY. IT
CC MAY BE INVOLVED IN REPLICATION.
CC -!- FUNCTION: NUCLEAR INCLUSION PROTEIN A HAS PROTEOLYTIC ACTIVITY.
CC -!- PPM: VPG IS COVALENTLY LINKED TO THE GENOMIC RNA.
CC -!- PPM: THE VIRAL RNA OF POTYVIRUSES IS EXPRESSED AS A SINGLE
CC POLYPROTEIN WHICH UNDERGOES POSTTRANSLATIONAL PROTEOLYTIC
CC PROCESSING RESULTING IN THE PRODUCTION OF AT LEAST EIGHT
CC INDIVIDUAL PROTEINS.
CC -!- SIMILARITY: HC PROTEINASE BELONGS TO PEPTIDASE FAMILY C6.
CC -!- SIMILARITY: NI-A PROTEINASE BELONGS TO PEPTIDASE FAMILY C4.
CC -!- SIMILARITY: BELONGS TO THE POTYVIRUSES POLYPROTEIN FAMILY.
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CC -----
CC ENBL; D10927; BAA01725.1; -
CC ENBL; D10601; BAA01452.1; -
CC PIR; JQ1168; JQ1168.
CC PIR; JQ1895; JQ1895.
CC MEROPS; C04.001; -.
CC DR InterPro; IPR001205; -
CC DR InterPro; IPR001410; -
CC DR InterPro; IPR001456; -
CC DR InterPro; IPR001592; -
CC DR InterPro; IPR001730; -
CC DR InterPro; IPR002540; -
CC Pfam; PF00270; DEAD; 1.
CC Pfam; PF00863; Peptidase_C4; 1.
CC Pfam; PF00851; Peptidase_C6; 1.
CC Pfam; PF01577; Poty_P1; 1.

Pfam; PF00767; Poty_coat; 1.
Pfam; PF00680; RNA_dep_RNA_pol; 1.
PRINTS; PR00966; NIAPOTYPASE.
KW Hydrolase; Transferase; Thiol protease; RNA-directed RNA polymerase;
KW Coat protein; Polyprotein; Covalent protein-RNA linkage; Helicase;
ATP-binding.
FT CHAIN 1 362 N-TERMINAL PROTEIN.
FT CHAIN 363 820 HELPER COMPONENT PROTEINASE.
FT CHAIN 821 1175 PROTEIN P3.
FT CHAIN 1176 1227 6 KDA PROTEIN 1.
FT CHAIN 1228 1870 CYTOPLASMIC INCLUSION PROTEIN.
FT CHAIN 1871 1923 6 KDA PROTEIN 2.
FT CHAIN 1924 2115 GENOME-LINKED PROTEIN.
FT CHAIN 2116 2358 NUCLEAR INCLUSION PROTEIN A.
FT CHAIN 2359 2875 NUCLEAR INCLUSION PROTEIN B.
FT CHAIN 2876 3163 COAT PROTEIN.
FT BINDING 1986 1986 COVALENT LINKAGE OF VIRAL RNA (BY
FT NP_BIND 1313 1320 SIMILARITY).
FT NP_BIND 1313 1320 ATP (POTENTIAL).
FT CONFLICT 2862 2862 E -> G (IN REF. 2).
SQ SEQUENCE 3163 AA; 357817 MW; 61B0F73B58DF6D59 CRC64;

Query Match 36.6%; Score 53; DB 1; Length 3163;
Best Local Similarity 44.4%; Pred. No. 17;
Matches 8; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

Qy 7 RVFOSWMDRNLGRGSSAP 24
    : |||: |||: |||: |
Db 1261 KTFASWNHQLSRGFTIP 1278

RESULT 9
ENV_FIVT2
ID ENV_FIVT2 STANDARD; PRT; 855 AA.
AC Q02282;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE ENV POLYPROTEIN PRECURSOR (GP150 POLYPROTEIN) [CONTAINS: GLYCOPROTEIN
DE GP100; GLYCOPROTEIN GP36].
DE GN ENV.
DE OS Feline immunodeficiency virus (isolate TM2) (FIV).
DE OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
DE OX NCBI_TaxID=31676;
DE RN [1]
DE RP SEQUENCE FROM N.A.
DE RX MEDLINE=91303718; PubMed=1649349;
DE RA Kiyomasu T., Miyazawa T., Furuya T., Shibata R., Sakai H.,
DE RA Sakuragi J.I., Fukasawa M., Maki N., Hasegawa A., Mikami T.,
DE RA Adachi A.;
DE RT "Identification of feline immunodeficiency virus rev gene activity.";
DE RL J. Virol. 65:4539-4542(1991).
DE RN [2]
DE RP SEQUENCE FROM N.A.
DE RX MEDLINE=92198230; PubMed=1312825;
DE RA Maki N., Miyazawa T., Fukasawa M., Hasegawa A., Hayami M., Miki K.,
DE RA Mikami T.;
DE RT "Molecular characterization and heterogeneity of feline
DE immunodeficiency virus isolates.";
DE RL Arch. Virol. 123:29-45(1992).
DE CC -----
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DE CC -----
DE CC ENBL; M59418; AAA43074.1; -
DE CC PIR; F45557; F45557.
DE DR Pfam; PF00429; ENV_polyprotein; 1.

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Page 6



CC -1- SIMILARITY: CONTAINS 3 TSP TYPE-1 DOMAINS.  
 CC -1- SIMILARITY: CONTAINS 7 TSP TYPE-3 DOMAINS.  
 CC  
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 CC -----  
 DR EMBL; AB005287; BAA21115.1; -  
 DR EMBL; X87618; CAA60950.1; -  
 DR EMBL; X87619; CAA60951.1; -  
 DR HSSP; P35555; 1EMO.  
 DR GlycoSuiteDB; Q28178; -  
 DR InterPro; IPR000561; -  
 DR InterPro; IPR000884; -  
 DR InterPro; IPR001007; -  
 DR InterPro; IPR001881; -  
 DR Pfam; PF00008; EGF; 2.  
 DR Pfam; PF00090; tsp.1; 3.  
 DR Pfam; PF00093; wvc; 1.  
 DR PROSITE; PS00022; EGF\_1; FALSE\_NEG.  
 DR PROSITE; PS01186; EGF\_2; FALSE\_NEG.  
 DR PROSITE; PS01208; WMFC; 1.  
 DR PROSITE; PS00092; TSP1; 3.  
 DR Glycoprotein; Cell adhesion; Calcium-binding; Heparin-binding; Repeat;  
 KW EGF-like domain; Signal.  
 FT SIGNAL 1 18  
 FT CHAIN 19 1170  
 FT DOMAIN 19 232  
 FT DOMAIN 316 373  
 FT DOMAIN 379 430  
 FT DOMAIN 435 491  
 FT DOMAIN 492 548  
 FT DOMAIN 549 587  
 FT DOMAIN 588 645  
 FT DOMAIN 646 690  
 FT DOMAIN 723 758  
 FT DOMAIN 759 781  
 FT DOMAIN 782 817  
 FT DOMAIN 818 840  
 FT DOMAIN 841 878  
 FT DOMAIN 879 914  
 FT DOMAIN 915 950  
 FT DOMAIN 951 1170  
 FT SITE 926 928  
 FT DISULFID 270 270  
 FT DISULFID 274 274  
 FT DISULFID 551 562  
 FT DISULFID 556 572  
 FT DISULFID 575 586  
 FT DISULFID 592 608  
 FT DISULFID 599 617  
 FT DISULFID 620 644  
 FT DISULFID 650 663  
 FT DISULFID 657 676  
 FT DISULFID 678 689  
 FT CARBOHYD 248 248  
 FT CARBOHYD 360 360  
 FT CARBOHYD 708 708  
 FT CARBOHYD 1067 1067  
 FT CARBOHYD 1085 1085  
 FT CONFLICT 805 805  
 CC SEQUENCE 1170 AA; 129533 MW; 0DD6ADF3E5FA031A CRC64;

Query Match 34.5% Score 50; DB 1; Length 1170;  
 Best Local Similarity 50.08; Pred. No. 16;  
 Matches 11; Conservative 2; Mismatches 3; Indels 6; Gaps 1;

Qy 1 QSSS-----WTRVFQSWDRN 16

Db 1030 QSSSRFYVVMKQVTSYWDN 1051  
 |||| | : | | : | | |  
 RESULT 12  
 TSP1\_HUMAN STANDARD; PRT; 1170 AA.  
 ID TSPI\_HUMAN AC P07996;  
 DT 01-AUG-1988 (Rel. 08, Created)  
 DT 01-AUG-1988 (Rel. 08, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE THROMBOSPONDIN 1 PRECURSOR.  
 GN THBS1 OR TSPI OR TSP.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Endothelial cells;  
 RX MEDLINE=87057617; PubMed=2430973;  
 RA Lawler J., Hynes R.O.;  
 RT "The structure of human thrombospondin, an adhesive glycoprotein with  
 RT multiple calcium-binding sites and homologies with several different  
 RT proteins.";  
 RL J. Cell Biol. 103:1635-1648(1986).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89139590; PubMed=2918029;  
 RA Hennessy S.W., Frazier B.A., Kim D.D., Deckwerth T.L.,  
 RA Baumgartel D.M., Rotwein P., Frazier W.A.;  
 RT "Complete thrombospondin mRNA sequence includes potential regulatory  
 RT sites in the 3' untranslated region.";  
 RL J. Cell Biol. 108:729-736(1989).  
 RN [3]  
 RP SEQUENCE OF 1-397 FROM N.A.  
 RX MEDLINE=87157592; PubMed=3030396;  
 RA Kobayashi S., Eden-McCutchan F., Framson P., Bornstein P.;  
 RT "Partial amino acid sequence of human thrombospondin as determined by  
 RT analysis of cDNA clones: homology to malarial circumsporozoite  
 RT proteins.";  
 RL Biochemistry 25:8418-8425(1986).  
 RN [4]  
 RP SEQUENCE OF 1-374 FROM N.A.  
 RX MEDLINE=86287276; PubMed=3461443;  
 RA Dixit V.M., Hennessy S.W., Grant G.A., Rotwein P., Frazier W.A.;  
 RT "Characterization of a cDNA encoding the heparin and collagen binding  
 RT domains of human thrombospondin.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 83:5449-5453(1986).  
 RN [5]  
 RP SEQUENCE OF 1-166 FROM N.A.  
 RX MEDLINE=89291870; PubMed=2544587;  
 RA Laherty C.D., Gierman T.M., Dixit V.M.;  
 RT "Characterization of the promoter region of the human thrombospondin  
 RT gene. DNA sequences within the first intron increase transcription.";  
 RL J. Biol. Chem. 264:11222-11227(1989).  
 RN [6]  
 RP SEQUENCE OF 1028-1170 FROM N.A.  
 RA Fleur M., Jobin C., Gauthier J., Kreis C.G.;  
 RL Submitted (XXX-1992) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: ADHESIVE GLYCOPROTEIN THAT MEDIATES CELL-TO-CELL AND  
 CC CELL-TO-MATRIX INTERACTIONS. CAN BIND TO FIBRINOGEN, FIBRONECTIN,  
 CC LAMININ AND TYPE V COLLAGEN.  
 CC -1- SUBUNIT: HOMOTRIMER, CROSS-LINKED BY DISULFIDE BONDS.  
 CC -1- SIMILARITY: BELONGS TO THE THROMBOSPONDIN FAMILY.  
 CC -1- SIMILARITY: CONTAINS 1 WMFC DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 3 EGF-LIKE DOMAINS.  
 CC -1- SIMILARITY: CONTAINS 3 TSP TYPE-1 DOMAINS.  
 CC -1- SIMILARITY: CONTAINS 7 TSP TYPE-3 DOMAINS.  
 CC -----  
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DR EMBL; M62465; AAA50611.1; JOINED.  
 DR EMBL; M62466; AAA50611.1; JOINED.  
 DR EMBL; M62467; AAA50611.1; JOINED.  
 DR EMBL; M62468; AAA50611.1; JOINED.  
 DR EMBL; M62469; AAA50611.1; JOINED.  
 DR EMBL; M82276; AAA50633.1; -.  
 DR EMBL; J05606; AAA40431.1; -.  
 DR EMBL; J05605; AAA40431.1; JOINED.  
 DR PIR; A40558; B42587.  
 DR PIR; B42587; B42587.  
 DR PIR; A37905; A37905.  
 DR HSP; P35555; LEMO.  
 DR MGD; MGI:98737; Ths1.  
 DR InterPro; IPR000561; -.  
 DR InterPro; IPR000884; -.  
 DR InterPro; IPR001007; -.  
 DR Pfam; PF00008; EGF; 2.  
 DR Pfam; PF00090; tsp\_1; 3.  
 DR Pfam; PF00093; vwc; 1.  
 DR PROSITE; PS00022; EGF\_1; FALSE\_NEG.  
 DR PROSITE; PS01186; EGF\_2; 1.  
 DR PROSITE; PS00092; TSP1; 3.  
 DR PROSITE; PS01208; VWFC; 1.  
 KW Glycoprotein; Cell adhesion; Calcium-binding; Heparin-binding; Repeat;  
 EGF-like domain; Signal.  
 FT SIGNAL 1 18  
 FT CHAIN 19 1170  
 FT DOMAIN 19 232  
 FT DOMAIN 316 373  
 FT DOMAIN 379 430  
 FT DOMAIN 435 491  
 FT DOMAIN 492 548  
 FT DOMAIN 549 587  
 FT DOMAIN 588 645  
 FT DOMAIN 646 690  
 FT DOMAIN 723 758  
 FT DOMAIN 759 781  
 FT DOMAIN 782 817  
 FT DOMAIN 818 840  
 FT DOMAIN 841 878  
 FT DOMAIN 879 914  
 FT DOMAIN 915 950  
 FT DOMAIN 951 1170  
 FT SITE 926 928  
 FT DISULFID 270 274  
 FT DISULFID 274 274  
 FT DISULFID 551 562  
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 FT DISULFID 592 608  
 FT DISULFID 599 617  
 FT DISULFID 620 644  
 FT DISULFID 650 663  
 FT DISULFID 657 676  
 FT DISULFID 678 689  
 FT CARBOHYD 248 248  
 FT CARBOHYD 360 360  
 FT CARBOHYD 708 708  
 FT CARBOHYD 1067 1067  
 FT CONFLICT 1025 1025  
 SQ SEQUENCE 1170 AA; 129646 MW; 0443E493615E7F06 CRC64;

Query Match 34.58; Score 50; DB 1; Length 1170;  
 Best Local Similarity 50.08; Pred. No. 16;  
 Matches 11; Conservative 2; Mismatches 3; Indels 6; Gaps 1;

Qy 1 QSSS-----WTRVFQSWDRN 16  
 ||||| : |||||  
 Db 1030 QSSRFYVWMKQYQSWDRN 1051

RESULT 14

POLG\_PVYHU STANDARD; PRT; 3061 AA.  
 ID POLG\_PVYHU  
 AC Q02963;  
 DT 01-JUL-1993 (Rel. 26, Created)  
 DT 01-JUL-1993 (Rel. 26, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE GENOME POLYPROTEIN [CONTAINS: N-TERMINAL PROTEIN (P1); HELPER  
 COMPONENT PROTEINASE (EC 3.4.22.-) (HC-PRO); 6 KDA PROTEIN 2 (6K2);  
 1 (6K1); CYTOPLASMIC INCLUSION PROTEIN (CI); 6 KDA PROTEIN A (NI-A) (NIA)  
 DE GENOME-LINKED PROTEIN (VPG); NUCLEAR INCLUSION PROTEIN A (NI-A) (NIA)  
 DE (EC 3.4.22.-) (49 KDA PROTEINASE) (49 KDA-PRO); NUCLEAR INCLUSION  
 DE PROTEIN B (NI-B) (NIB) (RNA-DIRECTED RNA POLYMERASE) (EC 2.7.7.48);  
 DE COAT PROTEIN (CP)].  
 OS Potato virus Y (strain Hungarian) (PVY).  
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Polyviridae;  
 OC Polyvirus.  
 OX NCBI\_TaxID=31739;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93154578; PubMed=8428653;  
 RA Thole V., Dalmay T., Burgyn J., Balazs E.;  
 RT "Cloning and sequencing of potato virus Y (Hungarian isolate) genomic  
 RNA.";  
 RL Gene 123:149-156(1993).  
 CC -!- FUNCTION: HELPER COMPONENT-PROTEINASE IS REQUIRED FOR APHID  
 TRANSMISSION AND ALSO HAS PROTEOLYTIC ACTIVITY.  
 CC -!- FUNCTION: CYTOPLASMIC INCLUSION PROTEIN HAS HELICASE ACTIVITY. IT  
 MAY BE INVOLVED IN REPLICATION.  
 CC -!- FUNCTION: NUCLEAR INCLUSION PROTEIN A HAS PROTEOLYTIC ACTIVITY.  
 CC -!- PTM: VPG IS COVALENTLY LINKED TO THE GENOMIC RNA.  
 CC -!- PTM: THE VIRAL RNA OF POTYVIRUSES IS EXPRESSED AS A SINGLE  
 POLYPROTEIN WHICH UNDERGOES POSTTRANSLATIONAL PROTEOLYTIC  
 PROCESSING RESULTING IN THE PRODUCTION OF AT LEAST EIGHT  
 INDIVIDUAL PROTEINS.  
 CC -!- SIMILARITY: HC PROTEINASE BELONGS TO PEPTIDASE FAMILY C6.  
 CC -!- SIMILARITY: NI-A PROTEINASE BELONGS TO PEPTIDASE FAMILY C4.  
 CC -!- SIMILARITY: BELONGS TO THE POTYVIRUSES POLYPROTEIN FAMILY.  
 -----  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
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 CC EMBL; M95491; AAB59762.1; -.  
 CC PIR; JN0545; JN0545.  
 CC MEROPS; C04.001; -.  
 CC MEROPS; C06.001; -.  
 CC MEROPS; S30.001; -.  
 CC InterPro; IPR001205; -.  
 CC InterPro; IPR001410; -.  
 CC InterPro; IPR001456; -.  
 CC InterPro; IPR001592; -.  
 CC InterPro; IPR001650; -.  
 CC InterPro; IPR001730; -.  
 CC InterPro; IPR002540; -.  
 CC Pfam; PF00270; DEAD; 1.  
 CC Pfam; PF00863; Peptidase\_C4; 1.  
 CC Pfam; PF00851; Peptidase\_C6; 1.  
 CC Pfam; PF01577; Poty\_P1; 1.  
 CC Pfam; PF00767; Poty\_Coat; 1.  
 CC Pfam; PF00680; RNA\_dep\_RNA\_pol; 1.  
 CC Pfam; PF00271; helicase\_C; 1.  
 CC PRINTS; PR00966; NIAPOTYPTASE.  
 KW Hydrolyase; Transferase; Thiol protease; RNA-directed RNA polymerase;  
 KW Coat protein; Polyprotein; Covalent protein-RNA linkage; Helicase;  
 KW ATP-binding.  
 FT CHAIN 1 275 N-TERMINAL PROTEIN.  
 FT CHAIN 276 824 HELPER COMPONENT PROTEINASE.  
 FT CHAIN 825 ? PROTEIN P3.  
 FT CHAIN ? 1157 6 KDA PROTEIN 1.

```
FT CHAIN 1158 1791 CYTOPLASMIC INCLUSION PROTEIN.
FT CHAIN 1792 1843 6 KDA PROTEIN 2.
FT CHAIN 1844 ? GENOME-LINKED PROTEIN.
FT CHAIN ? 2275 NUCLEAR INCLUSION PROTEIN A.
FT CHAIN 2276 2794 NUCLEAR INCLUSION PROTEIN B.
FT CHAIN 2795 3061 COAT PROTEIN.
FT BINDING 1907 1907 COVALENT LINKAGE OF VIRAL RNA (BY
SIMILARITY).
FT NP_BIND 1242 1249 ATP (POTENTIAL).
FT SEQUENCE 3061 AA; 347326 MW; 737FFBA215B56F99 CRC64;

Query Match 34.5%; Score 50; DB 1; Length 3061;
Best Local Similarity 43.8%; Pred. No. 43;
Matches 7; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 9 FQSWDRNLGRGSSAP 24
| | | | | : | : |
Db 1192 FSDWDRQIQMGHTLP 1207

RESULT 15
POLG_PVYN STANDARD; PRT: 3063 AA
AC F18247; Q85266; Q85267; Q85268; Q85269; Q85270; Q85271; Q85272;
AC Q85273;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE GENOME POLYPROTEIN [CONTAINS: N-TERMINAL PROTEIN (P1); HELPER
COMPONENT PROTEINASE (EC 3.4.22.-) (HC-PRO); PROTEIN P3; 6 KDA PROTEIN
1 (6K1); CYTOPLASMIC INCLUSION PROTEIN (CI); 6 KDA PROTEIN 2 (6K2);
GENOME-LINKED PROTEIN (VPG); NUCLEAR INCLUSION PROTEIN A (NI-A) (NIA)
(EC 3.4.22.-) (49 KDA PROTEINASE) (49 KDA-PRO); NUCLEAR INCLUSION
PROTEIN B (NI-B) (NIB) (RNA-DIRECTED RNA POLYMERASE) (EC 2.7.7.48);
COAT PROTEIN (CP)].
OS Potato virus Y (strain N) (PVY).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
OC Potyvirus.
OC NCBI_TaxID=122119;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89279275; PubMed=2732709;
RA Robaglia C., Durand-Tardif M., Tronchet M., Boudazin G.,
RA Astier-Manificier S., Casse-Delbart F.;
RT "Nucleotide sequence of potato virus Y (N Strain) genomic RNA.";
RL J. Gen. Virol. 70:935-947(1989).
RN [2]
RP REVISIONS.
RA Durand-Tardif M.;
RL Submitted (JAN-1994) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: HELPER COMPONENT-PROTEINASE IS REQUIRED FOR APHD
TRANSMISSION AND ALSO HAS PROTEOLYTIC ACTIVITY.
CC -!- FUNCTION: CYTOPLASMIC INCLUSION PROTEIN HAS HELICASE ACTIVITY. IT
MAY BE INVOLVED IN REPLICATION.
CC -!- FUNCTION: NUCLEAR INCLUSION PROTEIN A HAS PROTEOLYTIC ACTIVITY.
CC -!- PTM: VPG IS COVALENTLY LINKED TO THE GENOMIC RNA.
CC -!- PTM: THE VIRAL RNA OF POTYVIRUSES IS EXPRESSED AS A SINGLE
POLYPROTEIN WHICH UNDERGOES POSTTRANSLATIONAL PROTEOLYTIC
PROCESSING RESULTING IN THE PRODUCTION OF AT LEAST EIGHT
INDIVIDUAL PROTEINS.
CC -!- SIMILARITY: HC PROTEINASE BELONGS TO PEPTIDASE FAMILY C6.
CC -!- SIMILARITY: NI-A PROTEINASE BELONGS TO PEPTIDASE FAMILY C4.
CC -!- SIMILARITY: BELONGS TO THE POTYVIRUSES POLYPROTEIN FAMILY.
-----
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch)
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DR EMBL; X12456; CAA30988.1; -
DR EMBL; D00441; BAA00342.1; -
DR PIR; JS0166; JS0166.
DR MEROPS; C04.001; -
DR MEROPS; C06.001; -
DR MEROPS; S30.001; -
DR InterPro; IPR001205; -
DR InterPro; IPR001410; -
DR InterPro; IPR001456; -
DR InterPro; IPR001592; -
DR InterPro; IPR001650; -
DR InterPro; IPR001730; -
DR InterPro; IPR002540; -
DR Pfam; PF00270; DEAD; 1.
DR Pfam; PF00863; Peptidase_C4; 1.
DR Pfam; PF00851; Peptidase_C6; 1.
DR Pfam; PF01577; Poty_P1; 1.
DR Pfam; PF00767; Poty_coat; 1.
DR Pfam; PF00680; RNA_dep_RNA_pol; 1.
DR Pfam; PF00271; helicase_C; 1.
DR PRINTS; PR00966; NIAPOTYPASE.
KW Hydrolase; Transferase; Thiol protease; RNA-directed RNA polymerase;
KW Coat protein; Polyprotein; Covalent protein-RNA linkage; Helicase;
KW ATP-binding.
FT CHAIN 1 275 N-TERMINAL PROTEIN.
FT CHAIN 276 824 HELPER COMPONENT-PROTEINASE.
FT CHAIN 825 ? PROTEIN P3.
FT CHAIN ? 1157 6 KDA PROTEIN 1.
FT CHAIN 1158 1791 CYTOPLASMIC INCLUSION PROTEIN.
FT CHAIN 1792 1843 6 KDA PROTEIN 2.
FT CHAIN 1844 ? GENOME-LINKED PROTEIN.
FT CHAIN ? 2275 NUCLEAR INCLUSION PROTEIN A.
FT CHAIN 2276 2796 NUCLEAR INCLUSION PROTEIN B.
FT CHAIN 2797 3063 COAT PROTEIN.
FT BINDING 1907 1907 COVALENT LINKAGE OF VIRAL RNA (BY
SIMILARITY).
FT NP_BIND 1242 1249 ATP (POTENTIAL).
FT SEQUENCE 3063 AA; 347535 MW; 3EC79125DE33F1BB CRC64;

Query Match 34.5%; Score 50; DB 1; Length 3063;
Best Local Similarity 43.8%; Pred. No. 43;
Matches 7; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 9 FQSWDRNLGRGSSAP 24
| | | | | : | : |
Db 1192 FSDWDRQIQMGHTLP 1207

Search completed: October 9, 2001, 15:55:22
Job time: 197 sec
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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: October 9, 2001, 15:50:10 ; Search time 28.81 seconds  
(without alignments)  
444.197 Million cell updates/sec

Title: US-09-580-523-1  
Perfect score: 905  
Sequence: 1 MFQIPFEPSEQEDSSAER.....RVFSWDRNLGRGSSAPSQ 168

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_68.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	649	71.7	204	2 A55671	bad protein - mous
2	95	10.5	834	2 T42702	hypothetical prote
3	93.5	10.3	1729	2 T18396	erythrocyte membra
4	93	10.3	1300	2 T03166	probable immediate
5	92.5	10.2	336	2 T30757	hypothetical prote
6	91.5	10.1	2248	2 A35938	profilaggrin - hum
7	90	9.9	646	1 S15901	chromogranin B pre
8	90	9.9	2237	2 T45115	N-type calcium cha
9	90	9.9	2339	2 A42566	omega-conotoxin-se
10	89.5	9.9	449	1 A41520	chromogranin A pre
11	88.5	9.8	393	2 JC5614	RNB6 protein - rat
12	86.5	9.6	1077	2 A44067	serine-rich protei
13	86.5	9.6	1647	2 S45252	SNF2beta protein -
14	86.5	9.6	2715	2 T13049	eyelid - fruit fly
15	86	9.5	222	2 T43500	hypothetical prote
16	86	9.5	270	1 WJMS13	homeotic protein H
17	86	9.5	343	2 T05221	hypothetical prote
18	86	9.5	420	2 B38104	LFV floral meriste
19	85.5	9.4	254	2 A31488	filaggrin - mouse
20	85	9.4	337	2 T49431	endorepine related
21	85	9.4	380	2 S51797	vasodilator-stimul
22	85	9.4	1095	2 T00329	hypothetical prote
23	84.5	9.3	134	2 T54810	pHL ELF1 - human
24	84.5	9.3	380	2 T24786	hypothetical prote
25	84.5	9.3	1159	2 I38465	probable potassium
26	84.5	9.3	1323	2 T00037	hypothetical prote
27	84.5	9.3	1562	2 T29146	hypothetical prote
28	84	9.3	270	1 WJH01C	homeotic protein H
29	84	9.3	313	2 A28444	filaggrin precurs

30 84 9.3 381 2 S16506 hypothetical prote  
31 84 9.3 542 2 A44358 zixin - chicken  
32 84 9.3 886 2 S07132 hypothetical prote  
33 84 9.3 2023 2 T13154 polycomb protein e  
34 83.5 9.2 625 2 A34615 profilaggrin - rat  
35 83.5 9.2 672 2 T40333 tracheal colonizat  
36 83.5 9.2 1215 2 T32734 myosin-IA - Acanth  
37 83.5 9.2 1392 2 T51947 probable transcrip  
38 83.5 9.2 3759 2 A35085 trithorax protein  
39 83 9.2 263 1 E080A enkephalin e-12 pr  
40 83 9.2 743 2 T09173 EH domain protein  
41 83 9.2 760 2 T16726 hypothetical prote  
42 82.5 9.1 523 2 T36677 probable secretory  
43 82.5 9.1 558 2 A33616 heterogeneous ribo  
44 82.5 9.1 635 2 T09648 nucleolin homolog  
45 82.5 9.1 751 2 T02858 hypothetical prote

## ALIGNMENTS

RESULT 1

A55671  
bad protein - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 03-Mar-1995 #sequence\_revision 03-Mar-1995 #text\_change 05-Nov-1999  
C:Accession: A55671  
R:Yang, E.; Zha, J.; Jockel, J.; Boise, L.H.; Thompson, C.B.; Korsmeyer, S.J.  
Cell 80, 285-291, 1995  
A:Title: Bad, a heterodimeric partner for Bcl-x-L and Bcl-2, displaces Bax and promot  
A:Reference number: A55671; MUID:95136361  
A:Accession: A55671  
A:Status: preliminary; not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-204 <YAN>  
A:Cross-references: GB:L37296; NID:g639778; PIDN:AAA64465.1; PID:g639779  
C:Keywords: heterodimer

Query Match 71.7%; Score 649; DB 2; Length 204;  
Best Local Similarity 75.6%; Pred. No. 2.1e-45;  
Matches 127; Conservative 12; Mismatches 23; Indels 6; Gaps 3;

Oy 1 MFQIPFEPSEQEDSSAERGLGSPAGDGPSCGKHHKQAPGLLDASHOQEQPTSSSH 60  
Db 43 MFQIPFEPSEQEDASATDRGLGSLTEDQP---GPY--LAPGLLGSNIHQGRATNSH 97  
Oy 61 HGGAGAVEIRSRHSYPAGTDEDEGMGEPSFPRGRSRAPPNLWAAQRYGRELRRMSDE 120  
Db 98 HGGAGAMETRSRHSYPAGTDEDEGMGEELSPPFRGRSRAPPNLWAAQRYGRELRRMSDE 157  
Oy 121 FVDSFKKGLPRPKSAGTATOMRQSSSWTRVFQSWDRNLGRGSSAPSQ 168  
Db 158 FEGSF-KGLPRPKSAGTATOMRQSGWTRIIQSWWDRNLGRGSGSTPSQ 204

RESULT 2

T42702  
hypothetical protein DKFZp434F117.1 - human (fragment)  
N:Alternate names: hypothetical protein DKFZp434B239.1  
C:Species: Homo sapiens (man)  
C:Date: 11-Jan-2000 #sequence\_revision 11-Jan-2000 #text\_change 02-Jun-2000  
C:Accession: T42702; T46502  
R:Koehrer, K.; Beyer, A.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.  
submitted to the Protein Sequence Database, November 1999  
A:Reference number: Z22234  
A:Accession: T42702  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-834 <AAA>

A:Cross-references: EMBL:AL133028  
A:Experimental source: adult testis; clone DKFZp434F117  
R:Poustka, A.; Klein, M.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.

Db 1087 SVEKTPQQTWEAN 1100

C: Species: *Homo sapiens* (man)



Db	878	EPGAREERPRHSHSKEAAGPPPEARSERGPGPEGGRHHRR--GSPPEAAEREPRR	935
Qy	49	-SHQOEPTSSHHGGAGAV-EIRSHSSYP-AGTEDDEGMEGEPSPRGRSRAP	101
Db	936	RAHRHODPSKEC---AGAKGERRAHRHGPGRAGPEAES-GPEAPRRHRAHKAOP	987



Best Local Similarity 28.9%; Pred. No. 22;  
Matches 37; Conservative 17; Mismatches 47; Indels 27; Gaps 7;

QY 15 SSSEERGLGSPAGDPSG--SGKHRRQAFLGLWDASHOOEQPTSSSHHGAGAVEIRSR 72  
Db 678 SSSSSS---KKGDHPAAIISNVHHQ-----HSWYQSSTSYPRAL-----LTSP 721

QY 73 HSSYPACTEDDEGMGEPPFPGRGRSAPPNLMAAQRYGRELRRMSDFDYDSFKKGLRPR 132  
Db 722 KSPDVSGS--NGGGCKSPSHTGTKKRSPYSAGSPVDYGHSFYR--DPYA----GAGR 772

QY 133 KSAGTATQ 140  
Db 773 STGSASQ 780

RESULT 13  
S45252  
SNFbeta protein - human  
C:Species: Homo sapiens (man)  
C>Date: 10-Dec-1994 #sequence\_revision 17-Nov-1995 #text\_change 21-Jul-2000  
C:Accession: S45252  
R:Chiba, H.; Muramatsu, M.; Nomoto, A.; Kato, H.  
Nucleic Acids Res. 22, 1815-1820, 1994  
A:Title: Two human homologues of Saccharomyces cerevisiae SWI2/SNF2 and Drosophila br  
A:Reference number: S45251; MID:94268902  
A:Accession: S45252  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-1647 <CHI>  
A:Cross-references: GB:D26156; NID:g505087; PIDN:BAA05143.1; PID:g505088  
C:Superfamily: unassigned bromodomain proteins; bromodomain homology  
F:1485-1540/Domain: bromodomain homology <BRO>

Query Match 9.6%; Score 86.5; DB 2; Length 1647;  
Best Local Similarity 29.8%; Pred. No. 36;  
Matches 31; Conservative 9; Mismatches 55; Indels 9; Gaps 4;

QY 9 PSEQEDSSSAERGPGPAGDGPGSGSKH---RQAP-GLLWDASHOEOPTSSSHHGGA 64  
Db 30 PSPGPSPCSAHMMGPS---GPSAG--HPITQGPGYPQDNMHQMHRKPMESSHEKMG 84

QY 65 GAVEIRSRHSYPAGTEDDEGMGEPPFPGRGRSAPPNLMAAQ 108  
Db 85 SDPPRYNQMKGMGRSGGHAGMGPMPSPMDQHSGGYPSPLGGSE 128

RESULT 14  
TL13049  
eyelid - fruit fly (*Drosophila melanogaster*)  
C:Species: *Drosophila melanogaster*  
C>Date: 13-Aug-1999 #sequence\_revision 13-Aug-1999 #text\_change 17-Nov-2000  
C:Accession: TL13049  
R:Freiseman, J.E.; Luk, A.; Rubin, G.M.; Heberlein, U.  
submitted to the EMBL data Library, March 1998  
A:Reference number: Z17592  
A:Accession: TL13049  
A>Status: preliminary; translated from GB/EMBL/DDBBJ  
A:Molecule type: mRNA  
A:Residues: 1-2715 <TRE>  
A:Cross-references: EMBL:AF053091; NID:g2981220; PID:g2981221; PIDN:AAC06254.1  
C:Genetics:  
A:Gene: eld  
A:Cross-references: FlyBase:FBgn0003013  
C:Function:  
A>Description: could act as a transcription factor antagonistic to the Wg pathway  
C:Keywords: DNA binding

Query Match	9.6%	Score 86.5;	DB 2;	Length 2715;
Best Local Similarity	25.8%;	Pred. No. 61;		
Matches 41;	Conservative	11;	Mismatches 48;	Indels 59;
				Gaps 10;

Search completed: October 9, 2001, 15:54:03  
Job time: 233 sec





CC COMPLEXES, CONSISTING OF ALPHA-1, ALPHA-2, BETA AND DELTA SUBUNITS  
 CC IN A 1:1:1 RATIO. THE CHANNEL ACTIVITY IS DIRECTED BY THE PORE-  
 CC FORMING AND VOLTAGE-SENSITIVE ALPHA-1 SUBUNIT. IN MANY CASES, THIS  
 CC SUBUNIT IS SUFFICIENT TO GENERATE VOLTAGE-SENSITIVE CALCIUM  
 CC CHANNEL ACTIVITY. THE AUXILIARY SUBUNITS BETA AND ALPHA-2/DELTA  
 CC LINKED BY A DISULFIDE BRIDGE REGULATE THE CHANNEL ACTIVITY.

CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
 CC -1- ALTERNATIVE PRODUCTS: AT LEAST 7 ISOFORMS; BI-1/1A-2, BI-1(V1),  
 CC BI-1-GGCAG/1A-1 (SHOWN HERE), BI-1(V1)-GGCAG, BI-1(V2), BI-1(V2)-  
 CC GGCAG AND BI-1(V2.V3). ARE PRODUCED BY ALTERNATIVE SPLICING.  
 CC -1- TISSUE SPECIFICITY: BRAIN-SPECIFIC. MAINLY FOUND IN CEREBELLUM,  
 CC CEREBRAL CORTEX, THALAMUS AND HYPOTHALAMUS. NO EXPRESSION IN  
 CC HEART, KIDNEY, LIVER OR MUSCLE. PURKINJE CELLS CONTAIN  
 CC PREDOMINANTLY P-TYPE VSCC. THE Q-TYPE BEING A PROMINENT CALCIUM  
 CC CURRENT IN CEREBELLAR GRANULE CELLS.

CC -1- DOMAIN: EACH OF THE FOUR INTERNAL REPEATS CONTAINS FIVE  
 CC HYDROPHOBIC TRANSMEMBRANE SEGMENTS (S1, S2, S3, S5, S6) AND ONE  
 CC POSITIVELY CHARGED TRANSMEMBRANE SEGMENT (S4). S4 SEGMENTS  
 CC PROBABLY REPRESENT THE VOLTAGE-SENSOR AND ARE CHARACTERIZED BY A  
 CC SERIES OF POSITIVELY CHARGED AMINO ACIDS AT EVERY THIRD POSITION.  
 CC -1- POLYMORPHISM: THE POLY-GLN REGION OF CACNA1A IS POLYMORPHIC: 6 TO  
 CC 17 REPEATS IN THE NORMAL POPULATION, EXPANDED TO ABOUT 21 TO 30  
 CC REPEATS IN SPINOCEREBELLAR ATAXIA 6 (SCA6) PATIENTS. THERE SEEMS  
 CC TO BE A CORRELATION BETWEEN THE REPEAT NUMBER AND EARLIER ONSET OF  
 CC THE DISORDER.

CC -1- DISEASE: EXPANSION OF A CAG REPEAT IN THE CODING REGION OF CACNA1A  
 CC IS THE CAUSE OF ONE FORM OF SPINOCEREBELLAR ATAXIA 6 (SCA6). AN  
 CC AUTOSOMAL DOMINANT DISORDER CHARACTERIZED BY SLOWLY PROGRESSIVE  
 CC CEREBELLAR ATAXIA OF THE LIMBS AND GAIT, DYSPHAGIA, NYSTAGMUS,  
 CC AND MILD VIBRATORY AND PROPRIOCEPTIVE SENSORY LOSS. THESE SYMPTOMS  
 CC ARE PROBABLY EXPLAINED BY SEVERE LOSS OF CEREBELLAR PURKINJE  
 CC CELLS.

CC -1- DISEASE: DEFECTS IN CACNA1A ARE THE CAUSE OF FAMILIAL HEMIPLEGIC  
 CC MIGRAINE (FHM). ALSO KNOWN AS MIGRAINE FAMILIAL HEMIPLEGIC 1  
 CC (MHP1), EPISODIC ATAXIA TYPE 2 (EA-2), ACETAZOLAMIDE-RESPONSIVE  
 CC HEREDITARY PAROXYSMAL CEREBELLAR ATAXIA (APCA), AND POSSIBLY OTHER  
 CC COMMON TYPES OF MIGRAINES. FHM, A RARE AUTOSOMAL DOMINANT SUBTYPE  
 CC OF MIGRAINE WITH AURA, IS ASSOCIATED WITH ICTAL HEMIPARESIS AND,  
 CC IN SOME FAMILIES, PROGRESSIVE CEREBELLAR ATROPHY. EA-2 IS ANOTHER  
 CC AUTOSOMAL DOMINANT PAROXYSMAL CEREBELLAR DISEASE, CHARACTERIZED BY  
 CC ACETAZOLAMIDE-RESPONSIVE ATTACKS OF CEREBELLAR ATAXIA AND  
 CC MIGRAINE-LIKE SYMPTOMS, INTERICTAL NYSTAGMUS, AND CEREBELLAR  
 CC ATROPHY.

CC -1- SIMILARITY: BELONGS TO THE CALCIUM CHANNEL ALPHA-1 SUBUNITS  
 CC FAMILY.

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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC -----  
 CC EMBL: AF004884; AAB61613.1; -  
 CC EMBL: AF004883; AAB61612.1; -  
 CC EMBL: X9897; CAA68172.1; -  
 CC EMBL: Z80114; -; NOT\_ANNOTATED\_CDS.  
 CC EMBL: Z80115; -; NOT\_ANNOTATED\_CDS.  
 CC EMBL: U79666; AAB64179.1; -  
 CC EMBL: U79666; AAB49674.1; ALT\_INIT.  
 CC EMBL: U79664; AAB49675.1; ALT\_INIT.  
 CC EMBL: U79665; AAB49676.1; ALT\_INIT.  
 CC EMBL: U79667; AAB49677.1; ALT\_INIT.  
 CC EMBL: U79668; AAB49678.1; ALT\_INIT.  
 CC EMBL: S76537; AAB33068.1; -  
 CC EMBL: U06702; -; NOT\_ANNOTATED\_CDS.  
 CC MIM: 601011; -  
 CC MIM: 183086; -  
 CC MIM: 141500; -  
 CC InterPro: IPR000636; -  
 CC InterPro: IPR002077; -  
 CC Pfam: PF00520; Ion\_trans; 4.

DR PRINTS; PR00167; CACHANNEL.  
 KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;  
 KW Calcium channel; Glycoprotein; Repeat; Multigene family;  
 KW Calcium-binding; Phosphorylation; Alternative splicing; Polymorphism;  
 KW Disease mutation; triplet repeat expansion.  
 FT REPEAT 85 363 I.  
 FT REPEAT 473 717 II.  
 FT REPEAT 1231 1514 III.  
 FT REPEAT 1551 1814 IV.  
 FT DOMAIN 1 98 CYTOPLASMIC (POTENTIAL).  
 FT TRANSEM 99 117 S1 OF REPEAT I (POTENTIAL).  
 FT DOMAIN 118 135 EXTRACELLULAR (POTENTIAL).  
 FT TRANSEM 136 155 S2 OF REPEAT I (POTENTIAL).  
 FT DOMAIN 156 167 CYTOPLASMIC (POTENTIAL).  
 FT TRANSEM 168 185 S3 OF REPEAT I (POTENTIAL).  
 FT DOMAIN 186 190 EXTRACELLULAR (POTENTIAL).  
 FT TRANSEM 191 209 S4 OF REPEAT I (POTENTIAL).  
 FT DOMAIN 210 228 CYTOPLASMIC (POTENTIAL).  
 FT TRANSEM 229 248 S5 OF REPEAT I (POTENTIAL).  
 FT DOMAIN 249 335 EXTRACELLULAR (POTENTIAL).  
 FT TRANSEM 336 360 S6 OF REPEAT I (POTENTIAL).  
 FT DOMAIN 361 487 CYTOPLASMIC (POTENTIAL).  
 FT TRANSEM 488 506 S1 OF REPEAT II (POTENTIAL).  
 FT DOMAIN 507 521 EXTRACELLULAR (POTENTIAL).  
 FT TRANSEM 522 541 S2 OF REPEAT II (POTENTIAL).  
 FT DOMAIN 542 549 CYTOPLASMIC (POTENTIAL).  
 FT TRANSEM 550 568 S3 OF REPEAT II (POTENTIAL).  
 FT DOMAIN 569 578 EXTRACELLULAR (POTENTIAL).  
 FT TRANSEM 579 597 S4 OF REPEAT II (POTENTIAL).  
 FT DOMAIN 598 616 CYTOPLASMIC (POTENTIAL).  
 FT TRANSEM 617 636 S5 OF REPEAT II (POTENTIAL).  
 FT DOMAIN 637 689 EXTRACELLULAR (POTENTIAL).  
 FT TRANSEM 690 714 S6 OF REPEAT II (POTENTIAL).  
 FT DOMAIN 715 1242 CYTOPLASMIC (POTENTIAL).  
 FT TRANSEM 1243 1261 S1 OF REPEAT III (POTENTIAL).  
 FT DOMAIN 1262 1277 EXTRACELLULAR (POTENTIAL).  
 FT TRANSEM 1278 1297 S2 OF REPEAT III (POTENTIAL).  
 FT DOMAIN 1298 1309 CYTOPLASMIC (POTENTIAL).  
 FT TRANSEM 1310 1328 S3 OF REPEAT III (POTENTIAL).  
 FT DOMAIN 1329 1339 EXTRACELLULAR (POTENTIAL).  
 FT TRANSEM 1340 1358 S4 OF REPEAT III (POTENTIAL).  
 FT DOMAIN 1359 1377 CYTOPLASMIC (POTENTIAL).  
 FT TRANSEM 1378 1397 S5 OF REPEAT III (POTENTIAL).  
 FT DOMAIN 1398 1484 EXTRACELLULAR (POTENTIAL).  
 FT TRANSEM 1485 1509 S6 OF REPEAT III (POTENTIAL).  
 FT DOMAIN 1510 1564 CYTOPLASMIC (POTENTIAL).  
 FT TRANSEM 1565 1593 S1 OF REPEAT IV (POTENTIAL).  
 FT DOMAIN 1594 1598 EXTRACELLULAR (POTENTIAL).  
 FT TRANSEM 1599 1618 S2 OF REPEAT IV (POTENTIAL).  
 FT DOMAIN 1619 1626 CYTOPLASMIC (POTENTIAL).  
 FT TRANSEM 1627 1645 S3 OF REPEAT IV (POTENTIAL).  
 FT DOMAIN 1646 1652 EXTRACELLULAR (POTENTIAL).  
 FT TRANSEM 1653 1671 S4 OF REPEAT IV (POTENTIAL).

Query Match 10.7%; Score 97; DB 1; Length 2505;

Best Local Similarity 23.5%; Pred. No. 6.9;

Matches 48; Conservative 22; Mismatches 54; Indels 80; Gaps 11;

QY 5 PEPEPSEQD-----SSAERGLGSP---ACDGPSSGSKHROAP----- 42  
 Db 2313 PQQQQQQQQQQAVARPGRAATSGPRYPGPTAELAGDRPTGGTSGSRPMRVRPG 2372  
 QY 43 -----GLWDAS--HOEOPTSSHHGGAGAVEIRSHSSYPAGTDEDE--- 84  
 Db 2373 PARSESPRACHGGRWPASGPHVSEGGPPGPRHHG-----YRGSYDEADG 2419  
 QY 85 ---GMGEE-----PSPFR-----GRS-----RSAPPLWAAQRYGRLRMSDEFV 122  
 Db 2420 PGSGGGEEMAGAYDAPPVVRHASSGATGRSPRTPRASGPACASPSRHG----RRLPNGYY 2476  
 QY 123 DSPKKGLPRKSGAGTATQMROSSS 146  
 Db 2477 PA--HGLARPRGSGSRKGLHEPYS 2498

```
RESULT 4
CYAA_NEUCR STANDARD; PRT: 2300 AA.
AC Q01631;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE ADENYLATE CYCLASE (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (ADENYLATE
CYCLASE).
GN CR-1 OR NAC.
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RX MEDLINE=92000795; PubMed=1680356;
RA Kore-Eda S., Murayama T., Uno I.;
RT "Isolation and characterization of the adenylate cyclase structural
gene of Neurospora crassa."
RL Jpn. J. Genet. 66:317-334(1991).
CC -!- FUNCTION: PLAYS ESSENTIAL ROLES IN REGULATION OF CELLULAR
METABOLISM BY CATALYSING THE SYNTHESIS OF A SECOND MESSENGER,
CAMP.
CC -!- CATALYTIC ACTIVITY: ATP = 3',5'-CYCLIC AMP + PYROPHOSPHATE.
CC -!- SIMILARITY: BELONGS TO ADENYLATE CYCLASE CLASS-3 FAMILY.
CC -!- SIMILARITY: CONTAINS 23 LEUCINE-RICH REPEATS (LRR).
CC -!- SIMILARITY: CONTAINS A PP2C-LIKE DOMAIN.
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between the Swiss Institute of Bioinformatics and the EMBL outstation -
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modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
CC -----
DR EMBL; D00909; BAA00755.1; -
DR InterPro; IPR001611; -
DR InterPro; IPR001932; -
DR Pfam; PF00560; LRR; 13.
DR Pfam; PF00481; PP2C; 1.
DR PROSITE; P000019; LEURICHRPT.
DR PROSITE; P50125; GUANYLATE CYCLASES.2; 1.
KW Lyase; Repeat; Leucine-rich repeat; CAMP synthesis; Magnesium.
FT REPEAT 867 990
FT REPEAT 892 914
FT REPEAT 915 938
FT REPEAT 938 961
FT REPEAT 962 986
FT REPEAT 988 1008
FT REPEAT 1009 1031
FT REPEAT 1033 1055
FT REPEAT 1056 1079
FT REPEAT 1081 1097
FT REPEAT 1098 1120
FT REPEAT 1122 1142
FT REPEAT 1143 1165
FT REPEAT 1166 1188
FT REPEAT 1189 1211
FT REPEAT 1213 1234
FT REPEAT 1349 1369
FT REPEAT 1398 1420
FT REPEAT 1422 1445
FT REPEAT 1447 1469
FT REPEAT 1474 1497
FT REPEAT 1513 1538
FT REPEAT 1564 1829
FT DOMAIN 1830 2300
FT DOMAIN 49 52
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FT DOMAIN 204 221 POLY-GLN.
SQ SEQUENCE 2300 AA; 254752 MW; 52E79B90E6B17A7B CRC64;

Query Match 10.4%; Score 94.5; DB 1; Length 2300;
Best Local Similarity 24.2%; Pred. No. 9.7;
Matches 51; Conservative 23; Mismatches 74; Indels 63; Gaps 11;

QY 17 SAERGLGPSAGDGPSSGSKHHR---QAPGLLDASHOEOPTSSHH-----GGAGAV 67
Db 343 SSEISL-PPSHSGPMSTGKHSYSLPGS--GRSHDRNYSNATDHHPTSGSVSTV 399

QY 68 EIRSRHSS-----YPA-----GTEDECMGEEP-----SPFRGR---SRSA 100
Db 400 GGRDRDASPVPSPRPPTVPAPPEVVPFLYQEAADDIARYGEAPVTSLTGPDORRYIDSSQN 459

QY 101 PPNLWAAQRYGREL-----RMSDEYDFSKGLPRKPSAGT-----AT 139
Db 460 PPKTSSARSAGHSIVHLPGHHKHSNEDPRALKPSLSREDSAAFPARFNGSSMMGT 519

QY 140 QMRQSS---SWTRVFQSWDRNLGRGSSAPS 167
Db 520 RSRAQSPAPSWGTSRGLKANSISDGTSPA 550

RESULT 5
SG1_BOVIN STANDARD; PRT: 646 AA.
AC P23389; O02707;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE SECRETAGRANIN I PRECURSOR (SGI) (CHROMOGRANIN B) [CONTAINS: GAWK
PEPTIDE; SECRETOLYTIN].
GN CHGB.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Adrenal chromaffin;
RX MEDLINE=91223091; PubMed=2025642;
RA Bauer J.W., Fischer-Colbrie R.;
RT "Primary structure of bovine chromogranin B deduced from cDNA
sequence."
RL Biochim. Biophys. Acta 1089:124-126(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Adrenal medulla;
RX MEDLINE=97282588; PubMed=9136897;
RA Yoo S.H., Kang Y.K.;
RT "Identification of the secretory vesicle membrane binding region of
chromogranin B."
RL FEBS Lett. 406:259-262(1997).
RN [3]
RP SEQUENCE OF 21-646 FROM N.A.
RC TISSUE=Adrenal medulla;
RA Grandy D.K., Leduc R., Makam H., Flanagan T., Diliberto E.J.,
RA Thomas G., Civeilli O., Viveros O.H.;
RL Submitted (OCT-1990) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 634-646.
RC TISSUE=Adrenal chromaffin;
RX MEDLINE=95262699; PubMed=7744058;
RA Strud J.-M., Garcia-Sablone P., Lonning K., Taupenot L., Hubert P.,
RA van Dorsselaer A., Aunis D., Metz-Boutigue M.-H.;
RT "Processing of chromogranin B in bovine adrenal medulla.
RT Identification of secretolytin, the endogenous C-terminal fragment of
RT residues 614-626 with antibacterial activity."
RL Eur. J. Biochem. 229:356-368(1995).
RN [5]
```



RP CHARACTERIZATION OF SECRETOLYTIN.  
 RX MEDLINE-96184581; PubMed-8603705;  
 RA Strub J.M., Hubert P., Nullans G., Aunis D., Metz-Boutigue M.-H.;  
 RT "Antibacterial activity of secretolytin, a chromogranin B-derived  
 RL peptide (614-626), is correlated with peptide structure";  
 FEBS Lett. 379:273-278(1996).  
 CC -1- FUNCTION: SECRETOGROGANIN I IS A NEUROENDOCRINE SECRETORY GRANULE  
 CC PROTEIN, WHICH MAY BE THE PRECURSOR FOR OTHER BIOLOGICALLY ACTIVE  
 CC PEPTIDES. THE 16 PAIRS OF BASIC AA DISTRIBUTED THROUGHOUT ITS  
 CC SEQUENCE MAY BE USED AS PROTEOLYTIC CLEAVAGE SITES.  
 CC -1- FUNCTION: SECRETOLYTIN HAS ANTIBACTERIAL ACTIVITY.  
 CC -1- SUBCELLULAR LOCATION: NEUROENDOCRINE AND ENDOCRINE SECRETORY  
 CC GRANULES.  
 CC -1- PTM: O-GLYCOSYLATED (PROBABLE).  
 CC -1- SIMILARITY: BELONGS TO THE CHROMOGROGANIN / SECRETOGROGANIN PROTEIN  
 CC FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL; X55027; CAA38846.1; -;  
 DR EMBL; U88551; AAC48720.1; -;  
 DR EMBL; X55489; CAA39109.1; -;  
 DR PIR; S15901; S15901.  
 DR InterPro; IPR001819; -;  
 DR InterPro; IPR001990; -;  
 DR Pfam; PF01271; Granin; 1.  
 DR PRINTS; PR00659; CHROMOGROGANIN.  
 DR PROSITE; PS00422; GRANINS.1; 1.  
 DR PROSITE; PS00423; GRANINS.2; 1.  
 KW Sulfatation; Cleavage on pair of basic residues; Signal.  
 FT SIGNAL 1 20  
 FT CHAIN 21 646  
 FT PEPTIDE 418 484  
 FT PEPTIDE 634 646  
 FT DISULFID 36 57  
 FT MOD\_RES 158 158  
 FT MOD\_RES 315 315  
 FT CONFLICT 64 64  
 FT CONFLICT 70 70  
 FT CONFLICT 93 98  
 FT CONFLICT 181 181  
 FT CONFLICT 261 261  
 FT CONFLICT 386 386  
 FT CONFLICT 481 481  
 FT CONFLICT 597 597  
 SQ SEQUENCE 646 AA; 73339 MW; 420DB1178FD9E415 CRC64;  
 Query Match 9.9%; Score 90; DB 1; Length 646;  
 Best Local Similarity 28.7%; Pred. No. 5.7;  
 Matches 37; Conservative 16; Mismatches 52; Indels 24; Gaps 6;  
 Qy 9 PSEQEDSSAERGLGSPAGDPSGSKHH--RQAPGLLDASHQOEP--TSSSHHCGA 64  
 Db 246 PGESEDA-----SPEVDKRHSRPHRHGSRP-----DRSQEGNPLEESHVGTG 293  
 Qy 65 GAVETRSRHSYPAGTDECGMGPSPFRGRSRSAPNLAAQRYGR-----ELRRMS 118  
 Db 294 NSDEKARHPAHPFALESCAEGVEVR--RHSAQAQPGDLOGARFGGGRGEGHQAOLRRPS 351  
 Qy 119 DEFVDSFKK 127  
 Db 352 EESLEQENK 360  
 RESULT 6  
 CCAB\_HUMAN

CCAB\_HUMAN STANDARD; PRT; 2339 AA.  
 Q00975;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE VOLTAGE-DEPENDENT N-TYPE CALCIUM CHANNEL ALPHA-1B SUBUNIT (CALCIUM  
 DE CHANNEL, L TYPE, ALPHA-1 POLYPEPTIDE ISOFORM 5) (BRAIN CALCIUM CHANNEL  
 DE III) (BIIT).  
 GN CACNA1B OR CACNL1A5 OR CACH5.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORMS ALPHA-1B-1 AND ALPHA-1B-2).  
 RC TISSUE-Brain;  
 RX MEDLINE-92335886; PubMed-1321501;  
 RA Williams M.E., Brust P.F., Feldman D.H., Patthi S., Simerson S.,  
 RA Maroufi A., McCue A.F., Velicelebi G., Ellis S.B., Harpold M.M.;  
 RT "Structure and functional expression of an omega-conotoxin-sensitive  
 human N-type calcium channel";  
 RL Science 257:389-395(1992).  
 RN [2]  
 RP SEQUENCE OF 1-94 FROM N.A.  
 RC TISSUE-Lung fibroblast;  
 RA Kim D.S., Jung H.H., Park S.H., Chin H.;  
 RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: VOLTAGE-SENSITIVE CALCIUM CHANNELS (VSCC) MEDIATE THE  
 CC ENTRY OF CALCIUM IONS INTO EXCITABLE CELLS AND ARE ALSO INVOLVED  
 CC IN A VARIETY OF CALCIUM-DEPENDENT PROCESSES, INCLUDING MUSCLE  
 CC CONTRACTION, HORMONE OR NEUROTRANSMITTER RELEASE, GENE EXPRESSION,  
 CC CELL MOTILITY, CELL DIVISION AND CELL DEATH. THE ISOFORM ALPHA-1B  
 CC GIVES RISE TO N-TYPE CALCIUM CURRENTS. N-TYPE CALCIUM CHANNELS  
 CC BELONG TO THE "HIGH-VOLTAGE ACTIVATED" (HVA) GROUP AND ARE BLOCKED  
 CC BY OMEGA-CONOTOXIN-GVIA (OMEGA-CIX-GVIA) AND BY OMEGA-AGATOXIN-  
 CC IIIA (OMEGA-AGA-IIIA). THEY ARE HOWEVER INSENSITIVE TO  
 CC DIHYDROPYRIDINES (DHP), AND OMEGA-AGATOXIN-IVA (OMEGA-AGA-IVA).  
 CC CALCIUM CHANNELS CONTAINING ALPHA-1B SUBUNIT MAY PLAY A ROLE IN  
 CC DIRECTED MIGRATION OF IMMATURE NEURONS.  
 CC -1- SUBUNIT: VOLTAGE-DEPENDENT CALCIUM CHANNELS ARE MULTISUBUNIT  
 CC COMPLEXES, CONSISTING OF ALPHA-1, ALPHA-2, BETA AND DELTA SUBUNITS  
 CC IN A 1:1:1:1 RATIO. THE CHANNEL ACTIVITY IS DIRECTED BY THE PORE-  
 CC FORMING AND VOLTAGE-SENSITIVE ALPHA-1 SUBUNIT. IN MANY CASES, THIS  
 CC SUBUNIT IS SUFFICIENT TO GENERATE VOLTAGE-SENSITIVE CALCIUM  
 CC CHANNEL ACTIVITY. THE AUXILIARY SUBUNITS BETA AND ALPHA-2/DELTA  
 CC LINKED BY A DISULFIDE BRIDGE REGULATE THE CHANNEL ACTIVITY.  
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: ALPHA-1B-1 (SHOWN HERE) AND  
 CC ALPHA-1B-2; ARE PRODUCED BY ALTERNATIVE SPLICING.  
 CC -1- TISSUE SPECIFICITY: ALPHA-1B-1 AND ALPHA-1B-2 ARE EXPRESSED IN THE  
 CC CENTRAL NERVOUS SYSTEM, BUT NOT IN SKELETAL MUSCLE OR AORTA.  
 CC -1- DOMAIN: EACH OF THE FOUR INTERNAL REPEATS CONTAINS FIVE  
 CC HYDROPHOBIC TRANSMEMBRANE SEGMENTS (S1, S2, S3, S5, S6) AND ONE  
 CC POSITIVELY CHARGED TRANSMEMBRANE SEGMENT (S4). S4 SEGMENTS  
 CC PROBABLY REPRESENT THE VOLTAGE-SENSOR AND ARE CHARACTERIZED BY A  
 CC SERIES OF POSITIVELY CHARGED AMINO ACIDS AT EVERY THIRD POSITION.  
 CC -1- PTM: PHOSPHORYLATED IN VITRO BY CAM-KINASE II, CAPK, PKC AND CGPK  
 CC (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE CALCIUM CHANNEL ALPHA-1 SUBUNITS  
 CC FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL; M94172; AAA51897.1; -;  
 DR EMBL; M94173; AAA51898.1; -;  
 DR EMBL; U76666; AAC51138.1; -;  
 DR MIM; 601012; -;

DR InterPro: IPR000636; --  
 DR InterPro: IPR002077; --  
 DR Pfam: PF00520; ion\_trans: 4.  
 DR PRINTS: PR00167; CACHANNEL.  
 KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;  
 KW Calcium channel; Glycoprotein; Repeat; Multigene family;  
 KW Calcium-binding; Phosphorylation; ATP-binding; Alternative splicing.  
 FT REPEAT 82 359 I.  
 FT REPEAT 468 712 II.  
 FT REPEAT 1137 1419 III.  
 FT REPEAT 1456 1711 IV.  
 FT DOMAIN 1 95 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 96 114 S1 OF REPEAT I (POTENTIAL).  
 FT DOMAIN 115 132 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 133 152 S2 OF REPEAT I (POTENTIAL).  
 FT DOMAIN 153 163 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 164 183 S3 OF REPEAT I (POTENTIAL).  
 FT DOMAIN 184 187 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 188 206 S4 OF REPEAT I (POTENTIAL).  
 FT DOMAIN 207 225 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 226 245 S5 OF REPEAT I (POTENTIAL).  
 FT DOMAIN 246 331 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 332 356 S6 OF REPEAT I (POTENTIAL).  
 FT DOMAIN 357 482 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 483 501 S1 OF REPEAT II (POTENTIAL).  
 FT DOMAIN 502 516 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 517 536 S2 OF REPEAT II (POTENTIAL).  
 FT DOMAIN 537 544 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 545 562 S3 OF REPEAT II (POTENTIAL).  
 FT DOMAIN 563 573 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 574 592 S4 OF REPEAT II (POTENTIAL).  
 FT DOMAIN 593 611 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 612 631 S5 OF REPEAT II (POTENTIAL).  
 FT DOMAIN 632 684 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 685 709 S6 OF REPEAT II (POTENTIAL).  
 FT DOMAIN 710 1151 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 1152 1169 S1 OF REPEAT III (POTENTIAL).  
 FT DOMAIN 1170 1185 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 1186 1205 S2 OF REPEAT III (POTENTIAL).  
 FT DOMAIN 1206 1217 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 1218 1236 S3 OF REPEAT III (POTENTIAL).  
 FT DOMAIN 1237 1246 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 1247 1265 S4 OF REPEAT III (POTENTIAL).  
 FT DOMAIN 1266 1284 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 1285 1304 S5 OF REPEAT III (POTENTIAL).  
 FT DOMAIN 1305 1391 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 1392 1416 S6 OF REPEAT III (POTENTIAL).  
 FT DOMAIN 1417 1471 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 1472 1490 S1 OF REPEAT IV (POTENTIAL).  
 FT DOMAIN 1491 1505 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 1506 1525 S2 OF REPEAT IV (POTENTIAL).  
 FT DOMAIN 1526 1533 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 1534 1552 S3 OF REPEAT IV (POTENTIAL).  
 FT DOMAIN 1553 1563 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 1564 1601 S4 OF REPEAT IV (POTENTIAL).  
 FT DOMAIN 1583 1601 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 1602 1621 S5 OF REPEAT IV (POTENTIAL).  
 FT DOMAIN 1622 1663 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 1664 1708 S6 OF REPEAT IV (POTENTIAL).  
 FT DOMAIN 1709 2339 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 2050 2054 POLY-HIS.  
 FT DOMAIN 2118 2122 POLY-SER.  
 FT TRANSMEM 379 396 BINDING TO THE BETA SUBUNIT (BY SIMILARITY).  
 FT NP\_BIND 451 458 ATP (POTENTIAL).  
 FT SITE 314 314 CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).  
 FT SITE 663 663 CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).  
 FT SITE 1365 1365 CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).  
 FT SITE 1655 1655 CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).

FT MOD\_RES 1719 1719 PHOSPHORYLATION (BY CAPK) (POTENTIAL).  
 FT CALBIND 1737 1748 BY SIMILARITY.  
 FT CARBOHYD 256 256 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 1563 1563 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 1675 1675 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT VARSPLIC 2164 2339 GSGVNGSPLLSSTGASTPGRRGRLQPLTPRPSITYK  
 TANSPIHFAGATSLPAPSGRLSGSEHNALQORDPLS  
 QPLAPGRISGYLQRLDSEASVHALPDLTFEEAVAT  
 NSGRSRYSYSSLSQSHPRLRVNPGVHCTGLGSSGRAR  
 HSYHHPDQDQHC -> AGSAGVFNPVTCCTRETSPASMPPL  
 ALEALTLTWGSMVTVPLSTPLCLRTSLSRRLWPPTRAAP  
 PGLPTCPP (IN ISOFORM ALPHA-1B-2).  
 SQ SEQUENCE 2339 AA; 262494 MW; 17A45C6D1E76B39D CRC64;  
 Query Match 9.9%; Score 90; DB 1; Length 2339;  
 Best Local Similarity 30.8%; Pred. No. 21; Mismatches 35; Indels 30; Gaps 9;  
 Matches 36; Conservative 16;  
 QY 8 EPSEQED-----SSAERGLGFSPA-----GDGPSGSGKHHRQAPGLLWDA----- 48  
 DB 878 EPGAREPRPHRSKSKAAGPPEARSGRGPBGRRHRR--GSPEEAAREPRRH 935  
 QY 49 -SHQEQPTSSHHGGAGV-EIRSRHSYP-AGTEDDGMGEPS-PFRGRSRAP 101  
 DB 936 RAHRHODPSKEC-----AGAKGERARRHGRGPRAGPREAES-GEPPARRHRAKQAP 987  
 RESULT 7  
 IE18\_PRIVIF STANDARD; PRT; 1461 AA.  
 AC P11675;  
 DT 01-OCT-1989 (Rel. 12, Created)  
 DT 01-APR-1990 (Rel. 14, Last sequence update)  
 DT 01-FEB-1994 (Rel. 28, Last annotation update)  
 DE IMMEDIATE-EARLY PROTEIN IE180.  
 GN IE.  
 OS Pseudorabies virus (strain Indiana-Funkhauser / Becker) (PRV).  
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
 OC Alphaherpesvirinae; Varicellovirus.  
 OX NCBI\_TaxID=31523;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89315207; PubMed=2546124;  
 RT "DNA nucleotide sequence analysis of the immediate-early gene of  
 pseudorabies virus."  
 RL Nucleic Acids Res. 17:4637-4646(1989).  
 RN [2]  
 RP REVISIONS.  
 RA Cheung A.K.;  
 RL Submitted (NOV-1989) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: THIS IE PROTEIN IS A MULTIFUNCTIONAL PROTEIN CAPABLE  
 OF MIGRATING TO THE NUCLEUS, BINDING TO DNA, TRANS-ACTIVATING  
 OTHER VIRAL GENES, AND AUTOREGULATING ITS OWN SYNTHESIS.  
 CC -!- SUBCELLULAR LOCATION: NUCLEUS OF INFECTED CELLS.  
 CC -!- PTM: A LONG STRETCH OF SERINE RESIDUES MAY BE A MAJOR SITE OF  
 PHOSPHORYLATION.  
 CC -!- SIMILARITY: BELONGS TO THE ICP4/IE140/IE180 FAMILY.  
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 CC EMBL; X15120; CAA33214.1;  
 DR PIR; S04713; EDBEIF.  
 KW Early protein; Transcription regulation; Trans-acting factor;  
 KW DNA-binding; Phosphorylation; Nuclear protein.  
 FT DOMAIN 390 405 POLY-SER.







CC -!- SIMILARITY: CONTAINS 1 BROMODOMAIN.  
CC -!- SIMILARITY: BELONGS TO THE SNF2/RAD54 HELICASE FAMILY.  
CC -----  
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CC -----  
DR EMBL: U291175; AAB40977.1; -.  
DR EMBL: D26156; BAA05143.1; -.  
DR EMBL: AC006127; AAC97987.1; -.  
DR MIM: 603254; -.  
DR InterPro: IPR000330; -.  
DR InterPro: IPR001487; -.  
DR InterPro: IPR001650; -.  
DR Pfam: PF00176; SNF2\_N; 1.  
DR Pfam: PF00439; bromodomain; 1.  
DR Pfam: PF00271; helicase\_C; 1.  
DR PRINTS: PR00503; BROMODOMAIN.  
DR PROSITE: PS00633; BROMODOMAIN\_1; 1.  
DR PROSITE: PS0014; BROMODOMAIN\_2; 1.  
KW Transcription regulation; Nuclear protein; Activator; Bromodomain;  
KW ATP-binding; Helicase.  
FT DOMAIN 578 588 POLY-LYS.  
FT DOMAIN 663 672 POLY-GLU.  
FT NP\_BIND 779 786 ATP (POTENTIAL).  
FT SITE 881 884 DEGH BOX.  
FT DOMAIN 1360 1364 POLY-GLU.  
FT DOMAIN 1477 1547 BROMODOMAIN.  
FT DOMAIN 1571 1584 POLY-GLU.  
FT SEQUENCE 1647 AA; 184585 MW; 75785E7953277FID CRC64;

Query Match 9.6%; Score 86.5; DB 1; Length 1647;  
Best Local Similarity 29.8%; Pred. No. 27;  
Matches 31; Conservative 9; Mismatches 55; Indels 9; Gaps 4;  
QY 9 PSQEDSSAERGGLSPAGDGPSSGSKHH--RQAP-GLLWDASHQEQPTSSHHGGA 64  
DB 30 PSQPSFSGSAHSMWGSP---GPPSAG--HPITQGGYPQNMHQMHPMESHEKGM 84  
QY 65 GAVEIRSRHSSYPAGTDDDEGMGEPPSPFRGRSRAPPNNLWAAQ 108  
DB 85 SDDPRYNQKMGMRSGGHAGMGPPSPMDQHSQGYPSPLGGSE 128

RESULT 12  
ID HXA5\_MOUSE STANDARD; PRT; 270 AA.  
AC P09021;  
DT 01-NOV-1988 (Rel. 09, Created)  
DT 01-NOV-1988 (Rel. 09, Last sequence update)  
DT 01-OCT-1996 (Rel. 34, Last annotation update)  
DE HOMEBOX PROTEIN HOX-A5 (HOX-1.3) (M2).  
GN HOXA5 OR HOXA-5 OR HOX-1.3.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_Taxid=10090;  
RN [1]  
RN SEQUENCE FROM N.A.  
RX MEDLINE=88056292; PubMed=2890554;  
RA Odenwald W.F., Taylor C.F., Palmer-Hill F.J., Friedrich V. Jr.,  
RA Tani M., Lazzarini R.A.;  
RT "Expression of a homeo domain protein in noncontact-inhibited  
RL cultured cells and postmitotic neurons.";  
RL Genes Dev. 1:482-496(1987).  
RN [2]  
RN SEQUENCE FROM N.A.  
RX MEDLINE=88328807; PubMed=2901335;

RA Fibi M., Zink B., Kessel M., Colberg-Poley A.M., Labelt S.,  
RA Leirach H., Gruss P.;  
RT "Coding sequence and expression of the homeobox gene Hox 1.3.";  
RL Development 102:349-359(1988).  
RN [3]  
RN DNA-BINDING SPECIFICITY.  
RP MEDLINE=89232713; PubMed=2565857;  
RX Odenwald W.F., Garbern J., Arnheiter H., Tournier-Lasserre E.,  
RA Lazzarini R.A.;  
RT "The Hox-1.3 homeo box protein is a sequence-specific DNA-binding  
RT phosphoprotein.";  
RL Genes Dev. 3:158-172(1989).  
RN [4]  
RN CHARACTERIZATION.  
RP MEDLINE=96205869; PubMed=8635464;  
RX Zhao J.J., Lazzarini R.A., Pick L.;  
RT "Functional dissection of the mouse Hox-a5 gene.";  
RL EMBO J. 15:1313-1322(1996).  
CC -!- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF  
CC A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH  
CC SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.  
CC ALSO BINDS TO ITS OWN PROMOTER. BINDS SPECIFICALLY TO THE MOTIF:  
CC 5'-CYNNATTA[TC]Y-3'.  
CC -!- SUBCELLULAR LOCATION: NUCLEAR.  
CC -!- DEVELOPMENTAL STAGE: EXPRESSED DURING EMBRYOGENESIS AND IN ADULT  
CC KIDNEY.  
CC -!- SIMILARITY: BELONGS TO THE ANTP FAMILY OF HOMEBOX PROTEINS.  
CC -----  
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CC -----  
DR EMBL: M36604; AAA37838.1; -.  
DR EMBL: Y00208; CAA68364.1; -.  
DR EMBL: X16840; CAA34738.1; -.  
DR EMBL: M28021; AAA37837.1; -.  
DR PIR: S07812; WJMS13.  
DR HSP: P02833; ISAN.  
DR TRANSFAC: T00377; -.  
DR MGD; MGI:96177; Hoxa5.  
DR InterPro: IPR001356; -.  
DR InterPro: IPR001827; -.  
DR Pfam: PF00046; homeobox; 1.  
DR PRINTS: PR00024; HOMEBOX.  
DR PRINTS: PR00025; ANTENNAPEDIA.  
DR PROSITE: PS00027; HOMEBOX\_1; 1.  
DR PROSITE: PS00032; ANTENNAPEDIA; 1.  
DR PROSITE: PS00071; HOMEBOX\_2; 1.  
KW Homeobox; DNA-binding; Developmental protein; Nuclear protein;  
KW Transcription regulation.  
FT DOMAIN 176 181 ANTP-TYPE HEXAPEPTIDE.  
FT DNA\_BIND 195 254 HOMEBOX.  
FT SEQUENCE 270 AA; 29237 MW; DC4BDDA8FE62766E CRC64;

Query Match 9.5%; Score 86; DB 1; Length 270;  
Best Local Similarity 25.8%; Pred. No. 4.6;  
Matches 55; Conservative 13; Mismatches 63; Indels 82; Gaps 11;  
QY 10 SEQ-EDSSAERH-----LGPSPAGDGPSSGSKHHRQ-----APGLWDASHQ 51  
DB 31 SEQFRDSASMHSGRYGYNGMDLSVGRSGSGHFGSGERARSYAAGASAP-----AEPR 85  
QY 52 QEQTSS-----SHHG-----AGAVEIRSR-----72  
DB 86 YSQPATSTHSPDPPLPCSAVADSPGSDSHHGKNSLGNSSGASANAGSTHSSREGVGT 145  
QY 73 ----HSSYPAGTDEDEGMGEPPSPFRGRSRAPPNNLWAAQRYGRELPRMDEPVSFKKG 128





CC -!- PTM: MAJOR SUBSTRATE FOR CAMP-DEPENDENT (CAPK) AND CGMP-DEPENDENT  
CC PROTEIN KINASE (CGPK) IN PLATELETS.  
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CC -----  
DR EMBL; Z46389; CAA86523.1; -;  
DR EMBL; X98534; CAA67147.2; -;  
DR EMBL; X98533; CAA67147.2; JOINED.  
DR MIM; 601703; -;  
DR InterPro: IPR001960; -;  
DR Pfam: PF00568; WHI; 1; -;  
KW Phosphorylation; Actin-binding.  
FT DOMAIN 118 122 POLY-PRO.  
FT DOMAIN 170 186 POLY-PRO.  
FT DOMAIN 215 222 POLY-GLY.  
FT DOMAIN 259 262 POLY-GLY.  
FT DOMAIN 322 325 POLY-SER.  
FT MOD\_RES 137 157 PHOSPHORYLATION (BY CAPK AND CGPK).  
FT MOD\_RES 239 239 PHOSPHORYLATION (BY CAPK AND CGPK).  
FT MOD\_RES 278 278 PHOSPHORYLATION (BY CAPK AND CGPK).  
SQ SEQUENCE 380 AA; 39830 MW; 17634B8134DEBF59 CRC64;

Query Match 9.4%; Score 85; DB 1; Length 380;  
Best Local Similarity 24.9%; Pred. No. 7.8;  
Matches 43; Conservative 18; Mismatches 52; Indels 60; Gaps 10;  
QY 17 SAERGLG-----PSPAGDGPSSGKHHRQAPGL-----LWDASHQEQE---PTS- 57  
DB 195 AAHAGAGGPPPPAPPLPAAGPGGG---AGAPGLAAATAGAKLRVKQEAASGGPTAP 251  
QY 58 ---SSHHGGAGAVE-----IRSRHSSYPAG---TEDEGMGEEPS-----PPR 94  
DB 252 KAESGRSGGGLMEENAMLRARRKATQGEKTPKDESANQAEPEARVPAQSESVRPWE 311  
QY 95 GRSRAP-----PMLAAQYRGRELREMSDEFVDSFKKGLPRPK 133  
DB 312 KNSTTLPRMKSSSVTTSETQCTPSSSDYS-DLQVRKQELLEEVKKELQVR 363

RESULT 15  
ID Y553\_HUMAN STANDARD; PRT; 1089 AA.  
AC Q9UKJ3; O60300;  
DT 01-OCT-2000 (Rel. 40, Created)  
DT 01-OCT-2000 (Rel. 40, Last sequence update)  
DT 01-OCT-2000 (Rel. 40, Last annotation update)  
DE HYPOTHETICAL PROTEIN KIAA0553.  
GN KIAA0553.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RX MEDLINE=98290545; PubMed=9628581;  
RA Nagase T., Ishikawa K.-I., Miyajima N., Tanaka A., Kotani H.,  
RA Nomura N., Ohara O.;  
RT "Prediction of the coding sequences of unidentified human genes. IX.  
RT The complete sequences of 100 new cDNA clones from brain which can  
RT code for large proteins in vitro.";  
RL DNA Res.. 5:31-39(1998).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99408744; PubMed=10477733;  
RA Thornton M.A., Poncz M., Korosticishevsky M., Yakobson E., Usher S.,

RA Seligsohn U., Peretz H.;  
RT "The human platelet alphaIIb gene is not closely linked to its  
RT integrin partner beta3.";  
RL Blood 94:2039-2047(1999).  
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CC -----  
DR EMBL; AB011125; BAA25479.1; ALT\_INIT.  
DR EMBL; AF160252; AAF03681.1; -;  
KW Hypothetical protein.  
FT DOMAIN 263 266 POLY-LYS.  
FT DOMAIN 332 336 POLY-ARG.  
FT DOMAIN 359 362 POLY-GLY.  
FT DOMAIN 425 430 POLY-GLU.  
FT DOMAIN 456 461 POLY-SER.  
FT DOMAIN 971 977 POLY-ALA.  
FT DOMAIN 1059 1065 POLY-ALA.  
FT CONFLICT 207 207 K -> E (IN REF. 1).  
FT CONFLICT 267 267 E -> K (IN REF. 1).  
FT CONFLICT 278 278 P -> H (IN REF. 1).  
FT CONFLICT 846 846 G -> S (IN REF. 1).  
SQ SEQUENCE 1089 AA; 117999 MW; 4EF687F9D81A16A5 CRC64;

Query Match 9.4%; Score 85; DB 1; Length 1089;  
Best Local Similarity 19.9%; Pred. No. 23;  
Matches 58; Conservative 22; Mismatches 71; Indels 140; Gaps 11;  
QY 12 QEDSSA-----ERGLGPSPAGDGPSSGKHHRQAPGLLWDASHQEQE----- 55  
DB 304 KKNSSAPADSEKGPKEPPPGSGSPAPRRRAQ-----DQSQRSLPAEESSGKKDEG 359  
QY 56 ---TSSSHRG-----AGAV-EIRSRHSSYPAG----- 79  
DB 360 GGGSSQDHHGRKHKGELPPSCQRRAGTKRSRSHRSQSSGDESDSDASSHRLHQS 419  
QY 80 -----TEDEGMGEEPSFGRS-----RSAPPLNWAQR----- 109  
DB 420 PSQYSEEEEDSGSEHSRSRSGRRSHRSRYSYSSSDASSDQSCYSRQRSYSD 479  
QY 110 ----YGRELRMSDFVD----- 123  
DB 480 SYSDYSDRSRRHSHKSHDSDDYASSKHSRKHKYSDDDDYSLSCSRSRSHRTRE 539  
QY 124 -SFKKGLPRPKSAGTATQMRQSSSWTRVFSW-----WDRNLGRGSSAFSQ 168  
DB 540 RSRGRGRSSSSCSRSRKRKRSTTA--HSWQSRYSRDRSRSPSPSQ 588

Search completed: October 9, 2001, 15:55:20  
Job time: 195 sec





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OM protein - protein search, using sw model

Run on: October 9, 2001, 15:51:45 ; Search time 46.39 Seconds  
(without alignments)  
479.139 Million cell updates/sec

Title: US-09-580-523-1  
Perfect score: 905  
Sequence: 1 MFQIPEFEPSEQEDSSSAER.....RVFQSWDRNLGRSSAPSQ 168

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues  
Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL16:\*  
1: sp-archaea:\*  
2: sp-bacteria:\*  
3: sp-fungi:\*  
4: sp-human:\*  
5: sp-invertebrate:\*  
6: sp-mammal:\*  
7: sp-mhc:\*  
8: sp-organelle:\*  
9: sp-phage:\*  
10: sp-plant:\*  
11: sp-rodent:\*  
12: sp-unclassified:\*  
13: sp-vertebrate:\*  
14: sp-virus:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	905	100.0	168	014803	014803 homo sapien
2	636.5	70.3	205	11	035147
3	636.5	70.3	205	11	070256
4	446	49.3	220	11	09JHX1
5	207.5	22.9	95	13	09I9N2
6	100	11.0	608	14	09QSK9
7	98.5	10.9	569	13	09DF20
8	98	10.8	272	4	09NS37
9	98	10.8	355	2	09NDL8
10	97.5	10.8	867	10	09FV26
11	97	10.7	1146	5	09N8Q9
12	96.5	10.7	980	4	095387
13	96.5	10.7	2506	4	09NS88
14	95.5	10.6	923	5	09NKN4
15	95	10.5	622	4	09NTE2
16	95	10.5	701	4	09NTP8
17	95	10.5	803	4	09ULK9
18	94	10.4	474	5	09VA96
19	93.5	10.3	549	4	09H0B9

20	93.5	10.3	1203	4	Q9UPQ9	Q9upq9 homo sapien
21	93.5	10.3	1729	5	Q25734	Q25734 plasmodium
22	93	10.3	1300	14	Q36421	Q36421 alcelaphine
23	93	10.3	2472	4	Q9NS89	Q9ns89 homo sapien
24	92.5	10.2	336	14	Q98321	Q98321 molluscum c
25	92.5	10.2	1082	11	Q9EP02	Q9epu2 rattus norv
26	92.5	10.2	1398	11	Q09000	Q09000 mus musculu
27	92	10.2	670	5	Q9NEL2	Q9nel2 caenorhabdi
28	91.5	10.1	651	4	Q9NXI9	Q9nxi9 homo sapien
29	91.5	10.1	845	4	Q9HAU3	Q9hau3 homo sapien
30	91.5	10.1	990	4	Q15206	Q15206 homo sapien
31	91.5	10.1	1218	4	Q05331	Q05331 homo sapien
32	90.5	10.0	662	5	Q9VW76	Q9vw76 drosophila
33	90.5	10.0	947	10	Q9LWJ9	Q9lwj9 oryza sativ
34	90	9.9	476	10	Q9FFH8	Q9ffh8 arabidopsis
35	90	9.9	903	4	Q9UPX1	Q9upx1 homo sapien
36	89.5	9.9	845	4	Q9HBB5	Q9hbb5 macroopus ru
37	89	9.8	410	6	Q97645	Q97645 macroopus ru
38	89	9.8	414	11	Q9ERU8	Q9eru8 mus musculu
39	89	9.8	462	6	Q97643	Q97643 lama glama
40	89	9.8	735	11	Q9JIG4	Q9jig4 mus musculu
41	88.5	9.8	393	11	Q08719	Q08719 rattus norv
42	88.5	9.8	393	11	P70429	P70429 mus musculu
43	88.5	9.8	510	5	Q9VAI8	Q9vai8 drosophila
44	88.5	9.8	658	11	Q9JL61	Q9jl61 mus musculu
45	88.5	9.8	667	14	Q9PY84	Q9py84 rat cytomeg

ALIGNMENTS

RESULT 1  
O14803 PRELIMINARY; PRT; 168 AA.  
AC O14803;  
DT 01-JAN-1998 (TREMBLrel. 05, Created)  
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
DE 01-NOV-1998 (TREMBLrel. 08, Last annotation update)  
DE BCL-X/BCL-2 BINDING PROTEIN (FRAGMENT).  
GN BAD.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=97083574; PubMed=8929532;  
RA Wang H.G., Rapp U.R., Reed J.C.;  
RT "Bcl-2 targets the protein kinase Raf-1 to mitochondria.";  
RL Cell 87:629-638(1996).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Takayama S., Reed J.C.;  
RL Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RA Ottillie S., Diaz J.L., Horne W., Chang J., Wang Y., Wilson G.,  
RA Weeks S., McConnell M., Chang S., Fritz L.C., Oltersdorf T.;  
RL J. Biol. Chem. 0:0-0(1997).  
DR EMBL; AF021792; AAB72092.1; -;  
DR EMBL; AF031523; AAB88124.1; -;  
FT NON\_TER 1  
SQ SEQUENCE 168 AA; 18392 MW; 69FD8D27DDEE3241 CRC64;

Query Match 100.0%; Score 905; DB 4; Length 168;  
Best Local Similarity 100.0%; Pred. No. 5e-76;  
Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MFQIPEFEPSEQEDSSSAERGLGSPAGDPSGSGKHHRQAPGLLWDASHQEQPTSSSH 60  
DB 1 MFQIPEFEPSEQEDSSSAERGLGSPAGDPSGSGKHHRQAPGLLWDASHQEQPTSSSH 60

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QY 61 HGGAGAVEIRSRHSSYPAGTDEDEGMGEESPFRGRSRAPPNLWAAQRYGRELRRMSD 120
|||||
Db 61 HGGAGAVEIRSRHSSYPAGTDEDEGMGEESPFRGRSRAPPNLWAAQRYGRELRRMSD 120
|||||
QY 121 FVDSFKKGLPRPKSAGTATQMRQSSWTRVFQSWDRNLGRGSSAPSQ 168
|||||
Db 121 FVDSFKKGLPRPKSAGTATQMRQSSWTRVFQSWDRNLGRGSSAPSQ 168
|||||

RESULT 2
O35147 PRELIMINARY; PRT; 205 AA.
AC O35147;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE BCL-2 ASSOCIATED DEATH PROMOTER.
GN BAD.
OS Rattus norvegicus (Rat.).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=OVARY;
RX MEDLINE=98034386; PubMed=9369453;
RA Hsu S.Y., Hsueh A.J.W.;
RT "Interference of BAD (Bcl-xL/Bcl-2-associated death promoter)-induced
RT apoptosis in mammalian cells by 14-3-3 isoforms and P11.";
RL Mol. Endocrinol. 11:1858-1867(1997).
DR EMBL; AF003523; AAC53374.1; -.
SQ SEQUENCE 205 AA; 22468 MW; 04DD3EBA03B11168 CRC64;

Query Match 70.3%; Score 636.5; DB 11; Length 205;
Best Local Similarity 75.1%; Pred. No. 3.1e-51;
Matches 127; Conservative 11; Mismatches 24; Indels 7; Gaps 4;

QY 1 MFOIPEFEPSEQEDSSAERGLGSPAGDGPSSGKHHRQAPGLLWDASHQOE-QPTSSS 59
|||||
Db 43 MFOIPEFEPSEQEDASTDRGLGSLTEDQP---GPY--LAPGLLSIVQQPGQAANN 97
|||||

QY 60 HGGAGAVEIRSRHSSYPAGTDEDEGMGEESPFRGRSRAPPNLWAAQRYGRELRRMSD 119
|||||
Db 98 HGGAGTMTETRSRHSYPAGTDEDEGMGEELSPFRGRSRAPPNLWAAQRYGRELRRMSD 157
|||||

QY 120 EFVDSFKKGLPRPKSAGTATQMRQSSWTRVFQSWDRNLGRGSSAPSQ 168
|||||
Db 158 EFEGSP-KGLPRPKSAGTATQMRQSSWTRIIQSWDRNLGKGGSTPSQ 205
|||||

RESULT 4
Q9JHX1 PRELIMINARY; PRT; 220 AA.
AC Q9JHX1;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE BCL-2 ASSOCIATED DEATH AGONIST BETA.
GN BAD-BETA.
OS Rattus norvegicus (Rat.).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Hamer S., Arumne U., Li-Ying Y., Sun Y.-F., Saarma M., Lindholm D.;
RT "Functional characterization of two splice variants of rat bad and
RT their interaction with bcl-w in sympathetic neurons.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF279911; AAF91428.1; -.
SQ SEQUENCE 220 AA; 24278 MW; E27BCD7C969E90F CRC64;

Query Match 49.3%; Score 446; DB 11; Length 220;
Best Local Similarity 72.4%; Pred. No. 1.2e-33;
Matches 92; Conservative 8; Mismatches 21; Indels 6; Gaps 3;

QY 1 MFOIPEFEPSEQEDSSAERGLGSPAGDGPSSGKHHRQAPGLLWDASHQOE-QPTSSS 59
|||||
Db 43 MFOIPEFEPSEQEDASTDRGLGSLTEDQP---GPY--LAPGLLSIVQQPGQAANN 97
|||||

QY 60 HGGAGAVEIRSRHSSYPAGTDEDEGMGEESPFRGRSRAPPNLWAAQRYGRELRRMSD 119
|||||
Db 98 HGGAGTMTETRSRHSYPAGTDEDEGMGEELSPFRGRSRAPPNLWAAQRYGRELRRMSD 157
|||||

QY 120 EFVDSFK 126
Db 158 EFEGSPK 164
|||||

RESULT 5
Q9I9N2 PRELIMINARY; PRT; 95 AA.
AC Q9I9N2;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
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DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
DE 01-MAR-2001 (TREMBlrel. 16, Last annotation update)  
DE BAD (FRAGMENT).  
GN BAD.  
OS Brachydanio rerio (Zebrafish) (Zebra danio).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;  
OC Cypriniformes; Cyprinidae; Rasbora; Danio.  
OX NCBI\_TaxID=7955;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20373792; PubMed=10917738;  
RA Inohara N., Nunez G.;  
RT "Genes with Homology to Mammalian Apoptosis Regulators Identified in  
RT Zebrafish."  
RL Cell Death Differ. 7:509-510(2000).  
DR EMBL; AF231017; AAF66962.1; -  
FT NON\_TER  
SQ SEQUENCE 95 AA; 10804 MW; 77F5CDE879E69FF7 CRC64;

Query Match 22.9%; Score 207.5; DB 13; Length 95;  
Best Local Similarity 50.0%; Pred. No. 4.3e-12;  
Matches 45; Conservative 10; Mismatches 24; Indels 11; Gaps 3;  
QY 83 DEGMGEPP-----SPFRGRSRAPPNLMWAQRYGRELRRMSDEFVDSFKGLPRPKSAGTA 138  
D 13 ETGVAEDPHMLGDPPRRSRAPPALWAAKKYQQLRRMSDE---FDKMKRYKSAGTA 68  
QY 139 TOMROSSWTRVFQSWDRNLGRSSAPSQ 168  
D 69 ROMSQSPSWLAF-----WSHKESDAESRPAE 95

RESULT 6  
Q905K9  
ID Q905K9 PRELIMINARY; PRT; 608 AA.  
AC Q905K9;  
DT 01-MAY-2000 (TREMBlrel. 13, Created)  
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)  
DE NTR.  
OS Herpesvirus papio.  
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
OC Gammaherpesvirinae; Lymphocryptovirus.  
OX NCBI\_TaxID=10394;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BABOON LYMPHOCRYPTOVIRUS BA65;  
RA Zong J.-C., Ryan J., Ling P.D., Loeb D.D., Pagano J.S., Hayward S.D.,  
RA Hayward G.S.;  
RL Submitted (DSC-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF200364; AAF23950.1; -  
SQ SEQUENCE 608 AA; 60458 MW; 4BF82ACB0A029627 CRC64;

Query Match 11.0%; Score 100; DB 14; Length 608;  
Best Local Similarity 33.3%; Pred. No. 0.23; Indels 12; Gaps 3;  
Matches 37; Conservative 7; Mismatches 7;  
QY 9 PSEQDSSSAERGLGSPAGDGPSPGSGKHHQAPGLLWDASHQOQPTSSSHHG---GA 64  
D 502 PTERRRGSAQRGHPGPGAGQPSGPTGGHPAAGPACGPRSPRTERRRGSQRGHPPGA 561  
QY 65 GAVETRSHSSYPAGTDEDEGMGEPPFRGRSRAPPNLMWAQRYGREL 115  
D 562 G-----QPSGPTGGHPAAGPACGPPNPERGSGPAPP---AATRLPLEPR 604

RESULT 7  
Q9DF20  
ID Q9DF20 PRELIMINARY; PRT; 569 AA.  
AC Q9DF20;

DT 01-MAR-2001 (TREMBlrel. 16, Created)  
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)  
DE KH DOMAIN CONTAINING RNA-BINDING PROTEIN FMRL.  
OS Brachydanio rerio (Zebrafish) (Zebra danio).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;  
OC Cypriniformes; Cyprinidae; Rasbora; Danio.  
OX NCBI\_TaxID=7955;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20501263; PubMed=11046149;  
RA Wan L., Dockendorff T.C., Jongens T.A., Dreyfuss G.;  
RT "Characterization of dFMRL, a Drosophila melanogaster Homolog of the  
RT Fragile X Mental Retardation Protein."  
RL Mol. Cell. Biol. 20:8536-8547(2000).  
DR EMBL; AF305882; AAG22046.1; -  
SQ SEQUENCE 569 AA; 63906 MW; 2E66A0689F7EDFB5 CRC64;

Query Match 10.9%; Score 98.5; DB 13; Length 569;  
Best Local Similarity 32.3%; Pred. No. 0.29;  
Matches 31; Conservative 8; Mismatches 42; Indels 15; Gaps 3;  
QY 11 EQEDSSSAERGLGSPAGDGPSPGSGKHHQAP-----GLLWDASHQOQPTSSSHHGAGA 66  
D 391 EKESFMADNMGPSRGGKPFGRGRRGPTLASGTNSEASNAE---TESDH----- 442  
QY 67 VEIRSRHSSYPAGTDEDEGMGEPPFRGRSRAPP 102  
D 443 ---RDELSWLSLAPTDEESMGYPKRAPDGRKRGGGP 475

RESULT 8  
Q9NS37  
ID Q9NS37 PRELIMINARY; PRT; 272 AA.  
AC Q9NS37;  
DT 01-OCT-2000 (TREMBlrel. 15, Created)  
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)  
DE HCF-BINDING TRANSCRIPTION FACTOR ZHANGFEI.  
GN ZF.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20330366; PubMed=10871379;  
RA Lu R., Misra V.;  
RT "Zhangfei, a second cellular protein interacts with herpes simplex  
RT virus accessory factor HCF in a manner similar to Luman and VP16."  
RL Nucleic Acids Res. 28:2446-2454(2000).  
DR EMBL; AF039942; AAD28325.1; -  
DR InterPro; IPR001871; -  
DR Pfam; PF00170; bZIP; 1.  
DR SMART; SM00338; BRLZ; 1.  
SQ SEQUENCE 272 AA; 28859 MW; B1F94B438F0702BF CRC64;

Query Match 10.8%; Score 98; DB 4; Length 272;  
Best Local Similarity 28.2%; Pred. No. 0.15;  
Matches 40; Conservative 13; Mismatches 69; Indels 20; Gaps 4;  
QY 10 SEQEDSSSAERGLGSPAGDGPSPGSGKHHQAPGLLWDASHQOQPTSSSHHGAGAVEI 69  
D 92 SSSSDSGSAEKRRRKSPPGGGGGGSGNDNQA-----ATKSPRKAATAAARL 138  
QY 70 -RSRHSYPAGTDEDD-EGMGEPPFRGRSRAPPNLMWAQRYGRELRRMSDEFVDSFK 127  
D 139 NLRKKKYYMGLSESRVGLAAEQELRAENRELGRKRVQALQESRYLRA-----VLANET 193  
QY 128 GLPRPKSAGTATQMRQSSSWTR 149

OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
OC Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae;

RESULT	13
Q9NS88	
ID	Q9NS88
AC	PRELIMINARY; PRT; 2506 AA.
DT	
DC	Q9NS88;
DT	01-OCT-2000 (TREMBLrel. 15, Created)
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT	01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE	ALPHA-VOLTAGE-DEPENDENT CALCIUM CHANNEL.
GN	CACNA1A.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Qy 10 SEQEDSSAERGLGSPAGDPSGSGKHHRQAPGLLDASHQEQEQTSSSHHGGGAVEI 69

Db 802 AEQRTNTDDR-----SPSAGGPASADVEHRSASQPPQPHS-----HAGGSALV 845  
QY 70 RSRHSYPAGTEDEGMGEPPSPFRGR--SRSAAPPNLWAAQRYGRELRRMSDEFVDSFKK 127  
Db 846 SNSHNGVQAAA---SGTGRMSAANSRGVNGSVPP-----RNGRRRAPLAAILDTLTA 896  
QY 128 GLPRP 132  
Db 897 GPPQP 901

## RESULT 15

Q9NTE2  
ID Q9NTE2 PRELIMINARY; PRT; 622 AA.  
AC Q9NTE2;  
DT 01-OCT-2000 (TremBLrel. 15, Created)  
DT 01-OCT-2000 (TremBLrel. 15, Last sequence update)  
DT 01-OCT-2000 (TremBLrel. 15, Last annotation update)  
DE HYPOTHETICAL 67.3 KDA PROTEIN (FRAGMENT).  
GN DKFZP434B239.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=TESTIS;  
RA Poustka A., Klein M., Mewes H.W., Gassenhuber J., Wiemann S.;  
RL Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; ALI37336; CAB70699.1; -  
KW Hypothetical protein.  
FT NON\_TER 1  
SQ SEQUENCE 622 AA; 67337 MW; 11D6CDF0E2D06082 CRC64;

Query Match 10.5%; Score 95; DB 4; Length 622;  
Best Local Similarity 27.6%; Pred. No. 0.67;  
Matches 50; Conservative 17; Mismatches 50; Indels 64; Gaps 11;  
QY 13 EDSSSAERGLGSPSP--AGDPSGSGKHHRQAPGLLWDASHQEQPTSSSHHGAGAVEI 69  
Db 14 EEKKHAEAPAGENPPRPGDARAGSK-----AKPQESPSSAS--ALAEWASI 60  
QY 70 RSR-----HSSYPAGTEDDE-GMGEPPSP-----FRGRSRAPP-----NLWAAQRY--- 110  
Db 61 RSRILKNAESDPRSSERDQLRPGDESTPRGRCDSRGNQRKTPPVNAKFSIMPWQKFSDG 120  
QY 111 GRELRMSDEFVDSFKK-----GLPRPKSAGTATQMRQSSSWTRVFQSWWDRNLGR 161  
Db 121 GTETSKQSTE-AESIRKRPMLGPSEETAPQPPAGV-----RELGK 160  
QY 162 G 162  
Db 161 G 161

Search completed: October 9, 2001, 15:54:56  
Job time: 191 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 9, 2001, 15:50:04 ; Search time 44.37 Seconds  
(without alignments)  
229.543 Million cell updates/sec

Title: US-09-580-523-1

Perfect score: 905

Sequence: 1 MFQIEFEPSEQEDSSAER.....RVFSWDRNLGRGSSAPSQ 168

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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22: /SID58/gcgdata/geneseq/geneseq/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	905	100.0	168	19	AAW55779 Human Bcl-xL/Bcl-2
2	905	100.0	168	21	AA13512 Human cell prolif
3	905	100.0	168	22	AA13512 Human BAD mutant a
4	905	100.0	168	22	AA13512 Human BAD mutant a
5	751	83.0	166	18	AAW32476 BCC6 protein for r
6	649	71.7	162	22	AA170370 Shorter murine BAD
7	649	71.7	204	17	AA195168 bcl-x(L)/bcl-2 ass
8	649	71.7	204	19	AAW61315 Murine Bcl-xL/BCL-
9	649	71.7	204	19	AAW58832 Murine BAD protein
10	649	71.7	204	22	AA170369 Longer murine BAD
11	646	71.4	204	19	AAW61317 Mutant BCL-XL/BCL-

12	643	71.0	204	19	AAW61316	Mutant BCL-XL/BCL-
13	643	71.0	204	19	AAW61318	Mutant BCL-XL/BCL-
14	314	34.7	59	19	AAW61319	Mutant BCL-XL/BCL-
15	314	34.7	59	19	AAW61320	Mutant BCL-XL/BCL-
16	311	34.4	59	19	AAW61321	Mutant BCL-XL/BCL-
17	308	34.0	59	19	AAW61322	Mutant BCL-XL/BCL-
18	159	17.6	56	21	AAW62251	Human secreted pro
19	133	14.7	26	21	AAW96321	Mammalian Bad Bcl-
20	133	14.7	26	22	AAW70371	BAD BH3 consensus
21	120.5	13.3	27	21	AAW37003	Bcl2 polypeptide B
22	116	12.8	23	17	AAW95166	bcl-x(L)/bcl-2 ass
23	114	12.6	26	21	AAW37001	Bcl2 polypeptide B
24	114	12.6	26	21	AAW37002	Bcl2 polypeptide B
25	114	12.6	27	21	AAW37055	Bcl2 polypeptide B
26	114	12.6	28	21	AAW37055	Bcl2 polypeptide B
27	97	10.7	2510	16	AAW71007	Human neuronal cal
28	97	10.7	2510	21	AAW10579	Human calcium chan
29	96.5	10.7	1182	20	AAW33496	Human SCA6 protein
30	94	10.4	1931	13	AAW27649	Human calcium chan
31	93.5	10.3	395	21	AAW91951	Human cytoskeleton
32	93.5	10.3	549	21	AAW84901	A human proliferat
33	93.5	10.3	1726	17	AAW00385	Truncated Plasmodi
34	92.5	10.2	1447	20	AAW81029	Murine PCIP protei
35	90	9.9	397	21	AAW45048	Arabidopsis thalia
36	90	9.9	420	21	AAW45047	Arabidopsis thalia
37	90	9.9	434	17	AAW96420	Peptide fragment o
38	90	9.9	434	21	AAW12821	Human N-type calci
39	90	9.9	476	21	AAW45046	Arabidopsis thalia
40	90	9.9	2237	16	AAW71006	Human neuronal cal
41	90	9.9	2237	19	AAW63142	Human calcium chan
42	90	9.9	2237	21	AAW10573	Human calcium chan
43	90	9.9	2337	19	AAW37878	Human calcium chan
44	90	9.9	2339	14	AAW33549	Sequence of the al
45	90	9.9	2339	16	AAW71005	Human neuronal cal

#### ALIGNMENTS

RESULT 1

AAW55779 AAW55779 standard; Protein; 168 AA.

XX AC AAW55779;

XX DT 17-JUL-1998 (first entry)

XX DE Human Bcl-xL/Bcl-2 associated death promoting polypeptide.

XX KW Human; Bcl-xL/Bcl-2 associated death promoting polypeptide; Bad;

XX KW programmed cell death; apoptosis.

XX OS Homo sapiens.

XX PN WO9812328-A2.

XX PD 26-MAR-1998.

XX PF 18-SEP-1997; 97WO-US16991.

XX PR 20-SEP-1996; 96US-0717123.

XX PA (IDUN-) IDUN PHARM INC.

XX PI Horne WA, Oltersdorf T;

XX DR BCC6 protein for r

XX DR N-PSDB; AAW25877.

XX PT Bad gene mediating apoptosis - used to develop products for treating

XX PT e.g. neurodegenerative disease, cancers or autoimmune disease

XX PS Claim 8; Fig 1; 41pp; English.

XX The present sequence is the human Bcl-XL/Bcl-2 associated  
 CC death promoting polypeptide, Bad, the binding of which to Bcl-XL  
 CC results in the induction of programmed cell death, i.e. apoptosis.  
 CC Bad can be used in screening assays for compounds to treat or  
 CC prevent diseases characterised by apoptotic cell death, such as  
 CC neurodegenerative disorders, e.g. Alzheimer's and Parkinson's  
 CC disease, amyotrophic lateral sclerosis, retinitis pigmentosa and  
 CC cerebellar degeneration, and myelodysplastic syndromes, e.g.  
 CC aplastic anaemia and ischaemic injury including myocardial  
 CC infarction, stroke and reperfusion injury. Assays can also be  
 CC used to obtain apoptosis enhancing compounds to treat or prevent  
 CC diseases characterised by the loss of apoptotic cell death, such as  
 CC cancers, e.g. lymphoma and hormone dependent tumours, autoimmune  
 CC diseases, e.g. systemic lupus erythematosus and immune-mediated  
 CC glomerulonephritis and viral infections, e.g. herpesvirus,  
 CC poxvirus or adenovirus infection. Bad can also be used for  
 CC detection and diagnosis.  
 XX  
 SQ Sequence 168 AA;

Query Match 100.0%; Score 905; DB 19; Length 168;  
 Best Local Similarity 100.0%; Pred. No. 6.4e-88;  
 Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFQIPEFEPSEQEDSSAERGLGSPAGDGPSCGSKHHRQAPGLLDASHQEQPTSSSH 60  
 |||||  
 DB 1 mqiipfefseqedssaaerglgpsagdgpsgskhhrqapglldashqeqptsssh 60  
 |||||

QY 61 HGGAGAVEIRSHSSYPAGTDEDEGMGEFPSPFRGRSRAPPNLMAAQRYGRELRRMSDE 120  
 |||||  
 DB 61 hggagaveirshssypagteddegmggeepsfgrsrsappnlwaaqrygrellrmsde 120  
 |||||

QY 121 FVDSFKKGLPRPKSAGTATQMROSSSWTRVFQSWDNRNLGRGSSAPSQ 168  
 |||||  
 DB 121 fvdskkglprpksagtatqmrqssswtrvfqswdnrnlgrgssapsq 168  
 |||||

RESULT 2  
 AAB13512  
 ID AAB13512 standard; protein; 168 AA.  
 XX  
 AC AAB13512;  
 XX  
 DT 02-NOV-2000 (first entry)  
 XX  
 DE Human cell proliferation protein APOP-1.  
 XX  
 KW Human; cell proliferation; APOP-1; cancer; inflammation; infection;  
 KW trauma; neurodegenerative disease; ischaemic injury; wasting disease.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US6080847-A.  
 XX  
 PD 27-JUN-2000.  
 XX  
 PF 04-DEC-1997; 97US-0985335.  
 XX  
 PR 04-DEC-1997; 97US-0985335.  
 XX  
 PA (INCY-) INCYTE PHARM INC.  
 XX  
 PI Corley NC, Hillman JL, Yue H, Lal P, Shah P;  
 XX  
 DR WPI; 2000-451230/39.  
 DR N-PSDB; AAA63332.  
 XX  
 PT Novel polynucleotide and polypeptide sequences of proteins associated  
 PT with cell proliferation for diagnosis, prevention and treatment of e.g.  
 PT cancer, acquired immunodeficiency syndrome, and Parkinson's disease -

PS Example 8; Fig 1; 58pp; English.  
 XX  
 CC The present sequence is the human APOP-1 protein. This protein, which  
 CC shares structural and chemical homology with Bcl-2, is involved in cell  
 CC proliferation. Its coding sequence was isolated by screening a synovial  
 CC tissue cDNA library using a computer search for amino acid sequence  
 CC alignments. The gene and protein can be used in the treatment of various  
 CC cancers, disorders with associated inflammation such as Addison's  
 CC disease, adult respiratory distress syndrome, allergies, anaemia, asthma,  
 CC atherosclerosis, Crohn's disease, ulcerative colitis, diabetes mellitus,  
 CC emphysema, glomerulonephritis, gout, Graves' disease, irritable bowel  
 CC syndrome, lupus erythematosus, multiple sclerosis, myasthenia gravis,  
 CC myocardial or pericardial inflammation, osteoporosis, rheumatoid  
 CC arthritis, Sjogren's syndrome and autoimmune thyroiditis, complications  
 CC of cancer, haemodialysis and extracorporeal circulation, infections,  
 CC trauma, disorders with associated apoptosis including AIDS and other  
 CC infectious and genetic immunodeficiencies, neurodegenerative diseases  
 CC such as Alzheimer's disease and Parkinson's disease, ischaemic injuries  
 CC such as myocardial infarction, and wasting diseases including cachexia.  
 XX  
 SQ Sequence 168 AA;

Query Match 100.0%; Score 905; DB 21; Length 168;  
 Best Local Similarity 100.0%; Pred. No. 6.4e-88;  
 Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFQIPEFEPSEQEDSSAERGLGSPAGDGPSCGSKHHRQAPGLLDASHQEQPTSSSH 60  
 |||||  
 DB 1 mqiipfefseqedssaaerglgpsagdgpsgskhhrqapglldashqeqptsssh 60  
 |||||

QY 61 HGGAGAVEIRSHSSYPAGTDEDEGMGEFPSPFRGRSRAPPNLMAAQRYGRELRRMSDE 120  
 |||||  
 DB 61 hggagaveirshssypagteddegmggeepsfgrsrsappnlwaaqrygrellrmsde 120  
 |||||

QY 121 FVDSFKKGLPRPKSAGTATQMROSSSWTRVFQSWDNRNLGRGSSAPSQ 168  
 |||||  
 DB 121 fvdskkglprpksagtatqmrqssswtrvfqswdnrnlgrgssapsq 168  
 |||||

RESULT 3  
 AAB70368  
 ID AAB70368 standard; protein; 168 AA.  
 XX  
 AC AAB70368;  
 XX  
 DT 02-MAY-2001 (first entry)  
 XX  
 DE Human BAD mutant amino acid sequence SEQ ID NO:1.  
 XX  
 KW Bcl-XL/Bcl-2 associated cell death regulator; BAD; mutant; apoptosis;  
 KW immunostimulant; neuroprotective; nootropic; antiischaemic; vulnerary;  
 KW cytosolic; antiviral; antiarthritic; antiinflammatory; wound healing;  
 KW immunosuppressive; apoptosis inducer; apoptosis inhibitor; cancer;  
 KW immunodeficiency disease; neurodegenerative disease; viral infection;  
 KW ischaemic cell death; reperfusion cell death; arthritis; infertility;  
 KW lymphoproliferative condition; inflammation; autoimmune disease.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN WO200110888-A1.  
 XX  
 PD 15-FEB-2001.  
 XX  
 PF 30-MAY-2000; 2000WO-US11864.  
 XX  
 PR 28-MAY-1999; 99US-0136783.  
 XX  
 PA (APOP-) APOPTOSIS TECHNOLOGY INC.  
 XX  
 PI Zhou X;

DR WPI; 2001-138734/14.  
 XX New mutant Bcl-XL/Bcl-2 Associated Cell Death Regulator polypeptide,  
 PT useful for screening for candidate compounds which induce or inhibit  
 PT apoptosis, comprises amino acid substitutions at Ser118, Ser155 or  
 PT Ser113 -  
 XX  
 PS Claim 1; Page 147; 157pp; English.  
 XX  
 CC The present invention describes an isolated or synthetic polypeptide  
 CC (I) comprising a less than full length amino acid sequence of a mutant  
 CC Bcl-XL/Bcl-2 associated cell death regulator polypeptide (BAD) or its  
 CC fragment, which contains amino acid substitutions at Ser118 of a human  
 CC BAD, Ser155 of a murine BAD (longer murine BAD) or Ser113 of a murine  
 CC BAD (shorter murine BAD). (I) has immunostimulant, neuroprotective,  
 CC nootropic, antiischaemic, vulnerary, cytostatic, antiviral,  
 CC antiarthritic, antiinflammatory and immunosuppressive activities, and  
 CC can be used as an apoptosis inducer or inhibitor. BAD polypeptides and  
 CC polynucleotides can be used for screening candidate compounds and drugs  
 CC for activity that promote cell survival or apoptosis. Other uses include  
 CC inducing or inhibiting apoptosis in a cell. Candidate compounds  
 CC identified and (mutant) BAD polypeptides are useful in treating  
 CC immunodeficiency diseases, neurodegenerative diseases, ischaemic cell  
 CC death, reperfusion cell death, wound healing, cancer, viral infections,  
 CC lymphoproliferative conditions, arthritis, infertility, inflammation and  
 CC autoimmune diseases. The present sequence represents a specifically  
 CC claimed human BAD mutant amino acid sequence from the present invention.  
 XX  
 SQ Sequence 168 AA;

Query Match 100.0%; Score 905; DB 22; Length 168;  
 Best Local Similarity 100.0%; Pred. No. 6.4e-88;  
 Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MFQIPFEPSEQEDSSAERGLGSPAGDPSGSGKHHRQAPGLLWDASHQEQPTSSSH 60  
 DB 1 mfpifepseqedsssaerglgspagdgpsgskhhrqapglldashhqqeqptsssh 60  
 QY 61 HGCAGAVEIRSHSSYPAGTDECGMEEPSPFGRGRSAPPNLWAAQRYGRELRRMSDE 120  
 DB 61 hggagaveirshssypagtedecgmeeppfgrgrsappnlwaaorygrellrrmsde 120  
 QY 121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWMDRNLGRGSSAPSQ 168  
 DB 121 fvdskkglprpkagatqmrqssswtrvfgswmdrnlgrgssapsq 168

RESULT 4  
 AAB48287  
 ID AAB48287 standard; protein; 168 AA.  
 XX  
 AC AAB48287;  
 XX  
 DT 02-APR-2001 (first entry)  
 XX  
 DE Human Bad protein.  
 XX  
 KW S-phase kinase associated protein; SKP1; SKP2; SKP2-like protein; 2F;  
 KW CUL-1; cullin; CDC53; p27; cyclin E; Max; Mad; c-Myc; MDM2; p53; Bax;  
 KW Bad; Bcl-2; tumour; cytostatic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200075184-A1.  
 XX  
 PD 14-DEC-2000.  
 XX  
 PF 05-JUN-2000; 2000WO-US15449.  
 XX  
 PR 04-JUN-1999; 99US-0137494.  
 XX  
 PA (UYVA ) UNIV YALE.

XX Zhang H, Tsvetkov LM, Kondo T;  
 XX WPI; 2001-061703/07.  
 DR N-FSDB; AAC84599.  
 XX  
 PT Modulating polypeptide levels in a cell, diagnosing and treating tumor,  
 PT involves altering levels of proteins such as S-phase kinase associated  
 PT proteins 1, 2 and cullin/CDC53 proteins -  
 XX  
 PS Claim 5; Page 102-103; 162pp; English.  
 XX  
 CC The invention relates to methods of altering the polypeptide levels in a  
 CC cell, using proteins selected from S-phase kinase associated proteins 1  
 CC and 2 (SKP1, SKP2), SKP2-like proteins (2F) and CUL-1 (a member of the  
 CC cullin/CDC53 family of proteins). The method is useful for altering the  
 CC level of p27, cyclin E, Max, Mad, c-Myc, MDM2, p53, Bax, Bad or Bcl-2  
 CC polypeptide in a cell. SKP2 and SKP2-like protein levels are useful for  
 CC detecting tumours, and in monitoring tumor treatment in a mammal. Agents  
 CC that modulate interactions between SKP and target proteins are useful for  
 CC treating tumours.  
 XX  
 SQ Sequence 168 AA;  
 Query Match 100.0%; Score 905; DB 22; Length 168;  
 Best Local Similarity 100.0%; Pred. No. 6.4e-88;  
 Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MFQIPFEPSEQEDSSAERGLGSPAGDPSGSGKHHRQAPGLLWDASHQEQPTSSSH 60  
 DB 1 mfpifepseqedsssaerglgspagdgpsgskhhrqapglldashhqqeqptsssh 60  
 QY 61 HGCAGAVEIRSHSSYPAGTDECGMEEPSPFGRGRSAPPNLWAAQRYGRELRRMSDE 120  
 DB 61 hggagaveirshssypagtedecgmeeppfgrgrsappnlwaaorygrellrrmsde 120  
 QY 121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWMDRNLGRGSSAPSQ 168  
 DB 121 fvdskkglprpkagatqmrqssswtrvfgswmdrnlgrgssapsq 168  
 RESULT 5  
 AAW32476  
 ID AAW32476 standard; Protein; 166 AA.  
 XX  
 AC AAW32476;  
 XX  
 DT 15-JAN-1998 (first entry)  
 XX  
 DE BBC6 protein for regulating cell death.  
 XX  
 KW BBC6 gene; cell death; cell cycle; Bcl2; human.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US5663316-A.  
 XX  
 PD 02-SEP-1997.  
 XX  
 PF 18-JUN-1996; 96US-0665617.  
 XX  
 PR 18-JUN-1996; 96US-0665617.  
 XX  
 PA (CLON-) CLONTECH LAB INC.  
 XX  
 PI Xudong Y;  
 XX  
 DR WPI; 1997-447980/41.  
 DR N-FSDB; AAT91561.  
 XX  
 PT Isolated BBC6 gene - encodes a protein that regulates cell death  
 PT through interaction with Bcl-2  
 XX

XX PS Claim 1; Column 11-12; 7pp; English.

CC The present sequence represents a protein of 166 amino acids. The

CC sequence is disclosed as being a protein called Bcl-2 which regulates

CC cell death through interaction with Bcl-2. The DNA may be used for the

CC production of the recombinant protein, which can be used in unspecified

CC therapeutic or diagnostic procedures, as a molecular weight marker, and

CC to raise antibodies that can be used in unspecified diagnostic or

CC therapeutic applications and to reduce or eliminate the biological

CC activity of the Bcl-2 protein in vivo.

XX SQ Sequence 166 AA;

Query Match 83.0%; Score 751; DB 18; Length 166;

Best Local Similarity 84.0%; Pred. No. 1.2e-71;

Matches 147; Conservative 3; Mismatches 9; Indels 16; Gaps 3;

QY 1 MFQIPFEPSEQEDSSAERGLGPGAGDPSGKHHROAPG-----LLWDASHQOE 53

DB 1 mfgipefepseqedsssaerg-wrspagtq-----qapasiliarpqylwdashqoe 51

QY 54 QPTSSSHHGAGAVEIRSRHSSYPAGTDEDEGMGEPSPPFRGRSRGAPPNLAQRYGRE 113

DB 52 qptssshhgagaveirsrhssypagteddegmggeepsfgrgrarppppnlwaaqrygre 111

QY 114 LRRMSDEFVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWMDRNLGRGSSAPSQ 168

DB 112 lrrmsdefvdsfkkgiprksagtatqmrqssswtrvfqswmdrnlgrgtaapsq 166

RESULT 6

AAB70370

ID AAB70370 standard; protein; 162 AA.

XX AC AAB70370;

XX DT 02-MAY-2001 (first entry)

XX DT Shorter murine BAD mutant amino acid sequence SEQ ID NO:3.

XX DE Bcl-XL/Bcl-2 associated cell death regulator; BAD; mutant; apoptosis;

XX KW immunostimulant; neuroprotective; nontoxic; antiischaemic; vulnary;

XX KW cytostatic; antiviral; antitumor; antiinflammatory; wound healing;

XX KW immunosuppressive; apoptosis inducer; apoptosis inhibitor; cancer;

XX KW immunodeficiency disease; neurodegenerative disease; viral infection;

XX KW ischaemic cell death; reperfusion cell death; arthritis; infertility;

XX KW lymphoproliferative condition; inflammation; autoimmune disease.

XX OS Mus musculus.

XX OS Synthetic.

XX XX WO200110888-A1.

XX PN 15-FEB-2001.

XX PF 30-MAY-2000; 2000WO-US11864.

XX PF 28-MAY-1999; 99US-0136783.

XX PA (APOB-) APOPTOSIS TECHNOLOGY INC.

XX PI Zhou X;

XX PI WPI; 2001-138734/14.

XX DR New mutant Bcl-XL/Bcl-2 Associated Cell Death Regulator polypeptide,

XX PT useful for screening for candidate compounds which induce or inhibit

XX PT apoptosis, comprises amino acid substitutions at Ser118, Ser155 or

XX PT Ser113 -

XX PS Claim 7; Page 148-149; 157pp; English.

XX CC The present invention describes an isolated or synthetic polypeptide

CC (I) comprising a less than full length amino acid sequence of a mutant

CC Bcl-XL/Bcl-2 associated cell death regulator polypeptide (BAD) or its

CC fragment, which contains amino acid substitutions at Ser118 of a human

CC BAD, Ser155 of a murine BAD (longer murine BAD) or Ser113 of a murine

CC BAD (shorter murine BAD). (I) has immunostimulant, neuroprotective,

CC nontoxic, antiischaemic, vulnary, cytostatic, antiviral,

CC antitumor, antiinflammatory and immunosuppressive activities, and

CC can be used as an apoptosis inducer or inhibitor. BAD polypeptides and

CC polynucleotides can be used for screening candidate compounds and drugs

CC for activity that promote cell survival or apoptosis. Other uses include

CC inducing or inhibiting apoptosis in a cell. Candidate compounds

CC identified and (mutant) BAD polypeptides are useful in treating

CC immunodeficiency diseases, neurodegenerative diseases, ischaemic cell

CC death, reperfusion cell death, wound healing, cancer, viral infections,

CC lymphoproliferative conditions, arthritis, infertility, inflammation and

CC autoimmune diseases. The present sequence represents a specifically

CC claimed shorter murine BAD mutant amino acid sequence from the present

CC invention.

XX SQ Sequence 162 AA;

Query Match 71.7%; Score 649; DB 22; Length 162;

Best Local Similarity 75.6%; Pred. No. 6.7e-61;

Matches 127; Conservative 12; Mismatches 23; Indels 6; Gaps 3;

QY 1 MFQIPFEPSEQEDSSAERGLGPGAGDPSGKHHROAPGLLWDASHQOEPTSSSH 60

DB 1 mfgipefepseqedssatdrglpsitedqp---gpy--lapglglnhgggrraatnsh 55

QY 61 HGAGAVEIRSRHSSYPAGTDEDEGMGEPSPPFRGRSRGAPPNLAQRYGRELRMSDE 120

DB 56 hggagavetrshssypagteddegmggeelspfgrgrsappnlwaaqrygrelrmsde 115

QY 121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWMDRNLGRGSSAPSQ 168

DB 116 fegsf-kglprksagtatqmrqsgwttriigswdrlngkggstpsq 162

RESULT 7

AAR95168

ID AAR95168 standard; Protein; 204 AA.

XX AC AAR95168;

XX DT 06-JAN-1997 (first entry)

XX DE bcl-x(L)/bcl-2 associated death promoter protein.

XX KW Epitope; murine; bcl-x(L)/bcl-2 associated death promoter; Bad; stroke;

XX KW polypeptide; bcl-x; cell death; regulate; BH1; BH2; apoptotic cell death;

XX KW cytokine deprivation; IL-3 dependent cell line; immunodeficiency; AIDS;

XX KW neurodegenerative disease; senescence; ischaemia; neoplasia.

XX OS Mus musculus.

XX FH Location/Qualifiers

XX FT Region 147..149

XX FT /note= "BH1 conserved amino acids"

XX FT Region 191..192

XX FT /note= "BH2 conserved amino acids"

XX FT Domain 38..61

XX FT /note= "PEST sequence"

XX FT Domain 111..130

XX FT /note= "PEST sequence"

XX XX WO9613614-A1.

XX PN 09-MAY-1996.

XX PD 31-OCT-1995; 95WO-US14246.

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XX PR 31-OCT-1994; 94US-03333565.
XX XX (UNIW ) UNIV WASHINGTON.
XX XX Korsmeyer SJ;
XX XX WPI; 1996-251465/25.
XX DR N-PSDB; AAT29479.
XX XX Polynucleotide encoding bcl-x(L)/bcl-2 associated death promoter -
XX PT useful to treat neoplasia and apoptosis and to identify agents
XX PT inhibiting its binding to bcl-2 or bcl-x(L) to form heteromultimers
XX XX
XX PS Claim 3; Fig 1; 130pp; English.
XX XX
XX CC This sequence represents the murine bcl-x(L)/bcl-2 associated death
XX CC promoter (Bad) gene. Bad is a 22.1 kD protein which interacts with
XX CC bcl-2 and bcl-x proteins and regulates cell death. It has homology
XX CC to the bcl-2-related family clustered in the BHL and BH2 domain. Bad
XX CC has been found to hybridise to bcl-x(L) and bcl-2 in yeast two-hybrid
XX CC assays and in vivo in mammalian cells. Overexpressed Bad counters the
XX CC death inhibitory activity of bcl-x(L), but is much less effective at
XX CC countering the death inhibitory activity of bcl-2. Bad expression can
XX CC accelerate apoptotic cell death induced by cytokine deprivation in an
XX CC IL-3 dependent cell line expressing bcl-x(L), and its also counters the
XX CC death repressor activity of bcl-x(L). Bad competes with Bax for binding
XX CC to bcl-x(L). Bad may be used to identify agents which inhibit its
XX CC binding to bcl-2 or bcl-x(L) to form heterodimers. Such agents may be
XX CC used to treat neurodegenerative diseases, immunodeficiency diseases,
XX CC e.g. AIDS, senescence or ischaemia.
XX SQ Sequence 204 AA;

Query Match 71.7%; Score 649; DB 17; Length 204;
Best Local Similarity 75.6%; Pred. No. 9.1e-61;
Matches 127; Conservative 12; Mismatches 23; Indels 6; Gaps 3;

QY 1 MFQIPEPSPQEDSSAERGLGSPAGDGPSSGSKHHRQAPGLLWDASHOQPTSSSH 60
Db 43 mfiqpefepseqedasatdrglpsltedqp---gpy--lapglgsnihqggraatnsh 97

QY 61 HGGAGAVEIRSRHSSYPAGTDEDCMGEPSPFRGRSRSPPNLWAAQRYGRELRMSDE 120
Db 98 hggagametrshssypagteedegmeelspfgrsrsappnlwaaqrygrelrmsde 157

QY 121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWMDRNLGRGSSAPSQ 168
Db 158 fegsf-kglprpkagtatmrqsagwtrliqswdrlngkggstpsq 204

RESULT 8
AAW61315
ID AAW61315 standard; Protein; 204 AA.
XX XX
XX AC AAW61315;
XX XX
XX DT 07-OCT-1998 (first entry)
XX XX
XX DE Murine BCL-XL/BCL-2 associated cell death regulator.
XX KW Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein;
XX KW serine substituted mutant; apoptosis; cancer; viral infection.
XX OS Mus sp.
XX XX
XX PN W09817682-A1.
XX XX
XX PD 30-APR-1998.
XX XX
XX PF 17-OCT-1997; 97WO-US19175.
XX XX

18-OCT-1996; 96US-07333505.
XX XX (UNIW ) UNIV WASHINGTON.
XX XX Korsmeyer SJ;
XX XX WPI; 1998-261422/23.
XX DR N-PSDB; AAV27833.
XX XX New mutant BAD polypeptide with phosphorylatable serine replaced -
XX PT useful for, e.g. treating reduced apoptosis such as in cancer or
XX PT viral infection
XX XX
XX PS Claim 1; Fig 10; 95pp; English.
XX XX
XX CC The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell
XX CC death regulator) proteins, having an amino acid other than Ser at
XX CC position 112 and/or 136, relative to the murine BAD 204 aa sequence. The
XX CC present sequence is the murine BAD protein. Also described are: (1)
XX CC fragments of mutant BAD protein able to decrease cell viability; (2)
XX CC fusion proteins of mutant BAD with a heterologous polypeptide that
XX CC increases intracellular delivery. Mutant BAD proteins are used to treat
XX CC or prevent diseases associated with reduced apoptosis, e.g. cancer,
XX CC viral infection, lymphoproliferation, arthritis, infertility,
XX CC inflammation and autoimmune disease. Polynucleotide sequences encoding
XX CC mutant BAD proteins can be used similarly by gene therapy or to produce
XX CC transgenic animals for use as disease models or in drug screening. BAD
XX CC proteins phosphorylated at specified Ser are used to screen for enhancers
XX CC and inhibitors of serine-phosphatase. Inhibitors are potentially useful
XX CC in treatment of excessive apoptosis such as AIDS, neurodegeneration,
XX CC aging or ischaemic cell death. The apoptotic status of cells is
XX CC determined by measuring relative amounts of phosphorylated and non-
XX CC phosphorylated BAD, by usual immunoassays. Mutant BAD proteins have
XX CC greater death-promoting activity than wild-type BAD which can become
XX CC phosphorylated on the specified Ser, forming a product that does not
XX CC heterodimerise with BCL-2 or BCL-XL but instead binds to 14-3-3 family
XX CC proteins in the cytosol, thus promoting cell survival. The mutants with
XX CC Ser substituted cannot bind 14-3-3.
XX SQ Sequence 204 AA;

Query Match 71.7%; Score 649; DB 19; Length 204;
Best Local Similarity 75.6%; Pred. No. 9.1e-61;
Matches 127; Conservative 12; Mismatches 23; Indels 6; Gaps 3;

QY 1 MFQIPEPSPQEDSSAERGLGSPAGDGPSSGSKHHRQAPGLLWDASHOQPTSSSH 60
Db 43 mfiqpefepseqedasatdrglpsltedqp---gpy--lapglgsnihqggraatnsh 97

QY 61 HGGAGAVEIRSRHSSYPAGTDEDCMGEPSPFRGRSRSPPNLWAAQRYGRELRMSDE 120
Db 98 hggagametrshssypagteedegmeelspfgrsrsappnlwaaqrygrelrmsde 157

QY 121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWMDRNLGRGSSAPSQ 168
Db 158 fegsf-kglprpkagtatmrqsagwtrliqswdrlngkggstpsq 204

RESULT 9
AAW58832
ID AAW58832 standard; protein; 204 AA.
XX XX
XX AC AAW58832;
XX XX
XX DT 23-JUL-1998 (first entry)
XX XX
XX DE Murine BAD protein.
XX XX
XX KW BAD protein; Bcl-XL/Bcl-2 associated cell death regulator; 14-3-3;
XX KW serine phosphorylation; post-translational modification; apoptosis;
XX KW signal transduction regulator; phosphoserine phosphatase; senescence;
XX KW immunodeficiency disease; neurodegenerative disease; infertility;

```

KW cancer, viral infection; lymphoproliferative condition; arthritis;  
 KW inflammation; autoimmune diseases.  
 OS Mus sp.  
 XX WO9809643-A1.  
 PN 12-MAR-1998.  
 XX 09-SEP-1997; 97WO-US15871.  
 XX 09-SEP-1996; 96US-0707868.  
 PR (UNIV ) UNIV WASHINGTON.  
 XX PA Korschmeier SJ;  
 XX PI WPI; 1998-207049/18.  
 DR Serine-phosphorylated Bcl-X-L/Bcl-2 Associated cell Death regulator  
 PT polypeptide - useful for modulation of apoptosis associated with,  
 PT e.g. cancer and immunodeficiency diseases  
 XX Claim 3; Fig 8; 61pp; English.  
 PS This sequence represents a novel serine-phosphorylated protein, BAD  
 CC (Bcl-XL/Bcl-2 associated cell death regulator). The serine residue is  
 CC phosphorylated in a post-translational modification and allows binding  
 CC to the 14-3-3 protein which is a signal transduction regulator.  
 CC Modulators of phosphorylated BAD, which act through inhibition/activation  
 CC of a phosphoserine phosphatase, are useful for preventing/treating  
 CC increased/decreased apoptosis in a cell. The increased apoptosis may  
 CC result from immunodeficiency diseases, senescence, neurodegenerative  
 CC disease, ischaemic cell death, reperfusion cell death, infertility and  
 CC wound-healing. Decreased apoptosis may result from cancer, viral  
 CC infection, lymphoproliferative conditions, arthritis, infertility,  
 CC inflammation and autoimmune diseases. Measuring the amount of  
 CC phosphorylated compared to unphosphorylated BAD polypeptide and/or total  
 CC BAD in a cell is useful for determining the apoptotic state of a cell.  
 XX Sequence 204 AA;

Query Match 71.7%; Score 649; DB 19; Length 204;  
 Best Local Similarity 75.6%; Pred. No. 9.1e-61;  
 Matches 127; Conservative 12; Mismatches 23; Indels 6; Gaps 3;  
 QY 1 MFQIPFEFSEQEDSSAERGLGPGSPAGDGPSCGKHRRQAPGLLWDASHQQQPTSSSH 60  
 DB 43 mtfqipefseqedasatdrglpsitedqp---gpy--lapglgslnhqggraatsnsh 97  
 QY 61 HGGAGAVEIRSRHSSYPAGTDEDEGMEGEPSPPRGRSRGAPPNLMWAQRYGRELRRMSDE 120  
 DB 98 hggagameirsrhssypagteedegmeelsprgrsrsappnlwaqrygrellrmsde 157  
 QY 121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWMDNLRGSSAPSQ 168  
 DB 158 fegsf-kglprksagtatqmrqsagwtrliqswdrnlgkggstpsq 204

RESULT 10  
 AAB70369  
 ID AAB70369 standard; protein; 204 AA.  
 XX AAB70369;  
 XX 02-MAY-2001 (first entry)  
 XX Longer murine BAD mutant amino acid sequence SEQ ID NO:2.

DE Bcl-XL/Bcl-2 associated cell death regulator; BAD; mutant; apoptosis;  
 KW immunostimulant; neuroprotective; nontropic; antiischaemic; vulnerary;  
 KW cytostatic; antiviral; antiarthritic; antiinflammatory; wound healing;

KW immunosuppressive; apoptosis inducer; apoptosis inhibitor; cancer;  
 KW immunodeficiency disease; neurodegenerative disease; viral infection;  
 KW ischaemic cell death; reperfusion cell death; arthritis; infertility;  
 XX lymphoproliferative condition; inflammation; autoimmune disease.  
 OS Mus musculus.  
 OS Synthetic.  
 XX WO200110888-A1.  
 PN 15-FEB-2001.  
 XX 30-MAY-2000; 2000WO-US11864.  
 XX 28-MAY-1999; 99US-0136783.  
 XX (APOP-) APOPTOSIS TECHNOLOGY INC.  
 XX Zhou X;  
 XX WPI; 2001-138734/14.  
 XX New mutant Bcl-XL/Bcl-2 Associated Cell Death Regulator polypeptide,  
 PT useful for screening for candidate compounds which induce or inhibit  
 PT apoptosis, comprises amino acid substitutions at Ser118, Ser155 or  
 PT Ser113 -  
 XX Claim 4; Page 148; 157pp; English.  
 PS The present invention describes an isolated or synthetic polypeptide  
 CC (I) comprising a less than full length amino acid sequence of a mutant  
 CC Bcl-XL/Bcl-2 associated cell death regulator polypeptide (BAD) or its  
 CC fragment, which contains amino acid substitutions at Ser118 of a human  
 CC BAD, Ser155 of a murine BAD (longer murine BAD) or Ser113 of a murine  
 CC BAD (shorter murine BAD). (I) has immunostimulant, neuroprotective,  
 CC nontropic, antiischaemic, vulnerary, cytostatic, antiviral,  
 CC antiarthritic, antiinflammatory and immunosuppressive activities, and  
 CC can be used as an apoptosis inducer or inhibitor. BAD polypeptides and  
 CC polynucleotides can be used for screening candidate compounds and drugs  
 CC for activity that promote cell survival or apoptosis. Other uses include  
 CC inducing or inhibiting apoptosis in a cell. Candidate compounds  
 CC identified and (mutant) BAD polypeptides are useful in treating  
 CC immunodeficiency diseases, neurodegenerative diseases, ischaemic cell  
 CC death, reperfusion cell death, wound healing, cancer, viral infections,  
 CC lymphoproliferative conditions, arthritis, infertility, inflammation and  
 CC autoimmune diseases. The present sequence represents a specifically  
 CC claimed longer murine BAD mutant amino acid sequence from the present  
 CC invention.

Sequence 204 AA;

Query Match 71.7%; Score 649; DB 22; Length 204;  
 Best Local Similarity 75.6%; Pred. No. 9.1e-61;  
 Matches 127; Conservative 12; Mismatches 23; Indels 6; Gaps 3;  
 QY 1 MFQIPFEFSEQEDSSAERGLGPGSPAGDGPSCGKHRRQAPGLLWDASHQQQPTSSSH 60  
 DB 43 mtfqipefseqedasatdrglpsitedqp---gpy--lapglgslnhqggraatsnsh 97  
 QY 61 HGGAGAVEIRSRHSSYPAGTDEDEGMEGEPSPPRGRSRGAPPNLMWAQRYGRELRRMSDE 120  
 DB 98 hggagameirsrhssypagteedegmeelsprgrsrsappnlwaqrygrellrmsde 157  
 QY 121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWMDNLRGSSAPSQ 168  
 DB 158 fegsf-kglprksagtatqmrqsagwtrliqswdrnlgkggstpsq 204

RESULT 11  
 AAW61317  
 ID AAW61317 standard; Protein; 204 AA.  
 XX

AC AAW61317;  
XX 07-OCT-1998 (first entry)  
XX Mutant BCL-XL/BCL-2 associated cell death regulator #2.  
DE Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein;  
KW serine substituted mutant; apoptosis; cancer; viral infection.  
XX  
XX Mus sp.  
OS Synthetic.  
OS  
XX W09817682-A1.  
XX 30-APR-1998.  
XX 17-OCT-1997; 97WO-US19175.  
XX 18-OCT-1996; 96US-0733505.  
XX (UNIW ) UNIV WASHINGTON.  
XX PA Korsmeyer SJ;  
XX PI  
XX WPI; 1998-261422/23.  
DR N-PSDB; AAV27835.  
XX New mutant BAD polypeptide with phosphorylatable serine replaced -  
PT useful for, e.g. treating reduced apoptosis such as in cancer or  
PT viral infection  
XX  
XX Claim 7; Page 60; 95pp; English.  
XX The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell  
CC death regulator) proteins, having an amino acid other than Ser at  
CC position 112 and/or 136, relative to the murine BAD 204 aa sequence. The  
CC present sequence represents a mutant BAD protein. Also described are: (1)  
CC fragments of mutant BAD protein able to decrease cell viability; (2)  
CC fusion proteins of mutant BAD with a heterologous polypeptide that  
CC increases intracellular delivery. Mutant BAD proteins are used to treat  
CC or prevent diseases associated with reduced apoptosis, e.g. cancer,  
CC viral infection, lymphoproliferation, arthritis, infertility,  
CC inflammation and autoimmune disease. Polynucleotide sequences encoding  
CC mutant BAD proteins can be used similarly by gene therapy or to produce  
CC transgenic animals for use as disease models or in drug screening. BAD  
CC proteins phosphorylated at specified Ser are used to screen for enhancers  
CC and inhibitors of serine-phosphatase. Inhibitors are potentially useful  
CC in treatment of excessive apoptosis such as AIDS, neurodegeneration,  
CC aging or ischaemic cell death. The apoptotic status of cells is  
CC determined by measuring relative amounts of phosphorylated and non-  
CC phosphorylated BAD, by usual immunoassays. Mutant BAD proteins have  
CC greater death-promoting activity than wild-type BAD which can become  
CC phosphorylated on the specified Ser, forming a product that does not  
CC heterodimerise with BCL-2 or BCL-XL but instead binds to 14-3-3 family  
CC proteins in the cytosol, thus promoting cell survival. The mutants with  
CC Ser substituted cannot bind 14-3-3.  
XX Sequence 204 AA;  
XX  
XX Query Match 71.4%; Score 646; DB 19; Length 204;  
XX Best Local Similarity 75.0%; Pred. No. 1.9e-60;  
XX Matches 126; Conservative 13; Mismatches 23; Indels 6; Gaps 3;  
QY 1 MFQIPEFSEQEDSSAERGLGSPAGDPSGSGKHHRQAPGLLDASHQEQPTSSSH 60  
DB 43 mtfqipefseqedasatdrglgsitedqp---gpy--lapglglnlhqdggraatnsh 97  
QY 61 HGGAGAVETRSHSSYPAGTDEGMEPSPFRGSRSPAPNLWAAQRYGRELRRMSDE 120  
DB 98 hggagavetrshssypagtedegemeelspfrgsraapnlwaaqrygrelrrmsde 157  
QY 121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWMDRNLGRGSSAPSQ 168

Db 158 fegsf-kglprpksgatqmrqsagwttrliqswdrlngkgstpsq 204  
RESULT 12  
AAW61316  
ID AAW61316 standard; Protein; 204 AA.  
XX  
AC AAW61316;  
XX  
XX 07-OCT-1998 (first entry)  
XX Mutant BCL-XL/BCL-2 associated cell death regulator #1.  
XX Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein;  
KW serine substituted mutant; apoptosis; cancer; viral infection.  
XX  
XX Mus sp.  
OS Synthetic.  
XX W09817682-A1.  
XX 30-APR-1998.  
XX 17-OCT-1997; 97WO-US19175.  
XX 18-OCT-1996; 96US-0733505.  
XX (UNIW ) UNIV WASHINGTON.  
XX PA Korsmeyer SJ;  
XX PI  
XX WPI; 1998-261422/23.  
DR N-PSDB; AAV27834.  
XX New mutant BAD polypeptide with phosphorylatable serine replaced -  
PT useful for, e.g. treating reduced apoptosis such as in cancer or  
PT viral infection  
XX  
XX Claim 7; Page 59; 95pp; English.  
XX The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell  
CC death regulator) proteins, having an amino acid other than Ser at  
CC position 112 and/or 136, relative to the murine BAD 204 aa sequence. The  
CC present sequence represents a mutant BAD protein. Also described are: (1)  
CC fragments of mutant BAD protein able to decrease cell viability; (2)  
CC fusion proteins of mutant BAD with a heterologous polypeptide that  
CC increases intracellular delivery. Mutant BAD proteins are used to treat  
CC or prevent diseases associated with reduced apoptosis, e.g. cancer,  
CC viral infection, lymphoproliferation, arthritis, infertility,  
CC inflammation and autoimmune disease. Polynucleotide sequences encoding  
CC mutant BAD proteins can be used similarly by gene therapy or to produce  
CC transgenic animals for use as disease models or in drug screening. BAD  
CC proteins phosphorylated at specified Ser are used to screen for enhancers  
CC and inhibitors of serine-phosphatase. Inhibitors are potentially useful  
CC in treatment of excessive apoptosis such as AIDS, neurodegeneration,  
CC aging or ischaemic cell death. The apoptotic status of cells is  
CC determined by measuring relative amounts of phosphorylated and non-  
CC phosphorylated BAD, by usual immunoassays. Mutant BAD proteins have  
CC greater death-promoting activity than wild-type BAD which can become  
CC phosphorylated on the specified Ser, forming a product that does not  
CC heterodimerise with BCL-2 or BCL-XL but instead binds to 14-3-3 family  
CC proteins in the cytosol, thus promoting cell survival. The mutants with  
CC Ser substituted cannot bind 14-3-3.  
XX Sequence 204 AA;  
XX  
XX Query Match 71.0%; Score 643; DB 19; Length 204;  
XX Best Local Similarity 74.4%; Pred. No. 3.9e-60;  
XX Matches 125; Conservative 14; Mismatches 23; Indels 6; Gaps 3;  
QY 1 MFQIPEFSEQEDSSAERGLGSPAGDPSGSGKHHRQAPGLLDASHQEQPTSSSH 60

Db 43 mfgipefepseqedasatdrglpsltedqp---gpy--lapgllgnsihqggraatsnsh 97  
QY 61 HGAGAVEIRSRSSYPAGTEDEGMEEPSFPRGRSRSAPPNLWAAQRYGRELRRMSDE 120  
Db 98 hgagagmetrsrshsaypagteedegmeelsprfgrsraappnlwaaqrygrelrrmsde 157  
QY 121 FVDSFKKGLPRPKSAGTATOMROSSWTRVFQSWDNRNLGRGSSAPSQ 168  
Db 158 fegsf-kglprksagatqmrqsagwttriqlgswdwnlrgkggstpsq 204

RESULT 13  
AAW61318  
ID AAW61318 standard; Protein; 204 AA.  
XX  
AC AAW61318;  
XX  
DT 07-OCT-1998 (first entry)  
XX  
DE Mutant BCL-XL/BCL-2 associated cell death regulator #3.  
XX  
KW Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein;  
KW serine substituted mutant; apoptosis; cancer; viral infection.  
XX  
OS Mus sp.  
OS Synthetic.  
XX  
PN WO9817682-A1.  
XX  
PD 30-APR-1998.  
XX  
PF 17-OCT-1997; 97WO-US19175.  
XX  
PR 18-OCT-1996; 96US-0733505.  
XX  
PA (UNIW ) UNIV WASHINGTON.  
XX  
PI Korsmeyer SJ;  
XX  
DR WPI; 1998-261422/23.  
DR N-PSDB; AAV27836.  
XX  
PT New mutant BAD polypeptide with phosphorylatable serine replaced -  
PT useful for, e.g. treating reduced apoptosis such as in cancer or  
PT viral infection  
XX  
PS Claim 7; Page 60-61; 95pp; English.  
XX  
CC The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell  
CC death regulator) proteins, having an amino acid other than Ser at  
CC position 112 and/or 136, relative to the murine BAD 204 aa sequence. The  
CC present sequence represents a mutant BAD protein. Also described are: (1)  
CC fragments of mutant BAD protein able to decrease cell viability; (2)  
CC fusion proteins of mutant BAD with a heterologous polypeptide that  
CC increases intracellular delivery. Mutant BAD proteins are used to treat  
CC or prevent diseases associated with reduced apoptosis, e.g. cancer,  
CC viral infection, lymphoproliferation, arthritis, infertility,  
CC inflammation and autoimmune disease. Polynucleotide sequences encoding  
CC mutant BAD proteins can be used similarly by gene therapy or to produce  
CC transgenic animals for use as disease models or in drug screening. BAD  
CC proteins phosphorylated at specified Ser are used to screen for enhancers  
CC and inhibitors of serine-phosphatase. Inhibitors are potentially useful  
CC in treatment of excessive apoptosis such as AIDS, neurodegeneration,  
CC aging or ischaemic cell death. The apoptotic status of cells is  
CC determined by measuring relative amounts of phosphorylated and non-  
CC phosphorylated BAD, by usual immunoassays. Mutant BAD proteins have  
CC greater death-promoting activity than wild-type BAD which can become  
CC phosphorylated on the specified Ser, forming a product that does not  
CC heterodimerise with BCL-2 or BCL-XL but instead binds to 14-3-3 family  
CC proteins in the cytosol, thus promoting cell survival. The mutants with  
CC Ser substituted cannot bind 14-3-3.

SQ Sequence 204 AA;  
Query Match 71.0%; Score 643; DB 19; Length 204;  
Best Local Similarity 74.4%; Pred. No. 3.9e-60;  
Matches 125; Conservative 14; Mismatches 23; Indels 6; Gaps 3;  
QY 1 MFOIPEFEPSEQEDSSAERGLGSPAGDQPSGSGKHRRQAPGLLWDASHQQEQPTSSSH 60  
Db 43 mfgipefepseqedasatdrglpsltedqp---gpy--lapgllgnsihqggraatsnsh 97  
QY 61 HGAGAVEIRSRSSYPAGTEDEGMEEPSFPRGRSRSAPPNLWAAQRYGRELRRMSDE 120  
Db 98 hgagagmetrsrshsaypagteedegmeelsprfgrsraappnlwaaqrygrelrrmsde 157  
QY 121 FVDSFKKGLPRPKSAGTATOMROSSWTRVFQSWDNRNLGRGSSAPSQ 168  
Db 158 fegsf-kglprksagatqmrqsagwttriqlgswdwnlrgkggstpsq 204

RESULT 14  
AAW61319  
ID AAW61319 standard; Protein; 59 AA.  
XX  
AC AAW61319;  
XX  
DT 07-OCT-1998 (first entry)  
XX  
DE Mutant BCL-XL/BCL-2 associated cell death regulator #4.  
XX  
KW Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein;  
KW serine substituted mutant; apoptosis; cancer; viral infection.  
XX  
OS Mus sp.  
OS Synthetic.  
XX  
PN WO9817682-A1.  
XX  
PD 30-APR-1998.  
XX  
PF 17-OCT-1997; 97WO-US19175.  
XX  
PR 18-OCT-1996; 96US-0733505.  
XX  
PA (UNIW ) UNIV WASHINGTON.  
XX  
PI Korsmeyer SJ;  
XX  
DR WPI; 1998-261422/23.  
DR N-PSDB; AAV27837.  
XX  
PT New mutant BAD polypeptide with phosphorylatable serine replaced -  
PT useful for, e.g. treating reduced apoptosis such as in cancer or  
PT viral infection  
XX  
PS Claim 8; Page 73; 95pp; English.  
XX  
CC The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell  
CC death regulator) proteins, having an amino acid other than Ser at  
CC position 112 and/or 136, relative to the murine BAD 204 aa sequence. The  
CC present sequence represents a mutant BAD protein. Also described are: (1)  
CC fragments of mutant BAD protein able to decrease cell viability; (2)  
CC fusion proteins of mutant BAD with a heterologous polypeptide that  
CC increases intracellular delivery. Mutant BAD proteins are used to treat  
CC or prevent diseases associated with reduced apoptosis, e.g. cancer,  
CC viral infection, lymphoproliferation, arthritis, infertility,  
CC inflammation and autoimmune disease. Polynucleotide sequences encoding  
CC mutant BAD proteins can be used similarly by gene therapy or to produce  
CC transgenic animals for use as disease models or in drug screening. BAD  
CC proteins phosphorylated at specified Ser are used to screen for enhancers  
CC and inhibitors of serine-phosphatase. Inhibitors are potentially useful  
CC in treatment of excessive apoptosis such as AIDS, neurodegeneration,  
CC aging or ischaemic cell death. The apoptotic status of cells is



CC determined by measuring relative amounts of phosphorylated and non-phosphorylated BAD, by usual immunoassays. Mutant BAD proteins have greater death-promoting activity than wild-type BAD which can become phosphorylated on the specified Ser, forming a product that does not heterodimerise with BCL-2 or BCL-XL but instead binds to 14-3-3 family proteins in the cytosol, thus promoting cell survival. The mutants with Ser substituted cannot bind 14-3-3.

XX  
SQ Sequence 59 AA;

Query Match 34.7%; Score 314; DB 19; Length 59;  
Best Local Similarity 100.0%; Pred. No. 4.5e-26;  
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 63 GAGAVEIRSRHSSYPAGTDEDEGMGEPSPPFRGRSRAPPNLWAAQRYGRELRMSDEF 121  
Db 1 gagaveirsrhssypagteddegmgpepsppfrgrsrappnlwaaqrygreirrmsdef 59

RESULT 15  
AAW61320  
ID AAW61320 standard; Protein; 59 AA.  
XX  
AC AAW61320;  
XX  
DT 07-OCT-1998 (first entry)  
XX  
DE Mutant BCL-XL/BCL-2 associated cell death regulator #5.  
XX  
KW Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein; serine substituted mutant; apoptosis; cancer; viral infection.  
XX  
OS Mus sp.  
OS Synthetic.  
XX  
PN W09817682-A1.  
XX  
PD 30-APR-1998.  
XX  
PF 17-OCT-1997; 97WO-US19175.  
XX  
PR 18-OCT-1996; 96US-0733505.  
XX  
PA (UNIW ) UNIV WASHINGTON.  
XX  
PI Korsmeyer SJ;  
XX  
DR WPI; 1998-261422/23.  
DR N-PSDB; AAV27838.  
XX  
PT New mutant BAD polypeptide with phosphorylatable serine replaced -  
PT useful for, e.g. treating reduced apoptosis such as in cancer or  
PT viral infection  
XX  
PS Claim 8; Page 73; 95pp; English.

CC The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell death regulator) proteins, having an amino acid other than Ser at position 112 and/or 136, relative to the murine BAD 204 aa sequence. The present sequence represents a mutant BAD protein. Also described are: (1) fragments of mutant BAD protein able to decrease cell viability; (2) fusion proteins of mutant BAD with a heterologous polypeptide that increases intracellular delivery. Mutant BAD proteins are used to treat or prevent diseases associated with reduced apoptosis, e.g. cancer, viral infection, lymphoproliferation, arthritis, infertility, inflammation and autoimmune disease. Polynucleotide sequences encoding mutant BAD proteins can be used similarly by gene therapy or to produce transgenic animals for use as disease models or in drug screening. BAD proteins phosphorylated at specified Ser are used to screen for enhancers and inhibitors of serine-phosphatase. Inhibitors are potentially useful in treatment of excessive apoptosis such as AIDS, neurodegeneration, aging or ischaemic cell death. The apoptotic status of cells is

CC determined by measuring relative amounts of phosphorylated and non-phosphorylated BAD, by usual immunoassays. Mutant BAD proteins have greater death-promoting activity than wild-type BAD which can become phosphorylated on the specified Ser, forming a product that does not heterodimerise with BCL-2 or BCL-XL but instead binds to 14-3-3 family proteins in the cytosol, thus promoting cell survival. The mutants with Ser substituted cannot bind 14-3-3.

XX  
SQ Sequence 59 AA;

Query Match 34.7%; Score 314; DB 19; Length 59;  
Best Local Similarity 100.0%; Pred. No. 4.5e-26;  
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 63 GAGAVEIRSRHSSYPAGTDEDEGMGEPSPPFRGRSRAPPNLWAAQRYGRELRMSDEF 121  
Db 1 gagaveirsrhssypagteddegmgpepsppfrgrsrappnlwaaqrygreirrmsdef 59

Search completed: October 9, 2001, 15:53:27  
Job time: 203 sec



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OM protein - protein search, using sw model

Run on: October 9, 2001, 15:59:30 ; Search time 239.36 Seconds  
(without alignments)  
155.708 Million cell updates/sec

Title: US-09-580-523-1

Perfect score: 905  
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Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2803329 seqs, 221847457 residues

Total number of hits satisfying chosen parameters: 2803329

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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23: /cgn2\_6/ptodata/2/paa/US099\_COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	905	100.0	168	1	PCT-US00-11864-1
2	905	100.0	168	17	US-09-375-257-2
3	905	100.0	168	17	US-09-376-154-2
4	905	100.0	168	18	US-09-410-372-1
5	905	100.0	168	18	US-09-456-357-32
6	905	100.0	168	19	US-09-580-523-1
7	905	100.0	168	19	US-09-587-473-21
8	744	82.2	168	12	US-08-883-731-2
9	744	82.2	168	18	US-09-410-372-7
10	673	74.4	125	23	US-60-197-873-16338

11	649	71.7	162	1	PCT-US00-11864-3	Sequence 3, Appli
12	649	71.7	162	19	US-09-580-523-3	Sequence 3, Appli
13	649	71.7	204	1	PCT-US00-11864-2	Sequence 2, Appli
14	649	71.7	204	1	PCT-US97-15871-1	Sequence 1, Appli
15	649	71.7	204	1	PCT-US97-15871A-1	Sequence 1, Appli
16	649	71.7	204	1	PCT-US98-19765-41	Sequence 41, Appli
17	649	71.7	204	11	US-08-707-868-1	Sequence 1, Appli
18	649	71.7	204	11	US-08-733-505-1	Sequence 1, Appli
19	649	71.7	204	13	US-08-946-039-41	Sequence 41, Appli
20	649	71.7	204	19	US-09-580-523-2	Sequence 2, Appli
21	646	71.4	204	11	US-08-733-505-12	Sequence 12, Appli
22	646	71.4	204	11	US-08-733-505-13	Sequence 13, Appli
23	646	71.4	204	17	US-09-375-257-3	Sequence 3, Appli
24	646	71.4	204	17	US-09-376-154-3	Sequence 3, Appli
25	643	71.0	204	11	US-08-733-505-14	Sequence 14, Appli
26	643	71.0	567	20	US-09-639-245-4	Sequence 4, Appli
27	334	36.9	63	1	PCT-US97-15871A-12	Sequence 12, Appli
28	334	36.9	63	1	PCT-US98-19765-42	Sequence 42, Appli
29	334	36.9	63	13	US-08-946-039-42	Sequence 42, Appli
30	314	34.7	59	11	US-08-733-505-55	Sequence 55, Appli
31	311	34.4	59	11	US-08-733-505-56	Sequence 56, Appli
32	311	34.4	59	11	US-08-733-505-57	Sequence 57, Appli
33	308	34.0	59	11	US-08-733-505-58	Sequence 58, Appli
34	133	14.7	26	1	PCT-US00-11864-4	Sequence 4, Appli
35	133	14.7	26	1	PCT-US99-25285-5	Sequence 5, Appli
36	133	14.7	26	15	US-09-184-168A-5	Sequence 4, Appli
37	133	14.7	26	19	US-09-580-523-4	Sequence 4, Appli
38	132	14.6	25	20	US-09-656-399-10	Sequence 10, Appli
39	132	14.6	25	20	US-09-656-399A-10	Sequence 10, Appli
40	132	14.6	25	21	US-09-716-395-20	Sequence 20, Appli
41	129	14.3	25	20	US-09-656-399-17	Sequence 17, Appli
42	129	14.3	25	20	US-09-656-399A-17	Sequence 17, Appli
43	129	14.3	25	21	US-09-716-395-26	Sequence 26, Appli
44	128	14.1	25	20	US-09-656-399-15	Sequence 15, Appli
45	128	14.1	25	20	US-09-656-399-16	Sequence 16, Appli

ALIGNMENTS

RESULT 1  
PCT-US00-11864-1  
; Sequence 1, Application PC/TUS0011864  
; GENERAL INFORMATION:  
; APPLICANT: APOPTOSIS TECHNOLOGY, INC.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR REGULATING APOPTOSIS,  
; TITLE OF INVENTION: AND METHODS OF MAKING AND SCREENING FOR COMPOUNDS  
; TITLE OF INVENTION: THAT REGULATE APOPTOSIS  
; FILE REFERENCE: F137122  
; CURRENT APPLICATION NUMBER: PCT/US00/11864  
; CURRENT FILING DATE: 2000-05-30  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 168  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
PCT-US00-11864-1

Query Match	100.0%;	Score 905;	DB 1;	Length 168;
Best Local Similarity	100.0%;	Pred. No. 5.3e-71;		
Matches 168;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MFQIPEFPESEQEDSSAERGLGPSAGDGGSGSKHHRQAPGLLWDASHHQEQPTSSSH	60	
Db	1	MFQIPEFPESEQEDSSAERGLGPSAGDGGSGSKHHRQAPGLLWDASHHQEQPTSSSH	60	
Qy	61	HGGAGAVEIRSHSSYPAGTDEDCMGGEPSPFGRGRSAPPNLWAAORYGRELARMDE	120	
Db	61	HGGAGAVEIRSHSSYPAGTDEDCMGGEPSPFGRGRSAPPNLWAAORYGRELARMDE	120	
Qy	121	FVDSFKGLPRPKSAGTATQMRQSSSWTRVFQSWDRNLGRGSSAPSQ	168	

Db 121 FVDSFKKGLPRPKSAGTATQMRQSSWTRVFQSWWDRNLGRGSSAPSQ 168  
|||||

## RESULT 2

US-09-375-257-2  
; Sequence 2, Application US/09375257  
; GENERAL INFORMATION:  
; APPLICANT: Horne, William A.  
; APPLICANT: Oltersdorf, Tilman  
; TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC  
; FILE REFERENCE: 480140.428D1  
; CURRENT APPLICATION NUMBER: US/09/375,257  
; CURRENT FILING DATE: 1999-08-16  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 168  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-375-257-2

Query Match 100.0%; Score 905; DB 17; Length 168;  
Best Local Similarity 100.0%; Pred. No. 5.3e-71;  
Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFQIPEFEPSEQEDSSAERGLGSPAGDGPSSGKHHROAPGLLWDASHQEQPTSSSH 60  
|||||  
Db 1 MFQIPEFEPSEQEDSSAERGLGSPAGDGPSSGKHHROAPGLLWDASHQEQPTSSSH 60  
|||||  
QY 61 HCGAGAVEIRSRHSSYPAGTDEDEGMGEPPSPRGRSRAPPNLWAAQRYGRELRRMSDE 120  
|||||  
Db 61 HCGAGAVEIRSRHSSYPAGTDEDEGMGEPPSPRGRSRAPPNLWAAQRYGRELRRMSDE 120  
|||||  
QY 121 FVDSFKKGLPRPKSAGTATQMRQSSWTRVFQSWWDRNLGRGSSAPSQ 168  
|||||  
Db 121 FVDSFKKGLPRPKSAGTATQMRQSSWTRVFQSWWDRNLGRGSSAPSQ 168  
|||||

## RESULT 3

US-09-376-154-2  
; Sequence 2, Application US/09376154  
; GENERAL INFORMATION:  
; APPLICANT: Horne, William A.  
; APPLICANT: Oltersdorf, Tilman  
; TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC  
; FILE REFERENCE: 480140.428D2  
; CURRENT APPLICATION NUMBER: US/09/376,154  
; CURRENT FILING DATE: 1999-08-17  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 168  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-376-154-2

Query Match 100.0%; Score 905; DB 17; Length 168;  
Best Local Similarity 100.0%; Pred. No. 5.3e-71;  
Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFQIPEFEPSEQEDSSAERGLGSPAGDGPSSGKHHROAPGLLWDASHQEQPTSSSH 60  
|||||  
Db 1 MFQIPEFEPSEQEDSSAERGLGSPAGDGPSSGKHHROAPGLLWDASHQEQPTSSSH 60  
|||||  
QY 61 HCGAGAVEIRSRHSSYPAGTDEDEGMGEPPSPRGRSRAPPNLWAAQRYGRELRRMSDE 120  
|||||  
Db 61 HCGAGAVEIRSRHSSYPAGTDEDEGMGEPPSPRGRSRAPPNLWAAQRYGRELRRMSDE 120  
|||||

QY 121 FVDSFKKGLPRPKSAGTATQMRQSSWTRVFQSWWDRNLGRGSSAPSQ 168  
|||||  
Db 121 FVDSFKKGLPRPKSAGTATQMRQSSWTRVFQSWWDRNLGRGSSAPSQ 168  
|||||

## RESULT 4

US-09-410-372-1  
; Sequence 1, Application US/09410372  
; GENERAL INFORMATION:  
; APPLICANT: Hillman, Jennifer L.  
; APPLICANT: Yue, Henry  
; APPLICANT: Lal, Preeti  
; APPLICANT: Shah, Purvi  
; APPLICANT: Corley, Neil C.  
; TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL  
; TITLE OF INVENTION: PROLIFERATION  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSER: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Dr.  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/410,372  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/985,335  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J.  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0421 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-855-0555  
TELEFAX: 650-845-4166  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 168 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: SYNORAB01  
CLONE: 358673  
US-09-410-372-1

Query Match 100.0%; Score 905; DB 18; Length 168;  
Best Local Similarity 100.0%; Pred. No. 5.3e-71;  
Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFQIPEFEPSEQEDSSAERGLGSPAGDGPSSGKHHROAPGLLWDASHQEQPTSSSH 60  
|||||  
Db 1 MFQIPEFEPSEQEDSSAERGLGSPAGDGPSSGKHHROAPGLLWDASHQEQPTSSSH 60  
|||||  
QY 61 HCGAGAVEIRSRHSSYPAGTDEDEGMGEPPSPRGRSRAPPNLWAAQRYGRELRRMSDE 120  
|||||  
Db 61 HCGAGAVEIRSRHSSYPAGTDEDEGMGEPPSPRGRSRAPPNLWAAQRYGRELRRMSDE 120  
|||||  
QY 121 FVDSFKKGLPRPKSAGTATQMRQSSWTRVFQSWWDRNLGRGSSAPSQ 168  
|||||  
Db 121 FVDSFKKGLPRPKSAGTATQMRQSSWTRVFQSWWDRNLGRGSSAPSQ 168  
|||||

## RESULT 5

US-09-456-357-32

; Sequence 32, Application US/09456357  
; GENERAL INFORMATION:  
; APPLICANT: 3921-1-1-1  
; TITLE OF INVENTION: VIRAL VECTORS ENCODING APOPTOSIS-INDUCING PROTEINS AND  
; TITLE OF INVENTION: METHODS FOR MAKING AND USING THE SAME  
; FILE REFERENCE: 3921-1-1-1  
; CURRENT APPLICATION NUMBER: US/09/456,357  
; CURRENT FILING DATE: 1999-12-08  
; EARLIER APPLICATION NUMBER: 60/134,416  
; EARLIER FILING DATE: 1999-05-17  
; EARLIER APPLICATION NUMBER: 09/087,195  
; EARLIER FILING DATE: 1998-05-29  
; EARLIER APPLICATION NUMBER: 08/378,507  
; EARLIER FILING DATE: 1995-01-26  
; EARLIER APPLICATION NUMBER: 08/250,478  
; EARLIER FILING DATE: 1994-05-27  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 32  
; LENGTH: 168  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-456-357-32

Query Match 100.0%; Score 905; DB 18; Length 168;  
Best Local Similarity 100.0%; Pred. No. 5.3e-71;  
Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MFQIPEFPSEQDSSSAERGLGSPAGDGPSSGKHHRRQAPGLLWDASHQOQPTSSSH 60  
Db 1 MFQIPEFPSEQDSSSAERGLGSPAGDGPSSGKHHRRQAPGLLWDASHQOQPTSSSH 60  
Qy 61 HGGAGAVEIRSRHSSYPAGTDEDCMGEEPPFGRGSRSSAPPNLWAAQRYGRELRMSDE 120  
Db 61 HGGAGAVEIRSRHSSYPAGTDEDCMGEEPPFGRGSRSSAPPNLWAAQRYGRELRMSDE 120  
Qy 121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168  
Db 121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168

RESULT 6  
US-09-580-523-1  
; Sequence 1, Application US/09580523  
; GENERAL INFORMATION:  
; APPLICANT: Zhou, Xiao-Mai  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR REGULATING APOPTOSIS,  
; TITLE OF INVENTION: AND METHODS OF MAKING AND SCREENING FOR COMPOUNDS  
; TITLE OF INVENTION: THAT REGULATE APOPTOSIS  
; FILE REFERENCE: A7483  
; CURRENT APPLICATION NUMBER: US/09/580,523  
; CURRENT FILING DATE: 2000-05-30  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 168  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-580-523-1

Query Match 100.0%; Score 905; DB 19; Length 168;  
Best Local Similarity 100.0%; Pred. No. 5.3e-71;  
Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MFQIPEFPSEQDSSSAERGLGSPAGDGPSSGKHHRRQAPGLLWDASHQOQPTSSSH 60  
Db 1 MFQIPEFPSEQDSSSAERGLGSPAGDGPSSGKHHRRQAPGLLWDASHQOQPTSSSH 60  
Qy 61 HGGAGAVEIRSRHSSYPAGTDEDCMGEEPPFGRGSRSSAPPNLWAAQRYGRELRMSDE 120  
Db 61 HGGAGAVEIRSRHSSYPAGTDEDCMGEEPPFGRGSRSSAPPNLWAAQRYGRELRMSDE 120

Qy 121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168  
Db 121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168  
RESULT 7  
US-09-587-473-21  
; Sequence 21, Application US/09587473  
; GENERAL INFORMATION:  
; APPLICANT: Zhang, Hui  
; APPLICANT: Tsvetkov, Lyuben  
; TITLE OF INVENTION: Protein Knockout Technology  
; FILE REFERENCE: 44574-5047-WO  
; CURRENT APPLICATION NUMBER: US/09/587,473  
; CURRENT FILING DATE: 2000-06-05  
; PRIOR APPLICATION NUMBER: US 60/137,494  
; PRIOR FILING DATE: 1999-06-04  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 21  
; LENGTH: 168  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-587-473-21

Query Match 100.0%; Score 905; DB 19; Length 168;  
Best Local Similarity 100.0%; Pred. No. 5.3e-71;  
Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MFQIPEFPSEQDSSSAERGLGSPAGDGPSSGKHHRRQAPGLLWDASHQOQPTSSSH 60  
Db 1 MFQIPEFPSEQDSSSAERGLGSPAGDGPSSGKHHRRQAPGLLWDASHQOQPTSSSH 60  
Qy 61 HGGAGAVEIRSRHSSYPAGTDEDCMGEEPPFGRGSRSSAPPNLWAAQRYGRELRMSDE 120  
Db 61 HGGAGAVEIRSRHSSYPAGTDEDCMGEEPPFGRGSRSSAPPNLWAAQRYGRELRMSDE 120  
Qy 121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168  
Db 121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168

RESULT 8  
US-08-883-731-2  
; Sequence 2, Application US/08883731  
; GENERAL INFORMATION:  
; APPLICANT: Zhu, Li  
; APPLICANT: Xudong, Yin  
; TITLE OF INVENTION: Gene and Protein for Regulation Cell Death  
; FILE REFERENCE: D6120  
; CURRENT APPLICATION NUMBER: US/08/883,731  
; CURRENT FILING DATE: 1997-06-27  
; EARLIER APPLICATION NUMBER: US 08/665,617  
; EARLIER FILING DATE: 1996-06-18  
; NUMBER OF SEQ ID NOS: 3  
; SEQ ID NO 2  
; LENGTH: 168  
; TYPE: PRT  
; ORGANISM: unknown  
; FEATURE:  
; LOCATION:  
; OTHER INFORMATION: Protein encoded by the BBC6 gene.  
US-08-883-731-2

Query Match 82.2%; Score 744; DB 12; Length 168;  
Best Local Similarity 85.1%; Pred. No. 6.4e-57;  
Matches 143; Conservative 0; Mismatches 25; Indels 0; Gaps 0;  
Qy 1 MFQIPEFPSEQDSSSAERGLGSPAGDGPSSGKHHRRQAPGLLWDASHQOQPTSSSH 60  
Db 1 MFQIPEFPSEQDSSSAERGLGSPAGDGPSSGKHHRRQAPGLLWDASHQOQPTSSSH 60

Db 1 MFOIPEFPESEQEDSSAERGLGSPAGDGPSCGKHHRQAPGLLDASHQQEQPTSSSH 60  
QY 61 HGGAGAVEIRSRHSSYPAGTDEDEGMGEPPFRGRSRSPPNLWAAQRYGRELRRMSDE 120  
Db 61 HGRWCGDPESQQLPRGDGRRDRGGGAQPFGRSRSPPNLWAAQRYGRELRRMSDE 120  
QY 121 FVDSFKKGLPRPSAGTATQMRQSSSWTRVFQSWDRNLGRGSSAPSQ 168  
Db 121 FVDSFKKGLPRPSAGTATQMRQSSSWTRVFQSWDRNLGRGSSAPSQ 168  
RESULT 9  
US-09-410-372-7  
; Sequence 7, Application US/09410372  
; GENERAL INFORMATION:  
; APPLICANT: Hillman, Jennifer L.  
; APPLICANT: Yue, Henry  
; APPLICANT: Lal, Preeti  
; APPLICANT: Shah, Purvi  
; APPLICANT: Corley, Neil C.  
; TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Dr.  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/410,372  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/985,335  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Billings, Lucy J.  
; REGISTRATION NUMBER: 36,749  
; REFERENCE/DOCKET NUMBER: PF-0421 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-855-0555  
; TELEFAX: 650-845-4166  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 168 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: GenBank  
; CLONE: 1683637  
US-09-410-372-7  
Query Match 82.2%; Score 744; DB 18; Length 168;  
Best Local Similarity 85.1%; Pred. No. 6.4e-57;  
Matches 143; Conservative 0; Mismatches 25; Indels 0; Gaps 0;  
QY 1 MFOIPEFPESEQEDSSAERGLGSPAGDGPSCGKHHRQAPGLLDASHQQEQPTSSSH 60  
Db 1 MFOIPEFPESEQEDSSAERGLGSPAGDGPSCGKHHRQAPGLLDASHQQEQPTSSSH 60  
QY 61 HGGAGAVEIRSRHSSYPAGTDEDEGMGEPPFRGRSRSPPNLWAAQRYGRELRRMSDE 120  
Db 61 HGRWCGDPESQQLPRGDGRRDRGGGAQPFGRSRSPPNLWAAQRYGRELRRMSDE 120  
QY 121 FVDSFKKGLPRPSAGTATQMRQSSSWTRVFQSWDRNLGRGSSAPSQ 168

Db 121 FVDSFKKGLPRPSAGTATQMRQSSSWTRVFQSWDRNLGRGSSAPSQ 168  
RESULT 10  
US-60-197-873-16338  
; Sequence 16338, Application US/60197873  
; GENERAL INFORMATION:  
; APPLICANT: Bejanin, Stephane  
; APPLICANT: Tanaka, Hiroaki  
; APPLICANT: Dumas Milne Edwards, Jean Baptiste  
; APPLICANT: Jobert, Seyerin  
; APPLICANT: Giordano, Jean-Yves  
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.  
; FILE REFERENCE: 81 US1 PRO  
; CURRENT APPLICATION NUMBER: US/60/197,873  
; CURRENT FILING DATE: 2000-04-18  
; NUMBER OF SEQ ID NOS: 52153  
; SOFTWARE: Patent.pm  
; SEQ ID NO 16338  
; LENGTH: 125  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-60-197-873-16338  
Query Match 74.4%; Score 673; DB 23; Length 125;  
Best Local Similarity 100.0%; Pred. No. 7.2e-51;  
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MFOIPEFPESEQEDSSAERGLGSPAGDGPSCGKHHRQAPGLLDASHQQEQPTSSSH 60  
Db 1 MFOIPEFPESEQEDSSAERGLGSPAGDGPSCGKHHRQAPGLLDASHQQEQPTSSSH 60  
QY 61 HGGAGAVEIRSRHSSYPAGTDEDEGMGEPPFRGRSRSPPNLWAAQRYGRELRRMSDE 120  
Db 61 HGGAGAVEIRSRHSSYPAGTDEDEGMGEPPFRGRSRSPPNLWAAQRYGRELRRMSDE 120  
QY 121 FVDSF 125  
Db 121 FVDSF 125  
RESULT 11  
PCT-US00-11864-3  
; Sequence 3, Application PC/TUS0011864  
; GENERAL INFORMATION:  
; APPLICANT: APOPTOSIS TECHNOLOGY, INC.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR REGULATING APOPTOSIS,  
; TITLE OF INVENTION: AND METHODS OF MAKING AND SCREENING FOR COMPOUNDS  
; TITLE OF INVENTION: THAT REGULATE APOPTOSIS  
; FILE REFERENCE: F137122  
; CURRENT APPLICATION NUMBER: PCT/US00/11864  
; CURRENT FILING DATE: 2000-05-30  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 162  
; TYPE: PRT  
; ORGANISM: Mus musculus  
PCT-US00-11864-3  
Query Match 71.7%; Score 649; DB 1; Length 162;  
Best Local Similarity 75.6%; Pred. No. 1.2e-48;  
Matches 127; Conservative 12; Mismatches 23; Indels 6; Gaps 3;  
QY 1 MFOIPEFPESEQEDSSAERGLGSPAGDGPSCGKHHRQAPGLLDASHQQEQPTSSSH 60  
Db 1 MFOIPEFPESEQEDASATDRGLGSLTEQDQPGY--LAPGLGSLNHQOGRATNSH 55  
QY 61 HGGAGAVEIRSRHSSYPAGTDEDEGMGEPPFRGRSRSPPNLWAAQRYGRELRRMSDE 120

Db 56 HGGAGAMETRRSHSSYPAGTEDEGMEELSPPFRGRSRAPPNLWAAQRYGRELRRMSDE 115  
QY 121 FVDSFKKGLPRPKSAGTATQMRQSSWTRVFQSWWDRNLGRCSSAPSQ 168  
Db 116 FEGSF-KGLPRPKSAGTATQMRQSSAGWTRIIQSWWDRNLGKGGSTPSQ 162

RESULT 12  
US-09-580-523-3  
; Sequence 3, Application US/09580523  
; GENERAL INFORMATION:  
; APPLICANT: Zhou, Xiao-Mai  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR REGULATING APOPTOSIS,  
; TITLE OF INVENTION: AND METHODS OF MAKING AND SCREENING FOR COMPOUNDS  
; TITLE OF INVENTION: THAT REGULATE APOPTOSIS  
; FILE REFERENCE: A7483  
; CURRENT APPLICATION NUMBER: US/09/580,523  
; CURRENT FILING DATE: 2000-05-30  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 162  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-580-523-3

Query Match 71.7%; Score 649; DB 19; Length 162;  
Best Local Similarity 75.6%; Pred. No. 1.2e-48;  
Matches 127; Conservative 12; Mismatches 23; Indels 6; Gaps 3;  
QY 1 MFQIPEFPEEQEDSSAERGLGSPAGDGPSSGKHHQAPGLLWDASHQOQPTSSSH 60  
Db 1 MFQIPEFPEEQEDASATDRGLGSLTEDQP---GPY--LAPGLLGSNIHQGRAATNSH 55  
QY 61 HGGAGAVEIRSHSSYPAGTEDEGMEELSPFRGRSRAPPNLWAAQRYGRELRRMSDE 120  
Db 56 HGGAGAMETRRSHSSYPAGTEDEGMEELSPPFRGRSRAPPNLWAAQRYGRELRRMSDE 115  
QY 121 FVDSFKKGLPRPKSAGTATQMRQSSWTRVFQSWWDRNLGRCSSAPSQ 168  
Db 116 FEGSF-KGLPRPKSAGTATQMRQSSAGWTRIIQSWWDRNLGKGGSTPSQ 162

RESULT 13  
PCT-US00-11864-2  
; Sequence 2, Application PC/TUS0011864  
; GENERAL INFORMATION:  
; APPLICANT: APOPTOSIS TECHNOLOGY, INC.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR REGULATING APOPTOSIS,  
; TITLE OF INVENTION: AND METHODS OF MAKING AND SCREENING FOR COMPOUNDS  
; TITLE OF INVENTION: THAT REGULATE APOPTOSIS  
; FILE REFERENCE: F137122  
; CURRENT APPLICATION NUMBER: PCT/US00/11864  
; CURRENT FILING DATE: 2000-05-30  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 204  
; TYPE: PRT  
; ORGANISM: Mus musculus  
PCT-US00-11864-2

Query Match 71.7%; Score 649; DB 1; Length 204;  
Best Local Similarity 75.6%; Pred. No. 1.6e-48;  
Matches 127; Conservative 12; Mismatches 23; Indels 6; Gaps 3;  
QY 1 MFQIPEFPEEQEDSSAERGLGSPAGDGPSSGKHHQAPGLLWDASHQOQPTSSSH 60  
Db 43 MFQIPEFPEEQEDASATDRGLGSLTEDQP---GPY--LAPGLLGSNIHQGRAATNSH 97  
QY 61 HGGAGAVEIRSHSSYPAGTEDEGMEELSPFRGRSRAPPNLWAAQRYGRELRRMSDE 120

Db 98 HGGAGAMETRRSHSSYPAGTEDEGMEELSPPFRGRSRAPPNLWAAQRYGRELRRMSDE 157  
QY 121 FVDSFKKGLPRPKSAGTATQMRQSSWTRVFQSWWDRNLGRCSSAPSQ 168  
Db 158 FEGSF-KGLPRPKSAGTATQMRQSSAGWTRIIQSWWDRNLGKGGSTPSQ 204

RESULT 14  
PCT-US97-15871-1  
; Sequence 1, Application PC/TUS9715871  
; GENERAL INFORMATION:  
; APPLICANT: KORSMEYER, STANLEY J.  
; TITLE OF INVENTION: MODULATION OF APOPTOSIS BY SERINE  
; TITLE OF INVENTION: PHOSPHORYLATION OF BCL-XL/BCL-2 ASSOCIATED CELL DEATH  
; TITLE OF INVENTION: REGULATOR  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: HOWELL & HAFERKAMP, L.C.  
; STREET: 7733 FORSYTH BLVD., SUITE 1400  
; CITY: ST. LOUIS  
; STATE: MISSOURI  
; COUNTRY: USA  
; ZIP: 63146  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US97/15871  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: HOLLAND, DONALD R.  
; REGISTRATION NUMBER: 35,197  
; REFERENCE/DOCKET NUMBER: 965018  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (314) 727-5188  
; TELEFAX: (314) 727-6092  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 204 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
PCT-US97-15871-1

Query Match 71.7%; Score 649; DB 1; Length 204;  
Best Local Similarity 75.6%; Pred. No. 1.6e-48;  
Matches 127; Conservative 12; Mismatches 23; Indels 6; Gaps 3;  
QY 1 MFQIPEFPEEQEDSSAERGLGSPAGDGPSSGKHHQAPGLLWDASHQOQPTSSSH 60  
Db 43 MFQIPEFPEEQEDASATDRGLGSLTEDQP---GPY--LAPGLLGSNIHQGRAATNSH 97  
QY 61 HGGAGAVEIRSHSSYPAGTEDEGMEELSPFRGRSRAPPNLWAAQRYGRELRRMSDE 120  
Db 98 HGGAGAMETRRSHSSYPAGTEDEGMEELSPPFRGRSRAPPNLWAAQRYGRELRRMSDE 157  
QY 121 FVDSFKKGLPRPKSAGTATQMRQSSWTRVFQSWWDRNLGRCSSAPSQ 168  
Db 158 FEGSF-KGLPRPKSAGTATQMRQSSAGWTRIIQSWWDRNLGKGGSTPSQ 204

RESULT 15  
PCT-US97-15871A-1  
; Sequence 1, Application PC/TUS9715871A  
; GENERAL INFORMATION:  
; APPLICANT: KORSMEYER, STANLEY J.  
; TITLE OF INVENTION: MODULATION OF APOPTOSIS BY SERINE

;; TITLE OF INVENTION: PHOSPHORYLATION OF BCL-XL/BCL-2 ASSOCIATED CELL DEATH  
;; TITLE OF INVENTION: REGULATOR  
;; NUMBER OF SEQUENCES: 12  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: HOWELL & HAFERKAMP, L.C.  
;; STREET: 7733 FORSYTH BLVD., SUITE 1400  
;; CITY: ST. LOUIS  
;; STATE: MISSOURI  
;; COUNTRY: USA  
;; ZIP: 63105  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patent In Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: PCT/US97/15871A  
;; FILING DATE:  
;; CLASSIFICATION: 435  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: HOLLAND, DONALD R  
;; REGISTRATION NUMBER: 35,197  
;; REFERENCE/DOCKET NUMBER: 6029-1938  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (314) 727-5188  
;; TELEFAX: (314) 727-6092  
;; INFORMATION FOR SEQ ID NO: 1:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 204 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS:  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
PCT-US97-15871A-1

Query Match 71.7%; Score 649; DB 1; Length 204;  
Best Local Similarity 75.6%; Pred. No. 1.6e-48;  
Matches 127; Conservative 12; Mismatches 23; Indels 6; Gaps 3;  
  
QY 1 MFQIPEFEPSEQEDSSAERGLGPSAGDGPSCGKHHKQAPGLLWDASHQOQPTSSSH 60  
|||||:|||||:|||||:| | | : ||||| ||| : :||  
Db 43 MFQIPEFEPSEQEDASATDRGLGSLTEDQP---GPY--LAPGLLGSNIHQQGRAATNSH 97  
|||||:| |||||:|||||:||||| || ||||| ||||| ||||| |||||  
QY 61 HGGAGAVEIRSRHSSYPAGTEDEGMEEPSFGRSRSPPNLWAAQRYGRELRRMSDE 120  
|||||:| |||||:|||||:||||| || ||||| ||||| ||||| |||||  
Db 98 HGGAGAMETSRHSSYPAGTEDEGMEELSPFGRSRSPPNLWAAQRYGRELRRMSDE 157  
|||||:| |||||:|||||:||||| || ||||| ||||| ||||| |||||  
QY 121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWDRNLGRGSSAPSQ 168  
| || ||||| ||||| |||||: |||: ||||| |||||  
Db 158 FEGSF-KGLPRPKSAGTATQMRQSGWTRIIQSWDRNLGKGGTPSQ 204

Search completed: October 9, 2001, 16:07:48  
Job time: 498 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 9, 2001, 16:02:10 ; Search time 36.31 Seconds  
(without alignments)  
219.441 Million cell updates/sec

Title: US-09-580-523-1

Perfect score: 905

Sequence: 1 MFQIPEFPESEDESSAER.....RVFQSWDRNLGRGSSAPSQ 168

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 311045 seqs, 47428042 residues

Total number of hits satisfying chosen parameters: 311045

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending\_Patents\_AA\_New.\*

1: /cgn2\_6/ptodata/2/paa/PCT\_NEW\_COMB.pep.\*  
2: /cgn2\_6/ptodata/2/paa/US06\_NEW\_COMB.pep.\*  
3: /cgn2\_6/ptodata/2/paa/US07\_NEW\_COMB.pep.\*  
4: /cgn2\_6/ptodata/2/paa/US08\_NEW\_COMB.pep.\*  
5: /cgn2\_6/ptodata/2/paa/US09\_NEW\_COMB.pep.\*  
6: /cgn2\_6/ptodata/2/paa/US60\_NEW\_COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	905	100.0	168	5	US-09-922-378-2	Sequence 2, Appli
2	864	95.5	201	1	PCT-US01-18569-2762	Sequence 2762, Ap
3	673	74.4	125	5	US-09-834-366-16338	Sequence 16338, A
4	646	71.4	204	5	US-09-922-378-3	Sequence 3, Appli
5	223	24.6	142	5	US-09-758-466-434	Sequence 434, App
6	122.5	13.5	211	5	US-09-758-466-716	Sequence 716, App
7	102.5	11.3	123	5	US-09-760-476-1456	Sequence 1456, Ap
8	100.5	11.1	1401	1	PCT-US01-08631-54396	Sequence 54396, A
9	95.5	10.6	743	5	US-09-902-540-10164	Sequence 10164, A
10	93.5	10.3	535	5	US-09-760-461-53	Sequence 53, Appl
11	93.5	10.3	535	5	US-09-760-485-758	Sequence 758, App
12	93.5	10.3	1203	1	PCT-US01-08656-10232	Sequence 10232, A
13	92.5	10.2	1398	5	US-09-445-353C-3	Sequence 3, Appli
14	92	10.2	296	5	US-09-760-466-1147	Sequence 1147, Ap
15	91.5	10.1	1475	1	PCT-US01-08631-44993	Sequence 44993, A
16	91	10.1	430	5	US-09-764-853-564	Sequence 564, App
17	91	10.1	684	1	PCT-US01-08631-44485	Sequence 44485, A
18	90.5	10.0	91	5	US-09-758-473-759	Sequence 759, App
19	90.5	10.0	139	1	PCT-US01-08631-46558	Sequence 46558, A
20	89.5	9.9	205	5	US-09-758-462-1232	Sequence 1232, Ap
21	89	9.8	267	5	US-09-758-472-7113	Sequence 7113, Ap
22	89	9.8	287	1	PCT-US01-08631-51566	Sequence 51566, A
23	89	9.8	889	1	PCT-US01-14827-8068	Sequence 8068, Ap
24	88	9.7	230	1	PCT-US01-08631-38449	Sequence 38449, A
25	87.5	9.7	394	1	PCT-US01-08631-32117	Sequence 32117, A
26	87.5	9.7	486	1	PCT-US01-08656-7242	Sequence 7242, Ap
27	87	9.6	418	6	US-60-306-501-92	Sequence 92, Appl

#### ALIGNMENTS

RESULT 1

US-09-922-378-2

; Sequence 2, Application US/09922378

; GENERAL INFORMATION:

; APPLICANT: Horne, William A.

; APPLICANT: Oltersdorf, Tilmann

; TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC

; FILE OF INVENTION: ACIDS AND METHODS OF USE

; FILE REFERENCE: 480140.428D3

; CURRENT APPLICATION NUMBER: US/09/922,378

; CURRENT FILING DATE: 2001-08-03

; NUMBER OF SEQ ID NOS: 15

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 2

; LENGTH: 168

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-922-378-2

Query Match

Best Local Similarity 100.0%; Score 905; DB 5; Length 168;

Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFQIPEFPESEDESSAERGLGSPAGDPSGSGKHRRQAPGLLWDASHQEQPTSSSH 60

Db 1 MFQIPEFPESEDESSAERGLGSPAGDPSGSGKHRRQAPGLLWDASHQEQPTSSSH 60

Qy 61 HGGAGAVEIRSRHSSYPAGTDEDEGMGEPPSPFRGSRSPAPNLMAAORYGRELRRMSDE 120

Db 61 HGGAGAVEIRSRHSSYPAGTDEDEGMGEPPSPFRGSRSPAPNLMAAORYGRELRRMSDE 120

Qy 121 FVDSFKGLPRPKSAGTATQMRQSSSWTRVFQSWDRNLGRGSSAPSQ 168

Db 121 FVDSFKGLPRPKSAGTATQMRQSSSWTRVFQSWDRNLGRGSSAPSQ 168

RESULT 2

PCT-US01-18569-2762

; Sequence 2762, Application PC/TUS0118569

; GENERAL INFORMATION:

; APPLICANT: Human Genome Sciences, Inc.

; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

; FILE REFERENCE: PAL33PCT

; CURRENT APPLICATION NUMBER: PCT/US01/18569

; CURRENT FILING DATE: 2001-06-07

; PRIOR APPLICATION NUMBER: 60/209,467

; PRIOR FILING DATE: 2000-06-07

; NUMBER OF SEQ ID NOS: 4360

; SOFTWARE: PatentIn Ver. 2.0

Sequence 985, App  
Sequence 10231, A  
Sequence 38680, A  
Sequence 1172, Ap  
Sequence 49667, A  
Sequence 15089, A  
Sequence 21794, A  
Sequence 8997, Ap  
Sequence 1, Appli  
Sequence 50030, A  
Sequence 45662, A  
Sequence 48762, A  
Sequence 12, Appl  
Sequence 38447, A  
Sequence 585, App  
Sequence 1761, Ap  
Sequence 8173, Ap  
Sequence 49, Appl

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; SEQ ID NO 2762
; LENGTH: 201
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (37)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (146)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (169)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (174)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; PCT-US01-18569-2762
```

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Query Match 95.5%; Score 864; DB 1; Length 201;
Best Local Similarity 98.2%; Pred. No. 5.2e-54;
Matches 160; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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```
QY 1 MFQIPEFPESEQEDSSAERGLGSPAGDGPSCGKHHRQAPGLLWDASHQEQPTSSSH 60
Db 9 MFQIPEFPESEQEDSSAERGLGSPAGDGPSCGKHHRQAPGLLWDASHQEQPTSSSH 68
QY 61 HGGAGAVEIRSRHSSYPAGTDEDEGMEEPSPPRGRSRSAPPNLWAAQRYGRELRRMSDE 120
Db 69 HGGAGAVEIRSRHSSYPAGTDEDEGMEEPSPPRGRSRSAPPNLWAAQRYGRELRRMSDE 128
QY 121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWDNLGRGS 163
Db 129 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWDNLGRGS 171
```

```
RESULT 3
US-09-834-366-16338
; Sequence 16338, Application US/09834366
; GENERAL INFORMATION:
; APPLICANT: Bejanin, Stephane
; APPLICANT: Tanaka, Hiroaki
; APPLICANT: Dumas Milne Edwards, Jean Baptiste
; APPLICANT: Jobert, Severin
; APPLICANT: Giordano, Jean-Yves
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: 81.052.REG
; CURRENT APPLICATION NUMBER: US/09/834,366
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/197,873
; PRIOR FILING DATE: 2000-04-18
; NUMBER OF SEQ ID NOS: 52153
; SOFTWARE: Patent.pm
; SEQ ID NO 16338
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-834-366-16338
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Query Match 74.4%; Score 673; DB 5; Length 125;
Best Local Similarity 100.0%; Pred. No. 8.5e-41;
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 MFQIPEFPESEQEDSSAERGLGSPAGDGPSCGKHHRQAPGLLWDASHQEQPTSSSH 60
Db 1 MFQIPEFPESEQEDSSAERGLGSPAGDGPSCGKHHRQAPGLLWDASHQEQPTSSSH 60
QY 61 HGGAGAVEIRSRHSSYPAGTDEDEGMEEPSPPRGRSRSAPPNLWAAQRYGRELRRMSDE 120
Db 61 HGGAGAVEIRSRHSSYPAGTDEDEGMEEPSPPRGRSRSAPPNLWAAQRYGRELRRMSDE 120
```

```
QY 121 FVDSF 125
Db 121 FVDSF 125
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## RESULT 4

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US-09-922-378-3
; Sequence 3, Application US/09922378
; GENERAL INFORMATION:
; APPLICANT: Horne, William A.
; APPLICANT: Oltersdorf, Tilman
; TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC
; FILE REFERENCE: 480140.428D3
; CURRENT APPLICATION NUMBER: US/09/922,378
; CURRENT FILING DATE: 2001-08-03
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 204
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-922-378-3
```

```
Query Match 71.4%; Score 646; DB 5; Length 204;
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```
Best Local Similarity 75.0%; Pred. No. 1.1e-38;
Matches 126; Conservative 13; Mismatches 23; Indels 6; Gaps 3;
```

```
QY 1 MFQIPEFPESEQEDSSAERGLGSPAGDGPSCGKHHRQAPGLLWDASHQEQPTSSSH 60
Db 43 MFQIPEFPESEQEDASATDRGLGSLTDQP---GPY--LAPGLLGSNIHQOGRATNSH 97
QY 61 HGGAGAVEIRSRHSSYPAGTDEDEGMEEPSPPRGRSRSAPPNLWAAQRYGRELRRMSDE 120
Db 98 HGGAGAVEIRSRHSSYPAGTDEDEGMEEPSPPRGRSRSAPPNLWAAQRYGRELRRMSDE 157
QY 121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWDNLGRGSAPSO 168
Db 158 FEGSF-KGLPRPKSAGTATQMRQSSSWTRVFQSWDNLGRGSPTSO 204
```

## RESULT 5

```
US-09-758-466-434
; Sequence 434, Application US/09758466
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PM036
; CURRENT APPLICATION NUMBER: US/09/758,466
; CURRENT FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 814
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 434
; LENGTH: 142
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (97)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (120)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (129)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (136)
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; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
US-09-758-466-434

Query Match 24.6%; Score 223; DB 5; Length 142;  
Best Local Similarity 45.1%; Pred. No. 4.3e-09;  
Matches 60; Conservative 8; Mismatches 37; Indels 28; Gaps 7;  
  
Qy 1 MFOIPEFPEQEDSSAERGLGSPAGDPSGSGKHHRQAPGLLW-----DA 48  
|||||  
Db 26 MFOIPEFPEQEDSSAERGLGSPAGRGP-----QAPASIIARQASCGTPSPAG 77  
|||||  
  
Qy 49 SHQOQPTSSHHGAGAVEIRSRSSYPAGTEDDEGMGEPPSPFRGRSRAPPNLWAAQ 108  
: ||| : |||  
Db 78 AANQOOP--SWRRWCGDPE---SQOFPAGTEDDEGNRSPA-LLGPXGFGPPT-FGXT 130  
|||||  
  
Qy 109 RYGRRLRMSDEF 121  
||| :|||  
Db 131 GYGRN-XELNDDF 142

RESULT 6  
US-09-758-466-716  
; Sequence 716, Application US/09758466  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PM036  
; CURRENT APPLICATION NUMBER: US/09/758,466  
; CURRENT FILING DATE: 2001-01-11  
; PRIOR APPLICATION NUMBER: 60/179,065  
; PRIOR FILING DATE: 2000-01-31  
; PRIOR APPLICATION NUMBER: 60/180,628  
; PRIOR FILING DATE: 2000-02-04  
; NUMBER OF SEQ ID NOS: 814  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 716  
; LENGTH: 211  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (72)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
; NAME/KEY: SITE  
; LOCATION: (145)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
; NAME/KEY: SITE  
; LOCATION: (153)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
; NAME/KEY: SITE  
; LOCATION: (166)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
; NAME/KEY: SITE  
; LOCATION: (170)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
; NAME/KEY: SITE  
; LOCATION: (178)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
; NAME/KEY: SITE  
; LOCATION: (199)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
; NAME/KEY: SITE  
; LOCATION: (202)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
; NAME/KEY: SITE  
; LOCATION: (206)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
US-09-758-466-716

Query Match 13.5%; Score 122.5; DB 5; Length 211;  
Best Local Similarity 27.3%; Pred. No. 0.078;  
Matches 44; Conservative 15; Mismatches 75; Indels 27; Gaps 5;  
  
Qy 19 ERGLGSPAGDPSGSGKHHRQAPGLL-WDASHQEQEQPTSSS-----HHGAGAVEIR 70  
:||| |||||  
Db 65 ORGAWAQPQTGPGSGKHHRQAPGSCGPPVTSRSQPAAMIALGLWRSQVATAPTR 124  
|||  
  
Qy 71 SRHSYPAGTEDDEGMGEPPSPFRGRSRAPPNLWAAQRYGRELRRMSDEFV----DSFK 126  
: ||| : |||  
Db 125 XHRTT-----KMGWRSPAPFGAVRAXAPQLGSLXALWRAPEMSDDXWLXRRDFFA 176  
|||  
  
Qy 127 KGLPRPKSAGTATMRQSSWTRVFSQSWMDRLNLGRSSAPS 167  
: ||| : |||  
Db 177 RXARAHNCG-----KFHWKHFSILVGYXRNXXGQGFAPS 210

RESULT 7  
US-09-760-476-1456  
; Sequence 1456, Application US/09760476  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PC015  
; CURRENT APPLICATION NUMBER: US/09/760,476  
; CURRENT FILING DATE: 2001-01-16  
; Prior application data removed - consult PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 2602  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1456  
; LENGTH: 123  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-760-476-1456

Query Match 11.3%; Score 102.5; DB 5; Length 123;  
Best Local Similarity 62.9%; Pred. No. 1.1;  
Matches 22; Conservative 2; Mismatches 4; Indels 7; Gaps 2;  
  
Qy 77 PAGTEDDEGMGEPPSPFRGRSRAPPN-----LW 105  
:|||  
Db 83 PRGTEDDEGMGEPPSPFR-RARARRPQPLGSTALW 116

RESULT 8  
PCT-US01-08631-54396  
; Sequence 54396, Application PC/TUS0108631  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc  
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES  
; FILE REFERENCE: 21272-049  
; CURRENT APPLICATION NUMBER: PCT/US01/08631  
; CURRENT FILING DATE: 2001-03-30  
; PRIOR APPLICATION NUMBER: 09/540,217  
; PRIOR FILING DATE: 2000-03-31  
; PRIOR APPLICATION NUMBER: 09/649,167  
; PRIOR FILING DATE: 2000-08-23  
; NUMBER OF SEQ ID NOS: 60736  
; SOFTWARE: Custom  
; SEQ ID NO 54396  
; LENGTH: 1401  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: DOMAIN  
; LOCATION: (199)...(248)  
; OTHER INFORMATION: Eukaryotic RNA polymerase II heptapeptide repeat proteins  
; OTHER INFORMATION: domain identified by EMATRIX, accession number BL001152, p-val  
; OTHER INFORMATION: 7.221e-09, raw score of 3.12  
PCT-US01-08631-54396

```

;
; FEATURE:
;
; NAME/KEY: SITE
; LOCATION: (236)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
;
; NAME/KEY: SITE
; LOCATION: (344)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
;
; NAME/KEY: SITE
; LOCATION: (512)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-760-461-53

```

```

Query Match      10.3%; Score 93.5; DB 5; Length 535;
Best Local Similarity 25.0%; Pred. No. 23;
Matches 41; Conservative 17; Mismatches 57; Indels 49; Gaps 8

QY      9 PSEQEDSSAERGLGPPAGDPGSGGKHHRQA-----PGLLDASHQEQPTSSSH 60
      ||: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      346 PAKPEQSSASR---PVPASRGKTLCKGDQAQPPGPPARPPRPPWSAPPRAPSSTPC 402
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      61 HGGAGAVEIRSRHSYSYPAGTDEDEGMGEPEPSPFGRSRSAPNLWAAQRYGRELRRMSDE 120
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      403 PGGA-----VREDTYPVGTG-----VPSP--ALAQGGPGSRRFLQW----- 438

QY      121 FVDSFKKGLPRPKSAGTATQMRQSSWTRVF---QSWMDRNLGR 161
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      439 -----NSMPR-----LPTLDLVEGPFERHYDFRQSCWVAISLQ 471

```

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RESULT 11
US-09-760-485-758
; Sequence 758, Application US/09760485
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PJ217
; CURRENT APPLICATION NUMBER: US/09/760,485
; CURRENT FILING DATE: 2001-01-16
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1477
; SOFTWARE: PatentIn Ver. 2.0

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		Query Match	10.3%	Score 93.5;	DB 5;	Length 535;	
		Best Local Similarity	25.0%;	Pred. No. 23;			
		Matches	41;	Conservative	17;	Mismatches	57; Indels 49; Gaps
Qy	9	PSEGEDESSAERGLGPPAGDGPSPGGSGKHHRQA-----PGLIWDASHOQEPTSSH	60				
		:: ::      :: ::      :: ::      :: ::      :: ::					
Dd	346	PAKEEQSSASR--PVPSRGKTLCKGDRAOPPGPARFPPIWSAPPRAPSSTFC	402				
Qy	61	HGGAGAEIRGRHSYYPACTDEEGMGEEPSFPRGRKSAPPNLMAAQRYGRELRRMSDE	120				
		:: ::      :: ::      :: ::      :: ::      :: ::					
Dd	403	PGA-----VREDTYPVGTOG-----VPSP-ALACGPGGSNRFLOW-----	438				
Qy	121	FVDSFKKLPRPKSAGTAGTAMQRQSSWTRVF---QSWMDRNLGR	161				
		:: ::      :: ::      :: ::      :: ::      :: ::					



RESULT 15  
PCT-US01-08631-44993  
; Sequence 44993, Application PC/TUS0108631  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc  
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES  
; FILE REFERENCE: 21272-049  
; CURRENT APPLICATION NUMBER: PCT/US01/08631  
; CURRENT FILING DATE: 2001-03-30  
; PRIOR APPLICATION NUMBER: 09/540,217  
; PRIOR FILING DATE: 2000-03-31  
; PRIOR APPLICATION NUMBER: 09/649,167  
; PRIOR FILING DATE: 2000-08-23  
; NUMBER OF SEQ ID NOS: 60736  
; SOFTWARE: Custom  
; SEQ ID NO 44993  
; LENGTH: 1475  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc.feature  
; LOCATION: (1)..(1475)  
; OTHER INFORMATION: Xaa = X or \* as defined in Table 2  
PCT-US01-08631-44993

Query Match 10.1%; Score 91.5; DB 1; Length 1475;  
Best Local Similarity 33.3%; Pred No. 93;  
Matches 41; Conservative 8; Mismatches 49; Indels 25; Gaps 8;  
QY 5 PEFPESEQEDSSAERGLGSPAGDG-PSGS-GKHHRQAPGLIWDASHQOEPTSSSHHG 62  
Db 757 PAAAPSPRE-GRSAERGWC-PAGPCAPRGXRGGRAGAP-----QHPPSRASQRG 805  
QY 63 GAGAVEIRSRHS-----SYAGTDEDDGMGEPEPFRGRSRSPPNLWAAQRYGRELR 115  
Db 806 AAGAAPXRAVHSRKLTFRAHRLAGLAGQPCRPDPVRLRG----APPPC-APARHGASAR 860  
QY 116 RMS 118  
Db 861 APS 863

Search completed: October 9, 2001, 16:08:31  
Job time: 381 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 9, 2001, 15:50:05 ; Search time 25.99 Seconds  
(without alignments)  
133.097 Million cell updates/sec

Title: us-09-580-523-1

Perfect score: 905

Sequence: 1 MFQIPEFSEQEDSSSAER.....RVFQSWDRNLGRGSSAPSQ 168

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 197339 seqs, 20590346 residues

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents\_AA.\*

1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pap.\*

2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pap.\*

3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pap.\*

4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pap.\*

5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pap.\*

6: /cgn2\_6/ptodata/2/iaa/backfiles1.pap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	905	100.0	168	2	US-08-717-123-2
2	905	100.0	168	3	US-08-985-335-1
3	751	83.0	166	1	US-08-665-617-2
4	744	82.2	168	3	US-08-985-335-7
5	649	71.7	204	1	US-08-333-565-2
6	649	71.7	204	2	US-08-661-479-2
7	649	71.7	204	2	US-08-733-505A-1
8	646	71.4	204	2	US-08-733-505A-12
9	646	71.4	204	2	US-08-733-505A-13
10	646	71.4	204	2	US-08-717-123-3
11	643	71.0	204	2	US-08-733-505A-14
12	314	34.7	59	2	US-08-733-505A-55
13	311	34.4	59	2	US-08-733-505A-56
14	311	34.4	59	2	US-08-733-505A-57
15	308	34.0	59	2	US-08-733-505A-58
16	116	12.8	23	1	US-08-333-565-10
17	116	12.8	23	2	US-08-661-479-10
18	97	10.7	2509	2	US-08-149-097D-35
19	96.5	10.7	1182	4	US-09-041-886-21
20	90	9.9	434	1	US-08-337-602-3
21	90	9.9	434	3	US-08-558-135-3
22	90	9.9	2237	1	US-08-455-543A-48
23	90	9.9	2237	2	US-08-223-305C-48
24	90	9.9	2337	3	US-08-713-118-2
25	90	9.9	2337	4	US-09-452-007-2
26	90	9.9	2339	1	US-08-455-543A-47
27	90	9.9	2339	2	US-08-223-305C-47

28	88.5	9.8	393	2	US-09-026-587-3	Sequence 3, Appli
29	88.5	9.8	393	2	US-09-227-420-3	Sequence 3, Appli
30	87	9.6	418	2	US-09-026-587-1	Sequence 1, Appli
31	87	9.6	418	2	US-09-227-420-1	Sequence 1, Appli
32	86.5	9.6	378	2	US-08-986-217-6	Sequence 6, Appli
33	86	9.5	16	1	US-08-333-565-26	Sequence 26, Appli
34	86	9.5	16	2	US-08-661-479-26	Sequence 2, Appli
35	86	9.5	591	3	US-09-082-737-2	Sequence 2, Appli
36	85	9.4	380	2	US-09-026-587-4	Sequence 4, Appli
37	85	9.4	380	2	US-09-227-420-4	Sequence 4, Appli
38	84.5	9.3	1159	2	US-08-956-242-13	Sequence 13, Appli
39	84.5	9.3	1159	3	US-09-351-215-13	Sequence 13, Appli
40	84.5	9.3	1159	4	US-09-226-012-2	Sequence 2, Appli
41	84.5	9.3	1159	4	US-09-226-012-4	Sequence 4, Appli
42	84	9.3	16	1	US-08-333-565-17	Sequence 17, Appli
43	84	9.3	16	2	US-08-661-479-17	Sequence 17, Appli
44	84	9.3	575	3	US-08-922-865-2	Sequence 2, Appli
45	82	9.1	424	2	US-08-592-214A-16	Sequence 16, Appli

ALIGNMENTS

RESULT 1  
US-08-717-123-2  
; Sequence 2, Application US/08717123  
; Patent No. 5965703  
; GENERAL INFORMATION:  
; APPLICANT: Horne, William A.  
; TITLE OF INVENTION: Human BAD Polypeptides, Encoding Nucleic  
; TITLE OF INVENTION: Acids and Methods of Use  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; STREET: 4370 La Jolla Village Drive, Suite 700  
; CITY: San Diego  
; STATE: California  
; COUNTRY: United States  
; ZIP: 92122  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/717,123  
; FILING DATE: 20-SEP-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Campbell, Cathryn A.  
; REGISTRATION NUMBER: 31,815  
; REFERENCE/DOCKET NUMBER: P-ID 1929  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 535-9001  
; TELEFAX: (619) 535-8949  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 168 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-717-123-2

Query Match 100.0%; Score 905; DB 2; Length 168;  
Best Local Similarity 100.0%; Pred. No. 4.4e-86;  
Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFQIPEFSEQEDSSSAERGLGPGSGSKHHRQAPGLLWDASHQEQPTSSSH 60

DB 1 MFQIPEFSEQEDSSSAERGLGPGSGSKHHRQAPGLLWDASHQEQPTSSSH 60

[illegible]

```

RESULT      2
US-08-985-335-1
; Sequence 1, Application US/08985335
; Patent No. 6080847
;
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Yue, Henry
; APPLICANT: Lal, Preeti
; APPLICANT: Shah, Purvi
; APPLICANT: Corley, Nell C.
; TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
; TITLE OF INVENTION: PROLIFERATION
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
;

```

Db 121 FVDFEKKGLPPKAGTATQMRQSSWTRVFQSWWDRNLGRSSAPSQ 168

RESULT 3  
US-08-665-617-2  
; Sequence 2, Application US/08665617  
; Patent No. 5663316

RESULT<sup>4</sup>  
 US-08-985-335-7  
 ; Sequence 7, Application US/08985335  
 ; Patent No. 6080847  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hillman, Jennifer L.  
 ; APPLICANT: Yue, Henry  
 ; APPLICANT: Lal, Preeti  
 ; APPLICANT: Shah, Purvi  
 ; APPLICANT: Corley, Neil C.  
 ; TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL  
 ; TITLE OF INVENTION: PROLIFERATION



NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Dr.  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/985,335  
FILING DATE: Filed Herewith  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J.  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0421 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-855-0555  
TELEFAX: 650-845-4166  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 168 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: GenBank  
CLONE: 1683637  
US-08-985-335-7

Query Match 82.2%; Score 744; DB 3; Length 168;  
Best Local Similarity 85.1%; Pred. No. 1.8e-69;  
Matches 143; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

Qy 1 MFQIPEFPESEQEDSSAERGLGSPAGDPSGSGKHHRQAPGLLWDASHQEQPTSSSH 60  
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Db 1 MFQIPEFPESEQEDSSAERGLGSPAGDPSGSGKHHRQAPGLLWDASHQEQPTSSSH 60  
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Qy 61 HGGAGAVIRSHSYSPAGTDEGMEGPEPFRGSRSPAPNLWAAQRYGRELRRMSDE 120  
|||||  
Db 61 HGGAGCGDPESPQLLRGDCGRRDGGGAQFPFRGSRSPAPNLWAAQRYGRELRRMSDE 120  
|||||  
Qy 121 FVDSFKGLPRPKSAGTATQMRQSSSWTRVFQSWMDRNLGRGSSAPSQ 168  
|||||  
Db 121 FVDSFKGLPRPKSAGTATQMRQSSSWTRVFQSWMDRNLGRGSSAPSQ 168  
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RESULT 5  
US-08-333-565-2  
Sequence 2, Application US/08333565  
Patent No. 5622852  
GENERAL INFORMATION:  
APPLICANT: KORSMEYER, Stanley J.  
TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH  
NUMBER OF SEQUENCES: 59  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Khourie and Crew  
STREET: 379 Lytton Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: US  
ZIP: 94301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/333,565  
FILING DATE: 31-OCT-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 15726A-000700  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 326-2422  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 204 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..204  
OTHER INFORMATION: /note= "Deduced amino acid sequence  
OTHER INFORMATION: of mouse BAD."  
US-08-333-565-2

Query Match 71.7%; Score 649; DB 1; Length 204;  
Best Local Similarity 75.6%; Pred. No. 1.4e-59;  
Matches 127; Conservative 12; Mismatches 23; Indels 6; Gaps 3;

Qy 1 MFQIPEFPESEQEDSSAERGLGSPAGDPSGSGKHHRQAPGLLWDASHQEQPTSSSH 60  
|||||  
Db 43 MFQIPEFPESEQEDASATDRGLGSLTDEQP---GPY--LAPGLLGSNTHQGGRAATNSH 97  
|||||  
Qy 61 HGGAGAVIRSHSYSPAGTDEGMEGPEPFRGSRSPAPNLWAAQRYGRELRRMSDE 120  
|||||  
Db 98 HGGAGAMETRSHSYSPAGTEDEGMEELSPFRGSRSPAPNLWAAQRYGRELRRMSDE 157  
|||||  
Qy 121 FVDSFKGLPRPKSAGTATQMRQSSSWTRVFQSWMDRNLGRGSSAPSQ 168  
|||||  
Db 158 FEGSPF-KGLPRPKSAGTATQMRQSGAGWTRIIQSWMDRNLGKGSTPSQ 204  
|||||

RESULT 6  
US-08-661-479-2  
Sequence 2, Application US/08661479  
Patent No. 5834209  
GENERAL INFORMATION:  
APPLICANT: KORSMEYER, Stanley J.  
TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH  
NUMBER OF SEQUENCES: 59  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Khourie and Crew  
STREET: 379 Lytton Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: US  
ZIP: 94301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/661,479  
FILING DATE: 11-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/333,565



Db 43 MFQIPEPESQEDASATDRGLGSLTEDQP---GPY--LAPGLLGSNIHQGRAATNSH 97  
Qy 61 HGGAGAVEIRSRHSSYPAGTDEDEGMEEPSPFRGRSRAPPNLWAAQRYGRELRRMSDE 120  
Db 98 HGGAGAMETRSRHSYAPGTDEGMEELSPFRGRSRAPPNLWAAQRYGRELRRMSDE 157  
Qy 121 FVDSFKKGLPRPKSAGTATQMRQSSWTRVFQSWWDRNLGRGSSAPSQ 168  
Db 158 FEGSF-KGLPRKSAGTATQMRQSGWTRIIQSWWDRNLGRGGSPTPSQ 204

## RESULT 9

US-08-733-505A-13  
; Sequence 13, Application US/08733505A  
; Patent No. 5856445  
; GENERAL INFORMATION:  
; APPLICANT: KORSMEYER, STANLEY J.  
; TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF  
; TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR  
; NUMBER OF SEQUENCES: 60  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: HOWELL & HAFERKAMP, L.C.  
; STREET: 7733 FORSYTH BLVD., SUITE 1400  
; CITY: ST. LOUIS  
; STATE: MISSOURI  
; COUNTRY: USA  
; ZIP: 63105  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/733,505A  
; FILING DATE:  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: HOLLAND, DONALD R.  
; REGISTRATION NUMBER: 35,197  
; REFERENCE/DOCKET NUMBER: 965458  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (314) 727-5188  
; TELEFAX: (314) 727-6092  
; INFORMATION FOR SEQ ID NO: 13:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 204 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-733-505A-13

Query Match 71.4%; Score 646; DB 2; Length 204;  
Best Local Similarity 75.0%; Pred. No. 2.9e-59;  
Matches 126; Conservative 13; Mismatches 23; Indels 6; Gaps 3;

Qy 1 MFQIPEPESQEDSSSAERGLGSPAGDGPSPGSKHHRQAPGLLWDASHOEOPTSSSH 60  
Db 43 MFQIPEPESQEDASATDRGLGSLTEDQP---GPY--LAPGLLGSNIHQGRAATNSH 97  
Qy 61 HGGAGAVEIRSRHSSYPAGTDEDEGMEEPSPFRGRSRAPPNLWAAQRYGRELRRMSDE 120  
Db 98 HGGAGAMETRSRHSYAPGTDEGMEELSPFRGRSRAPPNLWAAQRYGRELRRMSDE 157  
Qy 121 FVDSFKKGLPRPKSAGTATQMRQSSWTRVFQSWWDRNLGRGSSAPSQ 168  
Db 158 FEGSF-KGLPRKSAGTATQMRQSGWTRIIQSWWDRNLGRGGSPTPSQ 204

## RESULT 10

US-08-717-123-3

; Sequence 3, Application US/08717123  
; Patent No. 5965703  
; GENERAL INFORMATION:  
; APPLICANT: Horne, William A.  
; APPLICANT: Oltersdorf, Tilman  
; TITLE OF INVENTION: Human BAD Polyptides, Encoding Nucleic  
; TITLE OF INVENTION: Acids and Methods of Use  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Campbell and Flores  
; STREET: 4370 La Jolla Village Drive, Suite 700  
; CITY: San Diego  
; STATE: California  
; COUNTRY: United States  
; ZIP: 92122  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/717,123  
; FILING DATE: 20-SEP-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Campbell, Cathryn A.  
; REGISTRATION NUMBER: 31,815  
; REFERENCE/DOCKET NUMBER: P-ID 1929  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 535-9001  
; TELEFAX: (619) 535-8949  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 204 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; US-08-717-123-3

Query Match 71.4%; Score 646; DB 2; Length 204;  
Best Local Similarity 75.0%; Pred. No. 2.9e-59;  
Matches 126; Conservative 13; Mismatches 23; Indels 6; Gaps 3;

Qy 1 MFQIPEPESQEDSSSAERGLGSPAGDGPSPGSKHHRQAPGLLWDASHOEOPTSSSH 60  
Db 43 MFQIPEPESQEDASATDRGLGSLTEDQP---GPY--LAPGLLGSNIHQGRAATNSH 97  
Qy 61 HGGAGAVEIRSRHSSYPAGTDEDEGMEEPSPFRGRSRAPPNLWAAQRYGRELRRMSDE 120  
Db 98 HGGAGAMETRSRHSYAPGTDEGMEELSPFRGRSRAPPNLWAAQRYGRELRRMTDE 157  
Qy 121 FVDSFKKGLPRPKSAGTATQMRQSSWTRVFQSWWDRNLGRGSSAPSQ 168  
Db 158 FEGSF-KGLPRKSAGTATQMRQSGWTRIIQSWWDRNLGRGGSPTPSQ 204

## RESULT 11

US-08-733-505A-14  
; Sequence 14, Application US/08733505A  
; Patent No. 5856445  
; GENERAL INFORMATION:  
; APPLICANT: KORSMEYER, STANLEY J.  
; TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF  
; TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR  
; NUMBER OF SEQUENCES: 60  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: HOWELL & HAFERKAMP, L.C.  
; STREET: 7733 FORSYTH BLVD., SUITE 1400  
; CITY: ST. LOUIS  
; STATE: MISSOURI  
; COUNTRY: USA  
; ZIP: 63105  
; COMPUTER READABLE FORM:



; Sequence 57, Application US/08733505A  
; Patent No. 5856445  
; GENERAL INFORMATION:  
; APPLICANT: KORSMEYER, STANLEY J.  
; TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF  
; BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR  
; NUMBER OF SEQUENCES: 60  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: HOWELL & HAFERKAMP, L.C.  
; STREET: 7733 FORSYTH BLVD., SUITE 1400  
; CITY: ST. LOUIS  
; STATE: MISSOURI  
; COUNTRY: USA  
; ZIP: 63105  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/733,505A  
; FILING DATE:  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: HOLLAND, DONALD R.  
; REGISTRATION NUMBER: 35,197  
; REFERENCE/DOCKET NUMBER: 965458  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (314) 727-5188  
; TELEFAX: (314) 727-6092  
; INFORMATION FOR SEQ ID NO: 57:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 59 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-733-505A-57

Query Match 34.4%; Score 311; DB 2; Length 59;  
Best Local Similarity 98.3%; Pred. No. 2e-25;  
Matches 58; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Qy 63 GAGAVEIRSRHSSYPAGTDEDEGMGEPPRGRSRAPPNLWAAQRYGRELRMSDEF 121  
|||||  
Db 1 GAGAVEIRSRHSSYPAGTDEDEGMGEPPRGRSRAPPNLWAAQRYGRELRMSDEF 59

RESULT 15  
US-08-733-505A-58  
; Sequence 58, Application US/08733505A  
; Patent No. 5856445  
; GENERAL INFORMATION:  
; APPLICANT: KORSMEYER, STANLEY J.  
; TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF  
; BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR  
; NUMBER OF SEQUENCES: 60  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: HOWELL & HAFERKAMP, L.C.  
; STREET: 7733 FORSYTH BLVD., SUITE 1400  
; CITY: ST. LOUIS  
; STATE: MISSOURI  
; COUNTRY: USA  
; ZIP: 63105  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/733,505A  
; FILING DATE:

; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: HOLLAND, DONALD R.  
; REGISTRATION NUMBER: 35,197  
; REFERENCE/DOCKET NUMBER: 965458  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (314) 727-5188  
; TELEFAX: (314) 727-6092  
; INFORMATION FOR SEQ ID NO: 58:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 59 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-733-505A-58  
  
Query Match 34.0%; Score 308; DB 2; Length 59;  
Best Local Similarity 96.6%; Pred. No. 4.1e-25;  
Matches 57; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
Qy 63 GAGAVEIRSRHSSYPAGTDEDEGMGEPPRGRSRAPPNLWAAQRYGRELRMSDEF 121  
|||||  
Db 1 GAGAVEIRSRHSSYPAGTDEDEGMGEPPRGRSRAPPNLWAAQRYGRELRMSDEF 59  
  
Search completed: October 9, 2001, 15:52:36  
Job time: 151 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 9, 2001, 15:54:57 ; Search time 46.39 seconds  
(without alignments)  
74.152 Million cell updates/sec

Title: US-09-580-523-1\_COPY\_143\_168

Perfect score: 145

Sequence: 1 QSSSWTRVFQSWDRNLGRGSSAPSQ 26

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_16:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phase:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_unclassified:\*
- 13: sp\_vertebrate:\*
- 14: sp\_virus:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	145	100.0	168	014803	014803 homo sapien
2	124	85.5	205	11 035147	035147 rattus norv
3	124	85.5	205	11 070256	070256 rattus norv
4	57	39.3	203	4 Q9H108	Q9H108 homo sapien
5	55	37.9	635	14 Q98808	Q98808 yam mosa
6	54	37.2	731	14 Q9E9R7	Q9E9R7 turnip mosa
7	53	36.6	169	5 Q9U749	Q9U749 trypanosoma
8	53	36.6	476	2 Q9HU59	Q9HU59 pseudomonas
9	53	36.6	807	3 Q74309	Q74309 schizosacch
10	53	36.6	3164	14 Q9IC12	Q9IC12 turnip mosa
11	51	35.2	208	14 Q89177	Q89177 feline immu
12	51	35.2	224	14 Q85536	Q85536 feline immu
13	51	35.2	242	14 P87681	P87681 feline immu
14	51	35.2	273	14 P89340	P89340 feline immu
15	51	35.2	362	9 Q9ZX99	Q9ZX99 bacterioph
16	51	35.2	410	5 Q9WIH3	Q9WIH3 drosophila
17	51	35.2	853	14 Q66935	Q66935 feline immu
18	51	35.2	855	14 Q69662	Q69662 feline immu
19	51	35.2	3255	14 Q9EAB6	Q9EAB6 lettuce mos

20	50.5	34.8	94	14	Q67611	Q67611 tomato leaf
21	50.5	34.8	197	14	Q9YU79	Q9YU79 human immun
22	50.5	34.8	328	2	Q9RTK3	Q9RTK3 deinococcus
23	50.5	34.8	361	14	Q9YL74	Q9YL74 tomato leaf
24	50	34.5	76	14	Q68831	Q68831 human cytom
25	50	34.5	144	14	Q04994	Q04994 feline immu
26	50	34.5	170	14	Q66944	Q66944 feline immu
27	50	34.5	224	14	Q85553	Q85553 feline immu
28	50	34.5	225	14	Q85528	Q85528 feline immu
29	50	34.5	264	5	Q9U2S2	Q9U2S2 caenorhabdi
30	50	34.5	299	2	Q9HVQ9	Q9HVQ9 pseudomonas
31	50	34.5	476	10	Q9MAA5	Q9MAA5 arabidopsis
32	50	34.5	634	14	Q06122	Q06122 potato viru
33	50	34.5	3061	14	Q85265	Q85265 potato viru
34	50	34.5	3081	14	Q85105	Q85105 potato viru
35	49.5	34.1	197	14	Q9YU93	Q9YU93 human immun
36	49.5	34.1	226	14	Q9WP12	Q9WP12 havana toma
37	49.5	34.1	350	14	Q71205	Q71205 potato yell
38	49.5	34.1	361	14	P89122	P89122 sida golden
39	49	33.8	158	11	Q9R0V8	Q9R0V8 rattus norv
40	49	33.8	169	14	Q66949	Q66949 feline immu
41	49	33.8	170	14	Q66939	Q66939 feline immu
42	49	33.8	460	10	Q82181	Q82181 arabidopsis
43	49	33.8	643	2	Q9I741	Q9I741 pseudomonas
44	49	33.8	726	2	Q9I0F3	Q9I0F3 pseudomonas
45	49	33.8	741	2	Q9I737	Q9I737 pseudomonas

## ALIGNMENTS

RESULT 1

014803 PRELIMINARY: PRT: 168 AA.

AC 014803;

DT 01-JAN-1998 (TREMELrel. 05, Created)

DT 01-JAN-1998 (TREMELrel. 05, Last sequence update)

DE 01-NOV-1998 (TREMELrel. 08, Last annotation update)

DE BCL-X/BCL-2 BINDING PROTEIN (FRAGMENT).

GN BAD.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=97083574; PubMed=8929532;

RA Wang H.G., Rapp U.R., Reed J.C.;

RT "Bcl-2 targets the protein kinase Raf-1 to mitochondria.";

RL Cell 87:629-638(1996).

RN [2]

RP SEQUENCE FROM N.A.

RA Takayama S., Reed J.C.;

RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.

RN [3]

RP SEQUENCE FROM N.A.

RA Otilie S., Diaz J.L., Horne W., Chang J., Wang Y., Wilson G.,

RA Weeks S., McConnell M., Chang S., Fritz L.C., Oltersdorf T.;

RL J. Biol. Chem. 0:0-0(1997).

DR EMBL; AF021792; AAB72092.1; -

DR EMBL; AF031523; AAB88124.1; -

FT NON\_TER 1

SQ SEQUENCE 168 AA; 18392 MW; 69FD8D27DDEE3241 CRC64;

Query Match 100.0%; Score 145; DB 4; Length 168;

Best Local Similarity 100.0%; Pred. No. 3.4e-13;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QSSSWTRVFQSWDRNLGRGSSAPSQ 26

Db 143 QSSSWTRVFQSWDRNLGRGSSAPSQ 168

Db 180 QSASWTRIIQSWWDNRNLGRGGSTPQ 205  
|||||: |||||: |||||: |||||

RESULT 4  
QH9H108 PRELIMINARY; PRT: 203 AA.  
ID Q9H108  
AC Q9H108;  
DT 01-MAR-2001 (TREMBLrel. 16, Created)  
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)  
DE DJ417L20.1 (CYSTEINE-RICH SECRETORY PROTEIN 3 (CRISP-3, SGP28))  
DE DE (FRAGMENT).  
GN DJ417L20.1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
ON NCBI\_TaxID=9606;  
RX [1]  
RN RP SEQUENCE FROM N.A.  
RA Phillimore B.  
RL Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.  
FT ENBL; ALI21974; CAC19654.1; -.  
DR NON\_TER 203  
SQ SEQUENCE 203 AA; 22912 MW; F80D707E0D81A2B CRC64;

Query Match 39.3%; Score 57; DB 4; Length 203;  
Best Local Similarity 39.3%; Pred.No. 1.2;  
Matches 11; Conservative 5; Mismatches 8; Indels 4;  
G

QY 2 SSSWTRVFQSWMWR----NLGRGSAPS 25  
|||||: |||||: | | | : | | |:  
DB 106 SSSWSQAISQSFEDYNDFGVGPKTPN 133

RESULT 5  
Q98808 PRELIMINARY; PRT: 635 AA.  
ID Q98808  
AC Q98808;  
DT 01-FEB-1997 (TREMBLrel. 02, Created)  
DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)  
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)  
DE PUTATIVE CI PROTEIN (FRAGMENT).  
DE YAM MOSAIC VIRUS.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;  
OC Potyvirus.  
OX NCBI\_TaxID=41460;  
RP [1]  
RE SEQUENCE FROM N.A.  
RC STRAIN=IVORY COAST;  
RX MEDLINE=96370790; PubMed=8774686;  
RA Aleman M.E., Marcos J.F., Brigidou C., Beachy R.N., Fauquet C.;  
RT "The complete nucleotide sequence of Yam mosaic virus (Ivory Coast isolate) genomic RNA."  
RT Arch.Virol. 141:1259-1278(1996).  
CC -1- SIMILARITY: TO HELICASE C-TERMINAL DOMAIN.  
DR ENBL; U42596; AAC5551.1; -.  
DR InterPro; IPR001410; -.  
DR InterPro; IPR001650; -.  
DR Pfam; PF00271; helicasase.C; 1.  
DR SMART; SM00487; DEXDC; 1.  
KW ATP-binding; Helicase.  
FT NON\_TER 1  
FT .NON\_TER 635  
SQ SEQUENCE 635 AA; 70671 MW; 450FIAELB53E6BD5 CRC64;

Query Match 37.9%; Score 55; DB 14; Length 635;  
Best Local Similarity 50.0%; Pred.No. 6.8;  
Matches 8; Conservative 3; Mismatches 5; Indels 0;  
G

QY 9 FQSWWDNRNLGRGSAP 24



35 FQTWDRQIVSGRTIP 50  
 11:1111 : | : |

RESULT 6  
 Q9E9R7 PRELIMINARY; PRT; 731 AA.  
 AC Q9E9R7;  
 DT 01-MAR-2001 (TREMBlrel. 16, Created)  
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
 DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)  
 DE CYLINDRICAL INCLUSION PROTEIN (FRAGMENT).  
 GN CIP.  
 OS Turnip mosaic virus (strain Japanese) (TuMV).  
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;  
 OC Potyvirus.  
 OX NCBI\_TaxID=12230;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=59J;  
 RX MEDLINE=20417337; PubMed=10963347;  
 RA Kundu A.K., Ohshima K., Sako N., Yaegashi H.;  
 RT "Cross-reactive and major virus-specific epitopes are located at the  
 RT N-terminal halves of the cylindrical inclusion proteins of turnip  
 RT mosaic and zucchini yellow mosaic potyviruses.";  
 RL Arch. Virol. 145:1437-1447(2000).  
 DR EMBL; AB030276; BAB16312.1; -.  
 FT NON\_TER 1 731  
 FT NON\_TER 731 731  
 SQ SEQUENCE 731 AA; 81927 MW; BD775412B970B834 CRC64;

Query Match 37.2%; Score 54; DB 14; Length 731;  
 Best Local Similarity 44.4%; Pred. No. 11;  
 Matches 8; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Qy 7 RVFQSWDRNLGRGSSAP 24  
 : | | | | : | | : |  
 Db 99 KTFASWNNHQLSRGTIP 116

RESULT 7  
 Q9U749 PRELIMINARY; PRT; 169 AA.  
 AC Q9U749;  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DE PUTATIVE 90 KDA SURFACE PROTEIN (FRAGMENT).  
 OS Trypanosoma cruzi.  
 OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.  
 OX NCBI\_TaxID=5693;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=G;  
 RA Cummings L.M., Araya J.E., Yoshida N., Franco da Silveira J.;  
 RT "Trypanosoma cruzi 90 kDa surface protein.";  
 RT Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF157837; AAF09450.1; -.  
 DR InterPro; IPR001594; -.  
 DR PRODOM; PD003041; -; 1.  
 FT NON\_TER 1 169  
 FT NON\_TER 169 169  
 SQ SEQUENCE 169 AA; 17147 MW; BE298D2CE8701265 CRC64;

Query Match 36.6%; Score 53; DB 5; Length 169;  
 Best Local Similarity 38.9%; Pred. No. 3.5;  
 Matches 7; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Qy 8 VFQSWDRNLGRGSSAPS 25  
 : | | | | : | : |  
 Db 54 ILESWERNLEKAATVAS 71

RESULT 8  
 Q9HU59 PRELIMINARY; PRT; 476 AA.  
 AC Q9HU59;  
 DT 01-MAR-2001 (TREMBlrel. 16, Created)  
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
 DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)  
 DE TWO-COMPONENT RESPONSE REGULATOR NTRC.  
 GN NTRC OR PA5125.  
 OS Pseudomonas aeruginosa.  
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;  
 OC Pseudomonas.  
 OX NCBI\_TaxID=287;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=PA01;  
 RX MEDLINE=20437337; PubMed=10984043;  
 RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warringer P.,  
 RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,  
 RA Garber R.L., Goltry L., Tolentino E., Westbrook-Wadman S., Yuan Y.,  
 RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,  
 RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.F.,  
 RA Reizer J., Salier M.H., Hancock R.E.W., Lory S., Olson M.V.;  
 RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an  
 RT opportunistic pathogen.";  
 RL Nature 406:959-964(2000).  
 DR EMBL; AE004925; AAG08510.1; -.  
 DR InterPro; IPR001789; -.  
 DR InterPro; IPR002078; -.  
 DR InterPro; IPR002197; -.  
 DR Pfam; PF00072; response\_reg; 1.  
 DR Pfam; PF00158; sigma54; 1.  
 DR PROSITE; PS00675; SIGMA54\_INTERACT\_1; 1.  
 DR PROSITE; PS00676; SIGMA54\_INTERACT\_2; 1.  
 DR PROSITE; PS00688; SIGMA54\_INTERACT\_3; 1.  
 DR PROSITE; PS00045; SIGMA54\_INTERACT\_4; 1.  
 SQ SEQUENCE 476 AA; 52753 MW; 7DEBD71BA300A773 CRC64;

Query Match 36.6%; Score 53; DB 2; Length 476;  
 Best Local Similarity 38.1%; Pred. No. 9.8;  
 Matches 8; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Qy 2 SSSWTRVFQSWDRNLGRSS 22  
 : | | : | : | | | |  
 Db 396 AANWEALRWADQALGRQS 416

RESULT 9  
 O74309 PRELIMINARY; PRT; 807 AA.  
 AC O74309;  
 DT 01-NOV-1998 (TREMBlrel. 08, Created)  
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)  
 DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)  
 DE HISTONE TRANSCRIPTIONAL REGULATOR HOMOLOG.  
 GN SPBC15D4.03.  
 OS Schizosaccharomyces pombe (Fission yeast).  
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;  
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;  
 OC Schizosaccharomycetes.  
 OX NCBI\_TaxID=4896;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=972H-;  
 RA Lyne M., Rajadream M.A., Barrell B.G., Lucas M., Gaillardin C.;  
 RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AL031349; CAA20478.1; -.  
 DR InterPro; IPR001680; -.  
 DR Pfam; PF00400; WD40; 5.  
 DR PROSITE; PS00678; WD\_REPEATS; UNKNOWN\_1.

DR SMART; SM00320; WD40; 1.  
KW Repeat; WD repeat.  
SQ SEQUENCE 807 AA; 90432 MW; B8BFB73852EB7B45 CRC64;

Query Match 36.6%; Score 53; DB 3; Length 807;  
Best Local Similarity 66.7%; Pred. No. 16;  
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 2 SSSWTRVFQSWW 13  
||||| : ||

Db 624 SSSWLRVSEGW 635

RESULT 10

O9IC12 PRELIMINARY; PRT; 3164 AA.

AC Q9IC12;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
DE POLYPROTEIN.

OS Turnip mosaic virus (strain Japanese) (TuMV).

OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;  
OC Potyvirus.

OX NCBI\_TaxID=12230;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=UK1.

RA Jenner C.E., Sanchez F., Ponz F., Walsh J.A.;

RT "The cylindrical inclusion gene of Turnip mosaic potyvirus encodes a  
pathogenic determinant to the Brassica resistance gene TuRB01.";

RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.

CC -1- SIMILARITY: TO DEAD/DEAH BOX HELICASE FAMILY.

DR EMBL: AF169561; AAF89676.1; -

DR InterPro: IPR001205; -

DR InterPro: IPR001254; -

DR InterPro: IPR001410; -

DR InterPro: IPR001456; -

DR InterPro: IPR001592; -

DR InterPro: IPR001730; -

DR InterPro: IPR002540; -

DR Pfam: PF00270; DEAD; 1.

DR Pfam: PF00680; RNA\_dep\_RNA\_pol; 1.

DR Pfam: PF00767; Poly\_coat; 1.

DR Pfam: PF00851; Peptidase\_C6; 1.

DR Pfam: PF00863; Peptidase\_C4; 1.

DR Pfam: PF01577; Poly\_P1; 1.

DR PRINTS; PR00966; NIAPOTYPTASE.

DR SMART; SM00487; DEXDC; 1.

KW ATP-binding; Helicase.

SQ SEQUENCE 3164 AA; 357537 MW; 59D7BAF3734B7991 CRC64;

Query Match 36.6%; Score 53; DB 14; Length 3164;  
Best Local Similarity 44.4%; Pred. No. 63;  
Matches 8; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

OY 7 RVFQSWDRNLGRGSSAP 24

: ||||| : ||| : |

Db 1261 KTFASWWSHQLSRGFTIP 1278

RESULT 11

O89177 PRELIMINARY; PRT; 208 AA.

AC O89177;

DT 01-NOV-1998 (TrEMBLrel. 08, Created)

DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)

DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)

DE ENVELOPE GLYCOPROTEIN (FRAGMENT).

GN ENV.

OS Feline immunodeficiency virus.

OC Viruses; Retroid viruses; Retroviridae; Lentivirus.

OX NCBI\_TaxID=11673;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=AIC02;

RA Nishimura Y., Goto Y., Hai P., Momoi Y., Endo Y., Mizuno T.,

RT Watarai T., Tsujimoto H., Hasegawa A.;

RT "Genetic heterogeneity of ENV gene of Feline immunodeficiency virus  
obtained from several districts in Japan.";

RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.

DR EMBL: AB010397; BAA31442.1; -

KW Envelope protein.

FT NON\_TER 1

FT NON\_TER 208

SQ SEQUENCE 208 AA; 24090 MW; CD2AAECE2CEA777B CRC64;

Query Match 35.2%; Score 51; DB 14; Length 208;  
Best Local Similarity 56.2%; Pred. No. 8.3;  
Matches 9; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 QSSSWTRVFQSWWDRN 16

||||| : |||

Db 24 QSGSWIRTSSWKORN 39

RESULT 12

O85536 PRELIMINARY; PRT; 224 AA.

ID Q85536;

AC Q85536;

DT 01-NOV-1996 (TrEMBLrel. 01, Created)

DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)

DE GP100 (FRAGMENT).

GN ENV.

OS Feline immunodeficiency virus.

OC Viruses; Retroid viruses; Retroviridae; Lentivirus.

OX NCBI\_TaxID=11673;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=USILBNY03B;

RX MEDLINE-94187063; PubMed-8139008;

RA Sodora D.L., Shpaer E.G., Kitchell B.E., Dow S.W., Hoover E.A.,

RT Mullins J.I.;

RT "Identification of three feline immunodeficiency virus (FIV) env gene  
subtypes and comparison of the FIV and human immunodeficiency virus

RT type 1 evolutionary patterns.";

RL J. Virol. 68:2230-2238(1994).

DR EMBL: U02418; AAA18042.1; -

FT NON\_TER 1

FT NON\_TER 224

SQ SEQUENCE 224 AA; 25902 MW; 05EFAB6FD45A0E4E CRC64;

Query Match 35.2%; Score 51; DB 14; Length 224;  
Best Local Similarity 56.2%; Pred. No. 9;  
Matches 9; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 QSSSWTRVFQSWWDRN 16

||||| : |||

Db 41 QSGSWIRTSSWKORN 56

RESULT 13

P87681

ID P87681

AC P87681;

DT 01-MAY-1997 (TrEMBLrel. 03, Created)

DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)

DT 01-JAN-1999 (TrEMBLrel. 09, Last annotation update)

DE ENV PROTEIN (FRAGMENT).

GN ENV.

OS Feline immunodeficiency virus.

```
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=111673;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LP9;
RX MEDLINE=96406913; PubMed=8811000;
RA Pecoraro M.R., Tomonaga K., Miyazawa T., Kawaguchi Y., Sugita S.,
RA Tohya Y., Kai C., Etcheverrigaray M.E., Mikami T.;
RT "Genetic diversity of Argentine isolates of feline immunodeficiency
RT virus.";
RL J. Gen. Virol. 77:2031-2035(1996).
DR EMBL; D84497; BAA12687.1; -.
FT NON_TER 1
FT NON_TER 242 242
SQ SEQUENCE 242 AA; 28035 MW; 3CF75A2F5E37DBF0 CRC64;

Query Match 35.2%; Score 51; DB 14; Length 242;
Best Local Similarity 56.2%; Pred. No. 9.7;
Matches 9; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Oy 1 QSSSWTRVFQSWWDRN 16
Db 33 QSGSWIRTSSWKQRN 48

RESULT 14
P89340
ID P89340 PRELIMINARY; PRT; 273 AA.
AC P89340;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03; Last sequence update)
DE 01-JAN-1999 (TrEMBLrel. 09, Last annotation update)
DE ENVELOPE POLYPEPTIDE (FRAGMENT).
OS Feline immunodeficiency virus.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=111673;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PBMC;
RX MEDLINE=97079094; PubMed=8920826;
RA Nishimura Y., Nakamura S., Goto N., Hasegawa T., Pang H., Goto Y.,
RA Kato H., Youn H.Y., Endo Y., Mizuno T., Momoi Y., Ohno K., Watari T.,
RA Tsujimoto H., Hasegawa A.;
RT "Molecular characterization of feline immunodeficiency virus genome
RT obtained directly from organs of a naturally infected cat with marked
RT neurological symptoms and encephalitis.";
RL Arch. Virol. 141:1933-1948(1996).
DR EMBL; D67064; BAA1080.1; -.
KW Polyprotein; Envelope protein.
FT NON_TER 1
FT NON_TER 273 273
SQ SEQUENCE 273 AA; 31263 MW; 33B3724B6EFD7D99 CRC64;

Query Match 35.2%; Score 51; DB 14; Length 273;
Best Local Similarity 56.2%; Pred. No. 11;
Matches 9; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Oy 1 QSSSWTRVFQSWWDRN 16
Db 25 QSGSWIRTSSWKQRN 40

RESULT 15
Q92X99
ID Q92X99 PRELIMINARY; PRT; 362 AA.
AC Q92X99;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10; Last sequence update)
DE 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE GP50.
GN 50.
```

```
OS Bacteriophage phi-C31.
OC Viruses; dsDNA viruses, no RNA stage; Tailed phages; Siphoviridae;
OC Lambda phage group.
OX NCBI_TaxID=10719;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NORWICH STOCK;
RA Smith M.C.M.;
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=NORWICH STOCK;
RX MEDLINE=99162580; PubMed=10051617;
RA Hendrix R.W., Smith M.C.M., Burns N., Ford M.E., Hatfull G.F.;
RT "Evolutionary relationships among diverse bacteriophages and
RT prophages: all the world's a phage.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:2192-2197(1999).
DR EMBL; AJ006589; CAA07120.1; -.
SQ SEQUENCE 362 AA; 38359 MW; 878AE3DA5E53DBCA CRC64;

Query Match 35.2%; Score 51; DB 9; Length 362;
Best Local Similarity 25.5%; Pred. No. 14;
Matches 12; Conservative 4; Mismatches 9; Indels 22; Gaps 1;

Oy 1 QSSSWTRVFQSW-
Db 36 QNQAACATFVSWAALQAGESAHYPTASCATGVNFRNKGWSAYPA 82

Search completed: October 9, 2001, 15:54:58
Job time: 193 sec
```



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: October 9, 2001, 15:57:35 ; Search time 24.69 seconds  
(without alignments)  
518.320 Million cell updates/sec

Title: 09-580523-1A  
Perfect score: 902  
Sequence: 1 MFQIPEFPESEQEDSSAER.....RVFQSWMDRNLGRGSSAPSQ 168

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_68.\*

1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	64.5	71.5	204	2 A55671	bad protein - mous
2	94.5	10.5	1729	2 T18396	erythrocyte membra
3	93	10.3	1300	2 T03166	probable immediate
4	91	10.1	834	2 T42702	hypothetical prote
5	91	10.1	2248	2 A35938	profilaggrin - hum
6	90	10.0	2237	2 T45115	N-type calcium cha
7	90	10.0	2339	2 A42566	omega-conotoxin-se
8	89.5	9.9	393	2 JC5614	RNB6 protein - rat
9	88.5	9.8	336	2 T30757	hypothetical prote
10	88.5	9.8	449	1 A41520	chromogranin A pre
11	87	9.6	222	2 T43500	hypothetical prote
12	86.5	9.6	1077	2 A44067	serine-rich protei
13	86.5	9.6	1647	2 S45252	SNF2beta protein -
14	86.5	9.6	2715	2 T13049	eyelid - fruit fly
15	86	9.5	270	1 WJMS13	homeotic protein H
16	86	9.5	343	2 T05221	hypothetical prote
17	86	9.5	420	2 B38104	LFY floral meriste
18	86	9.5	646	1 S15901	chromogranin B pre
19	84.5	9.4	134	2 I54810	pHL ELF1 - human
20	84.5	9.4	1323	2 T00037	hypothetical prote
21	84.5	9.4	1392	2 T51947	probable transcrip
22	84.5	9.4	1562	2 T29146	hypothetical prote
23	84	9.3	270	1 WJH01C	homeotic protein H
24	84	9.3	313	2 A28444	filaggrin precursor
25	84	9.3	380	2 S51797	vasodilator-stimul
26	84	9.3	381	2 S16506	hypothetical prote
27	84	9.3	542	2 A44358	zyxin - chicken
28	83.5	9.3	380	2 T24786	hypothetical prote
29	83.5	9.3	625	2 A34615	profilaggrin - rat

30 83.5 9.3 1159 2 I38465 probable potassium  
31 83 9.2 337 2 T49431 endoepine related  
32 83 9.2 886 2 S07132 hypothetical prote  
33 83 9.2 2023 2 T13134 polycomb protein e  
34 82.5 9.1 523 2 T36677 probable secretory  
35 82.5 9.1 558 2 A33616 heterogeneous ribo  
36 82.5 9.1 792 2 H83736 subtilisin-type al  
37 82.5 9.1 1097 2 T13033 cyclin T - fruit f  
38 82.5 9.1 1215 2 T32734 myosin-IA - Acanth  
39 82.5 9.1 1734 2 A54602 microtubule-associ  
40 82 9.1 424 2 A38104 LFY floral meriste  
41 82 9.1 539 2 T28770 hypothetical prote  
42 82 9.1 1021 2 T10748 mannan endo-1,4-be  
43 82 9.1 1095 2 T00329 hypothetical prote  
44 82 9.1 1115 2 T13955 period protein Per  
45 81.5 9.0 254 2 A31488 filaggrin - mouse

ALIGNMENTS

RESULT 1  
A55671  
bad protein - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 03-Mar-1995 #sequence\_revision 03-Mar-1995 #text\_change 05-Nov-1999  
C:Accession: A55671  
R:Yang, E.; Zha, J.; Jockel, J.; Boise, L.H.; Thompson, C.B.; Korsmeyer, S.J.  
Cell 80, 285-291, 1995  
A:Title: Bad, a heterodimeric partner for Bcl-x-L and Bcl-2, displaces Bax and promot  
A:Reference number: A55671; MUID:95136361  
A:Accession: A55671  
A:Status: preliminary; not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-204 <YAN>  
A:Cross-references: GB:I37296; NID:g639778; PIDN:AAA64465.1; PID:g639779  
C:Keywords: heterodimer

Query Match 71.5%; Score 645; DB 2; Length 204;  
Best Local Similarity 75.0%; Pred. No. 1.le-45;  
Matches 126; Conservative 12; Mismatches 24; Indels 6; Gaps 3;

Qy 1 MFQIPEFPESEQEDSSAERGLSPAGDGPSPGSGKHRRQAPGLLDASHQEQPTSSSH 60  
Db 43 MFQIPEFPESEQEDASATDRGLGSLTEDQP---GPY--LAPGLLGSNIHQGRATNSH 97  
Qy 61 HGGAGAVEIRSRHSYPAGTDEDEGMGEPSPFGRGRSAPPNLWAAQRYGRELRRMXDE 120  
Db 98 HGGAGAMETRSRHSYPAGTDEDEGMGEELSPFGRGRSAPPNLWAAQRYGRELRRMSDE 157  
Qy 121 FVDSFKGLPRKSNAGTATOMRQSSWTRVFSQWMDRNLGRGSSAPSQ 168  
Db 158 FEGSF-KGLPRKSNAGTATMRQSGWTRIIQSWMDRNLGRGSGTPSQ 204

RESULT 2  
T18396  
erythrocyte membrane protein variant 2 - malaria parasite (Plasmodium falciparum) (fr  
C:Species: Plasmodium falciparum  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jun-2000  
C:Accession: T18396  
R:Baruch, D.I.; Pasloske, B.L.; Singh, H.B.; Bi, X.; Ma, X.C.; Feldman, M.; Taraschi,  
Cell 82, 77-87, 1995  
A:Title: Cloning the P. falciparum gene encoding PfEMP1, a malarial variant antigen a  
A:Reference number: Z18925; MUID:95330812  
A:Accession: T18396  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-1729 <BAR>  
A:Cross-references: EMBL:U27339; NID:g914920; PID:g914921; PIDN:AAA89134.1  
C:Genetics:  
A:Gene: EMP1

```
Query Match      10.1%; Score 91; DB 2; Length 2248;
Best Local Similarity 26.6%; pred. No. 18;
Matches 38; Conservative 13; Mismatches 50; Indels 42; Gaps 4;
```

---

```
Qy    11 EQDSSAER-GLGFSFAGDGPSGGKHHHQAPGLLDASHQQEQPTSSHHGG----- 63
      || || | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db    152 EQARSSACERGHSHHQQSADSSRHSGIGHGQAATAVSDSGHRGVGQSADNEGHSESD 211

Qy    64 ----AGAVEIRSRHSYYPAGTEDDEGMGEESPFRGRSR-----SAP 101
      || | : ||| | : | : | : | : | : | : | : | : | : | : | : | : |
Db    212 SQSVAGQRASRRHQSHQESt-----RGRSGGSGRGSGFLYQVSTHEQSES 258

Qy    102 PNLWAAQRYGRELRMMXDEFVDS 124
       : || || | : | :
```



chromogranin A precursor [validated] - bovine  
N:Alternate names: pituitary secretory protein I; secretory protein I  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 18-Aug-2000  
C:Accession: A41520; A28033; A24175; A60306; A61114; S15847; S39016; I46008; S38976  
R:Facangelo, A.L.; Grimes, M.; Eiden, L.E.  
Mol. Endocrinol. 5, 1651-1660, 1991  
A:Title: The bovine chromogranin A gene: structural basis for hormone regulation and gene expression  
A:Reference number: A41520; MUID:92140395  
A:Accession: A41520  
A:Status: not compared with conceptual translation  
A:Molecule type: DNA  
A:Residues: 1-449 <IAC>  
A:Cross-references: GB:S79270; NID:q244423; PIDN:AA621297.1; PID:q244424  
R:Ahm, T.G.; Cohn, D.V.; Gorr, S.U.; Ornstein, D.L.; Kashdan, M.A.; Levine, M.A.  
Proc. Natl. Acad. Sci. U.S.A. 84, 5043-5047, 1987  
A:Title: Primary structure of bovine pituitary secretory protein I (chromogranin A) deduced from cDNA  
A:Reference number: A28033; MUID:87260925  
A:Accession: A28033  
A:Molecule type: mRNA  
A:Residues: 1-111, 'T', 113-190, 'Y', 192-253, 'P', 255-378, 'R', 380-449 <AHN>  
A:Cross-references: GB:M16971; NID:g163727; PIDN:AAA30765.1; PID:g163728  
A:Note: The authors translated the codon CCG for residue 391 as Gln  
R:Facangelo, A.; Alfolter, H.U.; Eiden, L.E.; Heribert, E.; Grimes, M.  
Nature 323, 82-86, 1986  
A:Title: Bovine chromogranin A sequence and distribution of its messenger RNA in endocrine tissues  
A:Reference number: A24175; MUID:86311345  
A:Accession: A24175  
A:Molecule type: mRNA  
A:Residues: 1-153, 'PQ', 156-158, 'R', 160-190, 'Y', 192-253, 'P', 255-449 <TA2>  
A:Cross-references: GB:X04298; NID:g217; PIDN:CAA27841.1; PID:g218  
R:Nakano, I.; Funakoshi, A.; Miyasaka, K.; Ishida, K.; Makk, G.; Angwin, P.; Chang, D.; Regul. Pept. 25, 207-213, 1989  
A:Title: Isolation and characterization of bovine pancreastatin.  
A:Reference number: A60306; MUID:893331945  
A:Accession: A60306  
A:Molecule type: protein  
A:Residues: 266-312 <NAK>  
R:Barbosa, J.A.; Gill, B.M.; Takiyuddin, M.A.; O'Connor, D.T.  
Endocrinology 128, 174-190, 1991  
A:Title: Chromogranin A: posttranslational modifications in secretory granules.  
A:Reference number: A61114; MUID:91099142  
A:Accession: A61114  
A:Molecule type: protein  
A:Residues: 19-34, 'X', 36-38; 97-111; 134-139 <BA2>  
R:Watkinson, A.; Joensson, A.C.; Davison, M.; Young, J.; Lee, C.M.; Moore, S.; Dockray, G.  
Biochem. J. 276, 471-479, 1991  
A:Title: Heterogeneity of chromogranin A-derived peptides in bovine gut, pancreas and adrenal medulla  
A:Reference number: S15847; MUID:91264803  
A:Accession: S15847  
A:Molecule type: protein  
A:Residues: 266-310, 'H', 312-318, 'K', 320-331 <WA2>  
A:Note: 311-Arg and 319-Glu were also found  
R:Watkinson, A.; Rogers, M.; Dockray, G.J.  
Biochem. J. 295, 649-654, 1993  
A:Title: Post-translational processing of chromogranin A: differential distribution of peptides in secretory granules  
A:Reference number: S39016; MUID:94059013  
A:Accession: S39016  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 303-331 <WAT>  
R:Benedum, U.M.; Baeuerle, P.A.; Konecki, D.S.; Frank, R.; Powell, J.; Mallet, J.; Hutterl. EMBO J. 5, 1495-1502, 1986  
A:Title: The primary structure of bovine chromogranin A: a representative of a class of secretory granule proteins  
A:Reference number: I46008; MUID:86300648  
A:Accession: I46008  
A:Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: mRNA  
A:Residues: 1-135, 'S', 137-190, 'Y', 192-253, 'P', 255-310, 'H', 312-318, 'K', 320-390, 'Q', 392-444  
A:Cross-references: EMBL:X04012; NID:g197; PIDN:CAA27636.1; PID:g198  
R:Yoo, S.H.; Ferretti, J.A.  
FEBS Lett. 334, 373-377, 1993

A:Title: Nature of the pH-induced conformational changes and exposure of the C-terminus  
A:Reference number: S38976; MUID:94063061  
A:Accession: S38976  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 19-26; 266-272 <YOO>  
C:Comment: Chromogranin A is the major protein of bovine chromaggin granules.  
C:Comment: Chromogranin activity has been demonstrated from proteolytic fragments of chromogranin A  
C:Genetics:  
A:Introns: 16/1; 31/3; 63/1; 86/1; 119/1; 266/1; 422/3  
C:Superfamily: chromogranin A  
C:Keywords: signal sequence #status predicted <SIG>  
F:1-18/Domain: signal sequence #status experimental <MAT>  
F:19-449/Product: chromogranin A #status predicted <MAT>  
F:142-161/Product: chromogranin #status predicted <MAT>  
F:266-312/Product: pancreastatin #status experimental <MAT>  
F:35-56/Disulfide bonds: #status predicted  
Query Match 9.8%; Score 88.5; DB 1; Length 449;  
Best Local Similarity 24.4%; Pred. No. 5;  
Matches 39; Conservative 19; Mismatches 57; Indels 45; Gaps 8;  
QY 6 EPEPSEQE---DSSSAERGLGSPAGDPSGSGKHHRRQAPGLLDASHQOEQTSSHHG 62  
Db 138 EYEKSEDESDGDRPQASPGLGPGP-----KVEEDNQAPG-----EEEEAPSNH-- 181  
QY 63 GAGAVEIRSHSSYPAGTDEDDGMEGPEPFRGSRSPAPNLWAAQRYGRELRRMD--- 119  
Db 182 --PLASLPKHPGPOAKEDSEGSQGP-----SREKGLSAEQ--GRTEREEEEK 230  
QY 120 -EFVDSFKKGLPR-----PKSAGTATQMRSSSW 147  
Db 231 WEEAEAREKAVEESPPPTAAFKAPSLGNKETQRAAPGW 270  
RESULT 11  
Hypothetical protein DKFp586G1721.1 - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 21-Jan-2000  
C:Accession: T43500  
R:Ottenwaelder, B.; Obermaier, B.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.  
submitted to the Protein Sequence Database, December 1999  
A:Reference number: Z22515  
A:Accession: T43500  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-222 <AAA>  
A:Cross-references: EMBL:AL133642  
A:Experimental source: adult uterus; clone DKFp586G1721  
C:Genetics:  
A:Note: DKFp586G1721.1  
Query Match 9.6%; Score 87; DB 2; Length 222;  
Best Local Similarity 27.3%; Pred. No. 3.1;  
Matches 41; Conservative 15; Mismatches 56; Indels 38; Gaps 6;  
QY 13 EDSSSAERGLGSPAGDPSGSGKHHRRQAPGLLDASHQOEQTSSHHGAGAVEISR 72  
Db 77 EDAS-----GGSPSPGTSKS-----DANR-----ASSGGGGGLMEEMNK 111  
QY 73 -----HSSYPAGTDEDDGMEGPEP--SPFRG--RSRSAPPNLWAAQRYGRELRRMD 119  
Db 112 LLAKRRKAASQSDKPAEKEDSEDSQMEDPSTSPGTRAAASQPPNSSEAGKPKWERSNSVE 171  
QY 120 EFVDSFKKGLPRPKSAGTATQMRSSSWTR 149  
Db 172 KPVSSILSRTSPVAKSPKSPQSQPHSR 201  
RESULT 12



A44067  
serine-rich protein hairless - fruit fly (Drosophila melanogaster)  
N:Alternate names: 109K basic protein H  
C:Species: Drosophila melanogaster  
C>Date: 10-Jun-1993 #sequence\_revision 26-Feb-1999 #text\_change 26-Feb-1999  
C:Accession: A44067; A58929; S33412; S24639  
R:Bang, A.G.; Posakony, J.W.  
Genes Dev. 6, 1752-1769, 1992  
A:Title: The Drosophila gene Hairless encodes a novel basic protein that controls alternative splicing  
A:Reference number: A44067; MUID:92387549  
A:Accession: A44067  
A:Molecule type: DNA  
A:Residues: 19-1077 <BAN>  
A:Cross-references: GB:M95192; NID:g157621; PID:g157622  
A:Note: sequence extracted from NCBI backbone (NCBIN:112622, NCBIPI:112623)  
R:Preiss, A.  
submitted to the EMBL Data Library, May 1994  
A:Description: Hairless, a Drosophila gene involved in neural development, encodes a novel basic protein  
A:Reference number: A58929  
A:Accession: A58929  
A:Molecule type: mRNA  
A:Residues: 1-1077 <PRE>  
A:Cross-references: EMBL:X67239; GB:S49642; NID:g578331; PID:g578332  
R:Maier, D.; Stumm, G.; Kuhn, K.; Preiss, A.  
Mech. Dev. 38, 143-156, 1992  
A:Title: Hairless, a Drosophila gene involved in neural development, encodes a novel, serine-rich protein  
A:Reference number: S33412; MUID:93041287  
A:Accession: S33412  
A:Molecule type: mRNA  
A:Residues: 1-150, 'A', 152-701, 'LL', 704-890, 'R', 892-963, 'RLLP', 968-973, 975-1077 <MAI>  
A:Cross-references: EMBL:X67239  
C:Genetics:  
A:Gene: FlyBase:H. hairless  
A:Cross-references: FlyBase:FBgn0001169

Query Match 9.6%; Score 86.5; DB 2; Length 1077;  
Best Local Similarity 28.9%; Pred. No. 19;  
Matches 37; Conservative 17; Mismatches 47; Indels 27; Gaps 7;  
QY 15 SSSAERGLGSPAGDPSG--SGKHHQAPGLLDASHQOQPTSSSHHGAGAVETR 72  
Db SSSSSG---KKGDPHAAIISNVHPQ-----HSMYQPSSSSYPRAL-----LTSP 721  
QY 73 HSSYPAGTDEDEGMGEPSRGRSRAPPNLAAQRYGRELRLMXDFVDFSEKKGGLPRP 132  
Db KSPDVSQS--NGGKGKSPSHGTGKRSPYPYSGSPVDYGHGSFYR--DPYA-----GAGRP 772  
QY 133 KSAGTATQ 140  
Db STSGSASQ 780

RESULT 13  
SNF2beta protein - human  
C:Species: Homo sapiens (man)  
C>Date: 10-Dec-1994 #sequence\_revision 17-Nov-1995 #text\_change 21-Jul-2000  
C:Accession: S45252  
R:Chiba, H.; Muramatsu, M.; Nomoto, A.; Kato, H.  
Nucleic Acids Res. 22, 1815-1820, 1994  
A:Title: Two human homologues of Saccharomyces cerevisiae SWI2/SNF2 and Drosophila brahma  
A:Reference number: S45251; MUID:94268902  
A:Accession: S45252  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-1647 <CHI>  
A:Cross-references: GB:D26156; NID:g505087; PIDN:BAA05143.1; PID:g505088  
C:Superfamily: unassigned bromodomain proteins; bromodomain homology  
F:1485-1540/Domain: bromodomain homology <BRO>

Query Match 9.6%; Score 86.5; DB 2; Length 1647;

Best Local Similarity 29.8%; Pred. No. 29;  
Matches 31; Conservative 9; Mismatches 55; Indels 9; Gaps 4;  
QY 9 PSEQEDSSAERGLGSPAGDPSGSGKHH---RQAP-GLLDASHQOQPTSSSHHGCA 64  
Db 30 PSPGSPGSAHMMGPPSP---GPPSAG--HPITQGGYPODNNHMHKPMESHHKGM 84  
QY 65 GAVETRSHSSYPAGTDEDEGMGEPSRGRSRAPPNLAAQ 108  
Db 85 SDDPRYNQMGMRSGGHAGMGPPSPMDQHSQGYPSPLGSE 128

RESULT 14  
Tl3049  
eyelid - fruit fly (Drosophila melanogaster)  
C:Species: Drosophila melanogaster  
C>Date: 13-Aug-1999 #sequence\_revision 13-Aug-1999 #text\_change 17-Nov-2000  
C:Accession: Tl3049  
R:Treisman, J.E.; Luk, A.; Rubin, G.M.; Heberlein, U.  
submitted to the EMBL Data Library, March 1998  
A:Reference number: 217592  
A:Accession: Tl3049  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-2715 <TRE>  
A:Cross-references: EMBL:AF053091; NID:g2981220; PID:g2981221; PIDN:AAC06254.1  
C:Genetics:  
A:Gene: eld  
A:Cross-references: FlyBase:FBgn0003013  
C:Function:  
A:Description: could act as a transcription factor antagonistic to the wg pathway  
C:Keywords: DNA binding

Query Match 9.6%; Score 86.5; DB 2; Length 2715;  
Best Local Similarity 25.8%; Pred. No. 50;  
Matches 41; Conservative 11; Mismatches 48; Indels 59; Gaps 10;  
QY 8 EPSQEDSSAERGLG-PSPADGDPGSGKHHQAPG-----LLDASHQOQEP----- 55  
Db DPSIQQQQNVAPHYGAAPPSPGSGPGG-----PPGDPAAVMVHHHLHQOQQOHPPPP 106  
QY 56 --TSSSHHGAGAVETRSHSSYPAGT--EDDEGMGE-----PSPFRGRSRAPPNL 104  
Db HMQQQHHGGFAPP-----PGAPAHAPGVKEEYTHLPPPHPAYGRYH-ADPNM 157  
QY 105 WAAQRYGRELRLMXDFVDFSEKKGGLPRPKSAGTATQMRQ 143  
Db 158 -----DPYRYGQPLP--GGKPPQOQQ 176

RESULT 15  
WMS13  
homeotic protein Hox A5 - mouse  
N:Alternate names: homeotic protein Hox 1.3; homeotic protein m2  
C:Species: Mus musculus (house mouse)  
C>Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 24-Sep-1999  
C:Accession: S07812; A27051; A38763  
R:Fibi, M.; Zink, B.; Kessel, M.; Colberg-Poley, A.M.; Labeit, S.; Lehrach, H.; Gruss  
Development 102, 349-359, 1988  
A:Title: Coding sequence and expression of the homeobox gene Hox 1.3.  
A:Reference number: A30340; MUID:88328807  
A:Accession: S07812  
A:Molecule type: mRNA  
A:Residues: 1-270 <FIB>  
A:Cross-references: EMBL:X16840; NID:g51470; PIDN:CAA34738.1; PID:g51471  
R:Odenwald, W.F.; Taylor, C.F.; Palmer-Hill, F.J.; Friedrich Jr., V.; Tan, L. M.; Lazza  
Genes Dev. 1, 482-496, 1987  
A:Title: Expression of a homeo domain protein in noncontact-inhibited cultured cells  
A:Reference number: A27051; MUID:88056292  
A:Accession: A27051  
A:Molecule type: DNA  
A:Residues: 1-270 <ODE>



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OM protein - protein search, using sw model

Run on: October 9, 2001, 15:58:35 ; Search time 15.11 seconds

(without alignments)  
380.868 Million cell updates/sec

Title: 09-580523-1A

Perfect score: 902

Sequence: 1 MFQIPEFPEQEDSSAER.....RVFQSWDRNLGRGSSAPSQ 168

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_39.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	740	82.0	168	1	BAD_HUMAN
2	645	71.5	204	1	BAD_MOUSE
3	96	10.6	2505	1	CYAA_HUMAN
4	90.5	10.0	2300	1	CYAA_NEUCR
5	90	10.0	2339	1	CCAB_HUMAN
6	87.5	9.7	449	1	CMGA_BOVIN
7	86.5	9.6	1077	1	HLES_DROME
8	86.5	9.6	1647	1	SN24_HUMAN
9	86	9.5	270	1	HXA5_MOUSE
10	86	9.5	646	1	SG1_BOVIN
11	85.5	9.5	510	1	DMP1_BOVIN
12	85.5	9.5	1461	1	TE18_PRTIF
13	84.5	9.4	215	1	ST13_MOUSE
14	84	9.3	270	1	HXA5_HUMAN
15	84	9.3	380	1	VASP_HUMAN
16	84	9.3	542	1	ZYX_CHICK
17	83.5	9.3	1159	1	HERG_HUMAN
18	83.5	9.3	1453	1	NKCR_MOUSE
19	83	9.2	962	1	ARVC_HUMAN
20	82.5	9.1	558	1	ROL_HUMAN
21	82.5	9.1	1097	1	CCT_DROME
22	82	9.1	336	1	FLTA_MOUSE
23	82	9.1	424	1	LFY_ARATH
24	82	9.1	591	1	PAK4_HUMAN
25	82	9.1	1021	1	MANA_RHOMR
26	82	9.1	1089	1	Y553_HUMAN
27	81.5	9.0	407	1	Z174_HUMAN
28	81.5	9.0	841	1	TE63_MCMVS
29	81.5	9.0	1191	1	NKCL_SQUAC
30	81	9.0	1081	1	SPS2_CRAPL
31	80	8.9	443	1	GAT3_HUMAN
32	80	8.9	502	1	VE2_HPV25
33	80	8.9	559	1	PAX1_CHICK

34 80 8.9 2145 1 CYAA\_PODAN Q01513 podospora a  
35 80 8.9 2339 1 CCAB\_RABIT Q05152 oryctolagus  
36 79.5 8.8 369 1 PSPD\_BOVIN P35246 bos taurus  
37 79.5 8.8 614 1 NRDL\_HUMAN P20393 homo sapien  
38 79.5 8.8 783 1 FYB\_HUMAN O15117 homo sapien  
39 79.5 8.8 2220 1 CABI\_HUMAN Q9Y6J0 homo sapien  
40 79.5 8.8 3726 1 TRX\_DROME P20659 drosophila  
41 79.5 8.8 247 1 GRPB\_RAT P08462 rattus norv  
42 79 8.8 263 1 PENK\_BOVIN P01211 bos taurus  
43 79 8.8 489 1 DMP1\_RAT P98193 rattus norv  
44 79 8.8 707 1 HTF4\_RAT P51514 rattus norv  
45 79 8.8 825 1 SE5\_RAT Q63003 rattus norv

#### ALIGNMENTS

RESULT 1  
ID BAD\_HUMAN STANDARD; PRT; 168 AA.  
AC O92934;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 01-OCT-2000 (Rel. 40, Last annotation update)  
DE BAD PROTEIN (BCL-2 BINDING COMPONENT 6).  
GN BAD OR BCL6 OR BCL2L8.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OC NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Yin D.X., Li Z., Huang B., Chen S., Zhou H.;  
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.  
CC -1- FUNCTION: PROMOTES CELL DEATH. SUCCESSFULLY COMPETES FOR THE  
CC BINDING TO BCL-X(L) AND BCL-2, THEREBY AFFECTING THE LEVEL  
CC HETERODIMERIZATION OF BOTH THESE PROTEINS WITH BAX. CAN REVERSE  
CC THE DEATH REPRESSOR ACTIVITY OF BCL-X(L), BUT NOT THAT OF BCL-2  
CC (BY SIMILARITY).  
CC -1- SUBUNIT: FORMS HETERODIMERS WITH BCL-X(L) AND BCL-2, BUT NOT WITH  
CC BAX, MCL-1, AL, OR BCL-X(S) (BY SIMILARITY).  
CC -1- TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES.  
CC -1- SIMILARITY: CONTAINS A BCL-2 HOMOLOG DOMAIN 1 (BH1).  
CC -1- SIMILARITY: CONTAINS A BCL-2 HOMOLOG DOMAIN 2 (BH2).  
CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.  
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CC  
CC EMBL; U66879; AAB36516.1; -  
CC MIN; 603167; -  
DR P01088 mus musculus  
KW Apoptosis.  
FT DOMAIN 101 121 BH1.  
FT DOMAIN 146 163 BH2.  
SQ SEQUENCE 168 AA; 18408 MW; BDF3D99587C222BE CRC64;

Query Match 82.0%; Score 740; DB 1; Length 168;  
Best Local Similarity 84.5%; Pred. No. 5,9e-50;  
Matches 142; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

Qy 1 MFQIPEFPEQEDSSAERGLGSPAGDPSGSGKHRRQAPGLLDASHOQEQPTSSSH 60  
|||||  
Db 1 MFQIPEFPEQEDSSAERGLGSPAGDPSGSGKHRRQAPGLLDASHOQEQPTSSSH 60  
|||||  
Qy 61 HGGAGAVEIRSHSYYPAGTDEDEGMEEPSPFRGSRSPAPNLWAAORYGRELRRMDE 120  
|||||  
Db 61 HGGRWGCGDPSPQLLPRGDRRRDGGGAQPFGRGSRSPAPNLWAAORYGRELRRMDE 120  
|||||

QY 121 FVDSFKGLPRKSGATATQMRQSSWTRVFQSWDRNLGRSSAFSQ 168  
 |||||  
 Db 121 FVDSFKGLPRKSGATATQMRQSSWTRVFQSWDRNLGRSSAFSQ 168

## RESULT 2

BAD\_MOUSE STANDARD; PRT; 204 AA.  
 AC O61337;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE BAD PROTEIN (BCL-2 BINDING COMPONENT 6).  
 GN BAD OR BBC6.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain, and Thymus;  
 RX MEDLINE=95136361; PubMed=7834748;  
 RA Yang E., Zha J., Jockel J., Boise L.H., Thompson C.B., Korsmeyer S.J.;  
 RT "Bad, a heterodimeric partner for Bcl-XL and Bcl-2, displaces Bax and  
 RT promotes cell death.";  
 RL Cell 80:285-291(1995).  
 CC -!- FUNCTION: PROMOTES CELL DEATH. SUCCESSFULLY COMPETES FOR THE  
 CC BINDING TO BCL-X(L) AND BCL-2. THEREBY AFFECTING THE LEVEL  
 CC HETERODIMERIZATION OF BOTH THESE PROTEINS WITH BAX. CAN REVERSE  
 CC THE DEATH REPRESSOR ACTIVITY OF BCL-X(L), BUT NOT THAT OF BCL-2.  
 CC -!- SUBUNIT: FORMS HETERODIMERS WITH BCL-X(L) AND BCL-2, BUT NOT WITH  
 CC BAX, MCL-1, AL, OR BCL-X(S).  
 CC -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 1 (BH1).  
 CC -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 2 (BH2).  
 CC -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.  
 CC  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 DR EMBL; L37296; AAA64465.1; -;  
 DR MGD; MGI:1096330; Bad.  
 KW Apoptosis. 138 158 BH1.  
 FT DOMAIN 182 199 BH2.  
 SQ SEQUENCE 204 AA; 22080 MW; 6C2BA910205053F7 CRC64;

Query Match 71.5%; Score 645; DB 1; Length 204;  
 Best Local Similarity 75.0%; Pred. No. 1.2e-42;  
 Matches 126; Conservative 12; Mismatches 24; Indels 6; Gaps 3;  
 QY 1 MFQIPFEFSEQEDSSAERGLGSPAGDGPSCSGRHHRAQCLLWDASHQEQPTSSSH 60  
 |||||  
 Db 43 MFQIPFEFSEQEDASATDRGLGFSITEQP---GPY--LAPGLGSLNIHQGRAATNSH 97  
 |||||  
 QY 61 HGGAGAVEIRSRHSSYPAGTDEDMGEFSPPRGRSRSAPPNLMWAAQRYGRELRRMXDE 120  
 |||||  
 Db 98 HGGAGAMETRSRHSYPAGTDEDMGEELSPPRGRSRSAPPNLMWAAQRYGRELRRMSDE 157  
 |||||  
 QY 121 FVDSFKGLPRKSGATATQMRQSSWTRVFQSWDRNLGRSSAFSQ 168  
 |||||  
 Db 158 FEGSF-KGLPRKSGATATQMRQSGAGWTRIIQSWDRNLGKGGSTFSQ 204  
 |||||

## RESULT 3

ID CCAA\_HUMAN STANDARD; PRT; 2505 AA.  
 CC

AC 000555; Q92690; Q16290; Q99790; Q99791; Q99792; Q99793; P78510;  
 AC P78511;  
 DT 15-JUL-1999 (Rel. 38, Created)  
 DT 15-JUL-1999 (Rel. 38, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE VOLTAGE-DEPENDENT P/Q-TYPE CALCIUM CHANNEL ALPHA-1A SUBUNIT (CALCIUM  
 DE CHANNEL, L TYPE, ALPHA-1 POLYPEPTIDE ISOFORM 4) (BRAIN CALCIUM CHANNEL  
 DE I) (BI).  
 GN CACNALA OR CACNL1A4 OR CACH4 OR CACN3.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORMS BI-1-GGCAG/1A-1 AND BI-1/1A-2).  
 RC TISSUE=Neuron;  
 RX MEDLINE=99158614; PubMed=10049321;  
 RA Hans M., Urrutia A., Deal C., Brust P.F., Stauderman K., Ellis S.B.,  
 RA Harbold M.M., Johnson E.C., Williams M.E.;  
 RT "Structural elements in domain IV that influence biophysical and  
 RT pharmacological properties of human alpha1A-containing  
 RT high-voltage-activated calcium channels.";  
 RL Biophys. J. 76:1384-1400(1999).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORM BI-1(V1)), AND VARIANTS FHM.  
 RC TISSUE=Cerebellum;  
 RX MEDLINE=97053792; PubMed=8898206;  
 RA Ophoff R.A., Terwindt G.M., Vergouwe M.N., van Eijk R., Oefner P.J.,  
 RA Hoffman S.M.G., Lamerding J.E., Mohrenweiser H.W., Bulman D.E.,  
 RA Ferrari M., Haan J., Lindhout D., van Ommen G.-J.B., Hofker M.H.,  
 RA Ferrari M.D., Frants R.R.;  
 RT "Familial hemiplegic migraine and episodic ataxia type-2 are caused by  
 RT mutations in the Ca2+ channel gene CACNL1A4.";  
 RL Cell 87:543-552(1996).  
 RN [3]  
 RP SEQUENCE FROM N.A. AND ALTERNATIVE SPLICING.  
 RC TISSUE=Brain;  
 RX MEDLINE=97141920; PubMed=8988170;  
 RA Zhuchenko O., Bailey J., Bonnen P.E., Ashizawa T., Stockton D.W.,  
 RA Amos C., Dobyns W.B., Subramony S.H., Zoghbi H.Y., Lee C.C.;  
 RT "Autosomal dominant cerebellar ataxia (SCA6) associated with small  
 RT polyglutamine expansions in the alpha 1A-voltage-dependent calcium  
 RT channel.";  
 RL Nat. Genet. 15:62-69(1997).  
 RN [4]  
 RP SEQUENCE OF 1693-1807 FROM N.A.  
 RC TISSUE=Lung carcinoma;  
 RX MEDLINE=95123449; PubMed=7823133;  
 RA Barry E.L.R., Viglione M.P., Kim Y.I., Froehner S.C.;  
 RT "Expression and antibody inhibition of P-type calcium channels in  
 RT human small-cell lung carcinoma cells.";  
 RL J. Neurosci. 15:274-283(1995).  
 RN [5]  
 RP SEQUENCE OF 2038-2258 FROM N.A.  
 RC TISSUE=Frontal cortex;  
 RX MEDLINE=96102310; PubMed=8525433;  
 RA Margolis R.L., Breschel T.S., Li S.H., Kidwai A.S., Antonarakis S.E.,  
 RA McGinnis M.G., Ross C.A.;  
 RT "Characterization of cDNA clones containing CCA trinucleotide repeats  
 RT derived from human brain.";  
 RL Somat. Cell Mol. Genet. 21:279-284(1995).  
 CC -!- FUNCTION: VOLTAGE-SENSITIVE CALCIUM CHANNELS (VSCC) MEDIATE THE  
 CC ENTRY OF CALCIUM IONS INTO EXCITABLE CELLS AND ARE ALSO INVOLVED  
 CC IN A VARIETY OF CALCIUM-DEPENDENT PROCESSES, INCLUDING MUSCLE  
 CC CONTRACTION, HORMONE OR NEUROTRANSMITTER RELEASE, GENE EXPRESSION,  
 CC CELL MOTILITY, CELL DIVISION AND CELL DEATH. THE ISOFORM ALPHA-1A  
 CC GIVES RISE TO P AND/OR Q-TYPE CALCIUM CURRENTS. P/Q-TYPE CALCIUM  
 CC CHANNELS BELONG TO THE "HIGH-VOLTAGE ACTIVATED" (HVA) GROUP AND  
 CC ARE BLOCKED BY THE FUNNEL TOXIN (FTX) AND BY THE OMEGA-AGATOXIN-  
 CC IVA (OMEGA-AGA-IVA). THEY ARE HOWEVER INSENSITIVE TO  
 CC DIHYDROPYRIDINES (DHP), AND OMEGA-CONOTOXIN-GVIA (OMEGA-CTX-  
 CC GVIA).  
 CC -!- SUBUNIT: VOLTAGE-DEPENDENT CALCIUM CHANNELS ARE MULTISUBUNIT



```
RESULT 4
ID CYNAL_NEUR  STANDARD; PRT; 2300 AA.
AC Q01611;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DE ADENYLATE CYCLASE (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (ADENYLYL
DE CYCLASE)
GN CR-1 OR NAC.
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92000795; PubMed=1680356;
RA Kore-Eda S., Murayama T., Uno I.;
RT "Isolation and characterization of the adenylate cyclase structural
RT gene of Neurospora crassa."
RL Jpn. J. Genet. 66:317-334(1991).
CC -!- FUNCTION: PLAYS ESSENTIAL ROLES IN REGULATION OF CELLULAR
CC METABOLISM BY CATALYSING THE SYNTHESIS OF A SECOND MESSENGER,
CC CAMP.
CC -!- CATALYTIC ACTIVITY: ATP = 3',5'-CYCLIC AMP + PYROPHOSPHATE.
CC -!- SIMILARITY: BELONGS TO ADENYLYL CYCLASE CLASS-3 FAMILY.
CC -!- SIMILARITY: CONTAINS 23 LEUCINE-RICH REPEATS (LRR).
CC -!- SIMILARITY: CONTAINS A PP2C-LIKE DOMAIN.
CC -----
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CC -----
CC EMBL; D00909; BAA00755.1; -
CC InterPro: IPR001611; -
CC InterPro: IPR001932; -
CC Pfam; PF00560; LRR; 13.
CC Pfam; PF00481; PP2C; 1.
CC PROSITE; P00019; LEURICHRPT.
CC PROSITE; P050125; GUANYLATE_CYCLASES_2; 1.
KW Lyase; Repeat; Leucine-rich repeat; CAMP synthesis; Magnesium.
FT REPEAT 867 890
FT REPEAT 892 914
FT REPEAT 915 938
FT REPEAT 938 961
FT REPEAT 962 986
FT REPEAT 988 1008
FT REPEAT 1009 1031
FT REPEAT 1033 1055
FT REPEAT 1056 1079
FT REPEAT 1081 1097
FT REPEAT 1098 1120
FT REPEAT 1122 1142
FT REPEAT 1143 1165
FT REPEAT 1166 1188
FT REPEAT 1189 1211
FT REPEAT 1213 1234
FT REPEAT 1349 1369
FT REPEAT 1373 1396
FT REPEAT 1398 1420
FT REPEAT 1422 1445
FT REPEAT 1447 1469
FT REPEAT 1474 1497
FT REPEAT 1513 1538
FT REPEAT 1564 1829
FT DOMAIN 1830 2300
FT DOMAIN 49 52
```

```
FT DOMAIN 204 221 POLY-GLN.
SQ SEQUENCE 2300 AA; 254752 MW; 52E79B90E6B17A7B CRC64;

Query Match 10.0%; Score 90.5; DB 1; Length 2300;
Best Local Similarity 23.7%; Pred. No. 17;
Matches 50; Conservative 23; Mismatches 75; Indels 63; Gaps 11;

QY 17 SAERGLGPGAGDPSGSGKHHR---QAPGLLDASHOQEQPTSSSH---GGAGAV 67
   || || || || || || || || || || || || || || || || || || ||
DB 343 SSEISL-PPSHSGPMSTGKEHRSHSYLPGS--GSHRDRNYSNATDHPSTFGSVTV 399
   || || || || || || || || || || || || || || || || || || ||
QY 68 EIKSRHS-----YPA-----GTEDDEGMGEPE-----SPFRGR---SRSA 100
   || || || || || || || || || || || || || || || || || || ||
DB 400 GGRDROASVPSPRPVPVPAPEVVPVFLYQEAADDIARYGEAPVRTSLTGPDRLDYIDSSQN 459
   || || || || || || || || || || || || || || || || || || ||
QY 101 PPNLWAAQRYGREL-----RMXDFVDSFKKGLPRPKSAGT-----AT 139
   || || || || || || || || || || || || || || || || || || ||
DB 460 PRTSSARSAGHSIVHLPGHHKHNKSNEDPRALKPSLRSDSAASFARFNGSSMMGT 519
   || || || || || || || || || || || || || || || || || || ||
QY 140 QMRQSS---SWTRVFOSWMDRNLGRGSSAPS 167
   || || || || || || || || || || || || || || || || || || ||
DB 520 RSRAQSPAPSWTGTSGRLKANSISDGTSSPA 550
   || || || || || || || || || || || || || || || || || || ||

RESULT 5
CCAB_HUMAN
ID CCAB_HUMAN STANDARD; PRT; 2339 AA.
AC Q00975;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE VOLTAGE-DEPENDENT N-TYPE CALCIUM CHANNEL ALPHA-1B SUBUNIT (CALCIUM
DE CHANNEL, L TYPE, ALPHA-1 POLYPEPTIDE ISOFORM 5) (BRAIN CALCIUM CHANNEL
DE III) (BIII).
DE CACNA1B OR CACNLIA5 OR CACHS5.
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS ALPHA-1B-1 AND ALPHA-1B-2)...
RX TISSUE=Brain;
RX MEDLINE=92335886; PubMed=1321501;
RA Williams M.E., Brust P.F., Feldman D.H., Patthi S., Simerson S.,
RA Maroufi A., McCue A.F., Velicelebi G., Ellis S.B., Harpold M.M.;
RT "Structure and functional expression of an omega-conotoxin-sensitive
RT human N-type calcium channel."
RT Science 257:389-395(1992).
RL [2]
RP SEQUENCE OF 1-94 FROM N.A.
RP TISSUE=Lung fibroblast;
RA Kim D.S., Jung H.H., Park S.H., Chin H.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: VOLTAGE-SENSITIVE CALCIUM CHANNELS (VSCC) MEDIATE THE
CC ENTRY OF CALCIUM IONS INTO EXCITABLE CELLS AND ARE ALSO INVOLVED
CC IN A VARIETY OF CALCIUM-DEPENDENT PROCESSES, INCLUDING MUSCLE
CC CONTRACTION, HORMONE OR NEUROTRANSMITTER RELEASE, GENE EXPRESSION,
CC CELL MOTILITY, CELL DIVISION AND CELL DEATH. THE ISOFORM ALPHA-1B
CC GIVES RISE TO N-TYPE CALCIUM CURRENTS. N-TYPE CALCIUM CHANNELS
CC BELONG TO THE "HIGH-VOLTAGE ACTIVATED" (HVA) GROUP AND ARE BLOCKED
CC BY OMEGA-CONOTOXIN-GVIA (OMEGA-CTX-GVIA) AND BY OMEGA-AGATOXIN-
CC IIIA (OMEGA-AGA-IIIA). THEY ARE HOWEVER INSENSITIVE TO
CC DIHYDROPYRIDINES (DHP). AND OMEGA-AGATOXIN-IVA (OMEGA-AGA-IVA).
CC CALCIUM CHANNELS CONTAINING ALPHA-1B SUBUNIT MAY PLAY A ROLE IN
CC DIRECTED MIGRATION OF IMMATURE NEURONS.
CC -!- SUBUNIT: VOLTAGE-DEPENDENT CALCIUM CHANNELS ARE MULTISUBUNIT
CC COMPLEXES, CONSISTING OF ALPHA-1, ALPHA-2, BETA AND DELTA SUBUNITS
CC IN A 1:1:1:1 RATIO. THE CHANNEL ACTIVITY IS DIRECTED BY THE PORE-
CC FORMING AND VOLTAGE-SENSITIVE ALPHA-1 SUBUNIT. IN MANY CASES, THIS
CC SUBUNIT IS SUFFICIENT TO GENERATE VOLTAGE-SENSITIVE CALCIUM
CC CHANNEL ACTIVITY. THE AUXILIARY SUBUNITS BETA AND ALPHA-2/DELTA
CC LINKED BY A DISULFIDE BRIDGE REGULATE THE CHANNEL ACTIVITY.
```



RX MEDLINE=92140395; PubMed=1779968;  
RA Tacangelo A.L., Grimes M., Eiden L.E.;  
RT "The bovine chromogranin A gene: structural basis for hormone  
RL regulation and generation of biologically active peptides.";  
RL Mol. Endocrinol. 5:1651-1660(1991).  
RN [2]  
RN SEQUENCE FROM N.A.  
RX MEDLINE=86300648; PubMed=3755681;  
RA Benedum U.M., Baeuerle P.A., Konecki D.S., Frank R., Powell J.,  
RA Mallet J., Huttner W.B.;  
RT "The primary structure of bovine chromogranin A: a representative of  
RT a class of acidic secretory proteins common to a variety of  
RT peptidergic cells.";  
RL EMBO J. 5:1495-1502(1986).  
RN [3]  
RN SEQUENCE FROM N.A.  
RX MEDLINE=86311345; PubMed=3018587;  
RA Tacangelo A., Affolter H.-U., Eiden L.E., Herbert E., Grimes M.;  
RT "Bovine chromogranin A sequence and distribution of its messenger RNA  
RT in endocrine tissues.";  
RL Nature 323:82-86(1986).  
RN [4]  
RN SEQUENCE FROM N.A.  
RX MEDLINE=87260925; PubMed=3474638;  
RA Ann T.G., Cohn D.V., Gorr S.U., Ornstein D.L., Kashdan M.A.,  
RA Levine M.A.;  
RT "Primary structure of bovine pituitary secretory protein I  
RT (chromogranin A) deduced from the cDNA sequence";  
RL Proc. Natl. Acad. Sci. U.S.A. 84:5043-5047(1987).  
RN [5]  
RN SEQUENCE FROM N.A.  
RX MEDLINE=97228583; PubMed=9074643;  
RA Kang Y.K., Yoo S.H.;  
RT "Identification of the secretory vesicle membrane binding region of  
RT chromogranin A.";  
RL FEBS Lett. 404:87-90(1997).  
RN [6]  
RN SEQUENCE OF 19-45, AND CALCIUM-BINDING.  
RX MEDLINE=90354431; PubMed=2387861;  
RA Yoo S.H., Albanesi J.P.;  
RT "Ca2(+)-induced conformational change and aggregation of chromogranin  
RT A.";  
RL J. Biol. Chem. 265:14414-14421(1990).  
RN [7]  
RN SEQUENCE OF 142-161, AND SYNTHESIS OF CHROMOSTATIN.  
RX MEDLINE=91142185; PubMed=1996343;  
RA Galindo E., Rill A., Bader M.-F., Aunis D.;  
RT "Chromostatin, a 20-amino acid peptide derived from chromogranin A,  
RT inhibits chromaffin cell secretion.";  
RL Proc. Natl. Acad. Sci. U.S.A. 88:1426-1430(1991).  
RN [8]  
RN ERRATUM.  
RA Galindo E., Rill A., Bader M.-F., Aunis D.;  
RL Proc. Natl. Acad. Sci. U.S.A. 91:832-832(1994).  
RN [9]  
RN SEQUENCE OF 266-312.  
RX MEDLINE=89331945; PubMed=2756155;  
RA Nakano I., Funakoshi A., Miyasaka K., Ishida K., Makk G., Angwin P.,  
RA Chang D., Tatemoto K.;  
RT "Isolation and characterization of bovine pancreastatin.";  
RL Regul. Pept. 25:207-213(1989).  
RN [10]  
RN SEQUENCE OF 191-212 (CHROMACIN).  
RX MEDLINE=97067080; PubMed=8910482;  
RA Strub J.-M., Goumon Y., Lugardon K., Capon C., Lopez M., Moniatte M.,  
RA van Dorsselaer A., Aunis D., Metz-Boutigue M.-H.;  
RT "Antibacterial activity of glycosylated and phosphorylated  
RT chromogranin A-derived peptide 173-194 from bovine adrenal medullary  
RT chromaffin granules.";  
RL J. Biol. Chem. 271:28533-28540(1996).  
RN [11]  
RN CHARACTERIZATION OF CATESTATIN.

RX MEDLINE=97439785; PubMed=9294131;  
RA Mahata S.K., O'Connor D.T., Mahata M., Yoo S.H., Taupenot L., Wu H.,  
RA Gill B.M., Farmer R.J.;  
RT "Novel autocrine feedback control of catecholamine release. A discrete  
RT chromogranin A fragment is a noncompetitive nicotinic cholinergic  
RT antagonist.";  
RL J. Clin. Invest. 100:1623-1633(1997).  
RN [12]  
RN CHARACTERIZATION OF CATESTATIN.  
RX MEDLINE=99000113; PubMed=9786174;  
RA Kennedy B.P., Mahata S.K., O'Connor D.T., Ziegler M.G.;  
RT "Mechanism of cardiovascular actions of the chromogranin A fragment  
RT catestatin in vivo.";  
RL Peptides 19:1241-1248(1998).  
RN [13]  
RN 3D-STRUCTURE MODELING OF CATESTATIN.  
RX MEDLINE=99025667; PubMed=9809795;  
RA Tsigelny I., Mahata S.K., Taupenot L., Preece N.E., Mahata M.,  
RA Khan I., Farmer R.J., O'Connor D.T.;  
RT "Mechanism of action of chromogranin A on catecholamine release:  
RT molecular modeling of the catestatin region reveals a beta-  
RT strand/loop/beta-strand structure secured by hydrophobic interactions  
RT and predictive of activity.";  
RL Regul. Pept. 77:43-53(1998).  
RN [14]  
RN CHARACTERIZATION OF VASOSTATIN-1.  
RX MEDLINE=20219105; PubMed=10753865;  
RA Lugardon K., Raffner R., Goumon Y., Corti A., Delmas A., Bulet P.,  
RA Aunis D., Metz-Boutigue M.-H.;  
RT "Antibacterial and antifungal activities of vasostatin-1, the N-  
RT terminal fragment of chromogranin A";  
RL J. Biol. Chem. 275:10745-10753(2000).  
RN [15]  
RN CARBOHYDRATE-BINDING SITES, PHOSPHORYLATION, AND DISULFIDE BOND.  
RX MEDLINE=99459228; PubMed=10527498;  
RA Bauer S.H., Zhang X.Y., Van Dongen W., Claeys M., Przybylski M.;  
RT "Chromogranin A from bovine adrenal medulla: molecular  
RT characterization of glycosylations, phosphorylations, and sequence  
RT heterogeneities by mass spectrometry.";  
RL Anal. Biochem. 274:69-80(1999).  
CC -!- FUNCTION: PANCREASTATIN STRONGLY INHIBITS GLUCOSE INDUCED INSULIN  
CC RELEASE FROM THE PANCREAS.  
CC -!- FUNCTION: CHROMOSTATIN COMPLETELY INHIBITS CATECHOLAMINE RELEASE  
CC FROM CHROMAFFIN CELLS.  
CC -!- FUNCTION: CHROMACIN HAS ANTIBACTERIAL ACTIVITY AGAINST MICROCOCCUS  
CC LUTEUS.  
CC -!- FUNCTION: CATESTATIN INHIBITS CATECHOLAMINE RELEASE FROM  
CC CHROMAFFIN CELLS AND NORADRENERGIC NEURONS BY ACTING AS A NON-  
CC COMPETITIVE NICOTINIC CHOLINERGIC ANTAGONIST.  
CC -!- FUNCTION: VASOSTATIN-1 HAS ANTIBACTERIAL ACTIVITY AGAINST GRAM-  
CC POSITIVE BACTERIA M.LUTEUS, B.MEGATERIUM, NOT ACTIVE AGAINST GRAM-  
CC POSITIVE BACTERIA B.CEREUS, B.SUBTILIS, S.PYROGENES, M.FORTUITUM,  
CC S.AUREUS AND L.MONOCYTOGENES AND AGAINST GRAM-NEGATIVE BACTERIA  
CC E.COLI, E.CLOACAE, S.TYPHIMURIUM, K.PNEUMONIAE AND P.AURUGINOSA.  
CC POSSESSES ANTIFUNGAL ACTIVITY AGAINST N.CRASSA, A.FUMIGATUS,  
CC A.BRASSICOLA, N.HEMATOCOCCA, F.CULMORUM AND F.OXYSPORUM AND  
CC AGAINST S.CEREVISIAE AND C.ALBICANS YEAST. INACTIVE AGAINST  
CC T.MENTAGROPHYTES.  
CC -!- SUBCELLULAR LOCATION: NEUROENDOCRINE AND ENDOCRINE SECRETORY  
CC GRANULES.  
CC -!- MASS SPECTROMETRY: MW=8584.9; METHOD=MALDI; RANGE=19-94.  
CC -!- MISCELLANEOUS: BINDS CALCIUM WITH A LOW-AFFINITY.  
CC -!- SIMILARITY: BELONGS TO THE CHROMOGRANIN / SECRETOGRANIN PROTEIN  
CC FAMILY.  
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CC -----  
CC





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FT DOMAIN 1571 1584 POLY-GLU.
SQ SEQUENCE 1647 AA; 184585 MW; 7B785E7953277FID CRC64;

Query Match 9.6%; Score 86.5; DB 1; Length 1647;
Best Local Similarity 29.8%; Pred. No. 24;
Matches 31; Conservative 9; Mismatches 55; Indels 9; Gaps 4;

QY 9 PSEQDSSSSAERGLGSPAGDGPSSGSKH-- --ROAP-GLLWDASHOQEQPTSSSHHGA 64
   || :||| || :||| || :||| || :||| || :||| || :||| || :|||
Db 30 PSPGSPGSAHSMWGSP---GPPSAG--HPITQPGGYPQDNMHQHKPMESMHEKGM 84
   : : ||| ||| : : ||| ||| : : ||| ||| : : ||| ||| : : ||| |||
QY 65 GAVEIRSHRSYSPAGTDEDDGMEGEPSFPRGRSRAPPNLWAAQ 108
   : : ||| ||| : : ||| ||| : : ||| ||| : : ||| |||
Db 85 SDDPRYNQMGMRSGGHAGMGPFPSPMDQHSOGYPSPLGGSE 128
   : : ||| ||| : : ||| ||| : : ||| ||| : : ||| |||

RESULT. 9
HXA5_MOUSE
ID HXA5_MOUSE STANDARD; PRT; 270 AA.
AC P09021;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DE 01-OCT-1996 (Rel. 34, Last annotation update)
DE DE HOMEBOX PROTEIN HOX-A5 (HOX-1.3) (M2).
GN HOXA5 OR HOXA-5 OR HOX-1.3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88056292; PubMed=2890554;
RA Odenwald W.F., Taylor C.F., Palmer-Hill F.J., Friedrich V. Jr.,
RA Tani M., Lazzarini R.A.;
RT "Expression of a homeo domain protein in noncontact-inhibited
RT cultured cells and postmitotic neurons.";
RL Genes Dev. 1:482-496(1987).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=88328807; PubMed=2901335;
RA Fibi M., Zink B., Kessel M., Colberg-Poley A.M., Labelt S.,
RA Lechrad H., Gruss P.;
RT "Coding sequence and expression of the homeobox gene Hox 1.3.";
RL Development 102:349-359(1988).
RN [3]
RP DNA-BINDING SPECIFICITY.
RX MEDLINE=89232713; PubMed=2565857;
RA Odenwald W.F., Garber J., Arnheiter H., Tournier-Lasserre E.,
RA Lazzarini R.A.;
RT "The Hox-1.3 homeo box protein is a sequence-specific DNA-binding
RT phosphoprotein.";
RL Genes Dev. 3:158-172(1989).
RN [4]
RP CHARACTERIZATION.
RX MEDLINE=96205869; PubMed=8635464;
RA Zhao J.J., Lazzarini R.A., Pick L.;
RT "Functional dissection of the mouse Hox-a5 gene.";
RN [5]
RP EMBO J. 15:1313-1322(1996).
CC -1- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF
CC A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
CC SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.
CC ALSO BINDS TO ITS OWN PROMOTER. BINDS SPECIFICALLY TO THE MOTIF:
CC 5'-CYTNATTA[GTGY]-3'.
CC -1- SUBCELLULAR LOCATION: NUCLEAR.
CC -1- DEVELOPMENTAL STAGE: EXPRESSED DURING EMBRYOGENESIS AND IN ADULT
CC KIDNEY.
CC -1- SIMILARITY: BELONGS TO THE ANTP FAMILY OF HOMEBOX PROTEINS.
CC -----
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DR EMBL; M36604; AAA37838.1; -
DR EMBL; Y00208; CAA68364.1; -
DR EMBL; X16840; CAA34738.1; -
DR EMBL; M28021; AAA37837.1; -
DR PIR; S07812; WJMS13.
DR HSSP; P02833; 1SAN.
DR TRANSFAC; T00377; -
DR MGD; MGI:96177; Hoxa5.
DR InterPro; IPR001356; -
DR InterPro; IPR001827; -
DR Pfam; PF00046; homeobox.1.
DR PRINTS; PR00024; HOMEBOX.
DR PRINTS; PR00025; ANTENNAPEDIA.
DR PROSITE; PS00027; HOMEBOX.1; 1.
DR PROSITE; PS00032; ANTENNAPEDIA; 1.
DR PROSITE; PS00071; HOMEBOX.2; 1.
DR PROSITE; PS00071; HOMEBOX.2; 1.
KW Homeobox; DNA-binding; Developmental protein; Nuclear protein;
KW Transcription regulation.
FT DOMAIN 176 181 ANTP-TYPE HEXAPEPTIDE.
FT DNA_BIND 195 254 HOMEBOX.
SQ SEQUENCE 270 AA; 29237 MW; DC4BDDA8FE62766E CRC64;

Query Match          9.58; Score 86; DB 1; Length 270;
Best Local Similarity 25.88; Pred. No. 4;
Matches 55; Conservative 13; Mismatches 63; Indels 82; Gaps 11;

Qy 10 SEQ-EDSSABERG-----LGPSPAGDGPSPGSGKHHRQ-----APGLLDASHQ 51
   ||| ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 31 SEQFRDSAMHSGRYGYNGMDLSVGRSGHGRGSRARSYAAGASAP-----AEPR 85
   ||| ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 52 QEQPTSS-----SHGG-----AGAVEIRSR----- 72
   || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 86 YSQPATSTHPPDPLPCSAVAPSPGSDSHGKNSLGNSSGASANAGTHISSREGVGT 145
   || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 73 ----HSSYPACTDEGMEEPSPFRGRSAPPNLMQAAYGRELRMXDEEVDSPKKG 128
   || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 146 ASAAEDAPASSE-QAGAQSESP-----APPAQPIYPMWRKLHSHDNI-----G 191

Qy 129 LPRPKSACTATQMRQSSSWTRVFQSWMDRNLGR 161
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 192 GPEGKRARTATRYOTLEKEFH--FNRYLTR 222
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 10
SG1_BOVIN
AC P23389; STANDARD; PRT; 646 AA.
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE SECRETOGRANIN I PRECURSOR (SGI) (CHROMOGRANIN B) [CONTAINS: GAWK
DE PEPTIDE; SECRETOLYTIN].
GN CHGB.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUP-Adrenal Chromaffin;
RA MEDLINE=91223091; PubMed=2025642;
RX Bauer J.W., Fischer-Colbrie R.;
"Primary structure of bovine chromogranin B deduced from cDNA
sequence.";
RL Biochim. Biophys. Acta 1089:124-126(1991).
RN [2]
RP SEQUENCE FROM N.A.

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RC TISSUP-Adrenal medulla;
RX MEDLINE=97282588; PubMed=9136897;
RA Yoo S.H., Kang Y.K.;
RT "Identification of the secretory vesicle membrane binding region of
chromogranin B.";
FEBL Lett. 406:259-262(1997).
[3]
RN SEQUENCE OF 21-646 FROM N.A.
RP TISSUP-Adrenal medulla;
RA Grandy D.K., Leduc R., Makam H., Flanagan T., Diliberto E.J.,
Thomas G., Civelli O., Viveros O.H.;
RL Submitted (OCT-1990) to the EMBL/GenBank/DBJ databases.
[4]
RN SEQUENCE OF 634-646.
RP TISSUP-Adrenal chromaffin;
RX MEDLINE=95262699; PubMed=7744058;
RA Strub J.-M., Garcia-Sablone P., Lonning K., Taupenot L., Hubert P.,
van Dorselaer A., Aunis D., Metz-Boutigue M.-H.;
"Processing of chromogranin B in bovine adrenal medulla.
Identification of secretolytin, the endogenous C-terminal fragment of
residues 614-626 with antibacterial activity.";
Eur. J. Biochem. 229:356-368(1995).
[5]
RN CHARACTERIZATION OF SECRETOLYTIN.
RP MEDLINE=96184581; PubMed=8603705;
RA Strub J.M., Hubert P., Nullans G., Aunis D., Metz-Boutigue M.-H.;
"Antibacterial activity of secretolytin, a chromogranin B-derived
peptide (614-626), is correlated with peptide structure.";
FEBL Lett. 379:273-278(1996).
CC -1- FUNCTION: SECRETOGRANIN I IS A NEUROENDOCRINE SECRETORY GRANULE
PROTEIN, WHICH MAY BE THE PRECURSOR FOR OTHER BIOLOGICALLY ACTIVE
PEPTIDES. THE 16 PAIRS OF BASIC AA DISTRIBUTED THROUGHOUT ITS
SEQUENCE MAY BE USED AS PROTEOLYTIC CLEAVAGE SITES.
CC -1- FUNCTION: SECRETOLYTIN HAS ANTIBACTERIAL ACTIVITY.
CC -1- SUBCELLULAR LOCATION: NEUROENDOCRINE AND ENDOCRINE SECRETORY
GRANULES.
CC -1- PTM: O-GLYCOSYLATED (PROBABLE).
CC -1- SIMILARITY: BELONGS TO THE CHROMOGRANIN / SECRETOGRANIN PROTEIN
FAMILY.
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DR EMBL; X55027; CAA38846.1; -
DR EMBL; U88551; AAC48720.1; -
DR EMBL; X55489; CAA39109.1; -
DR PIR; S15901; S15901.
DR InterPro; IPR001819; -
DR InterPro; IPR001990; -
DR Pfam; PF01271; Granin; 1.
DR PRINTS; PR00659; CHROMOGRANIN.
DR PROSITE; PS00422; GRANINS.1; 1.
DR PROSITE; PS00423; GRANINS.2; 1.
KW Sulfatation; Cleavage on pair of basic residues; Signal.
FT SIGNAL 1 20
FT CHAIN 21 646 SECRETOGRANIN I.
FT PEPTIDE 418 484 GAWK PEPTIDE.
FT PEPTIDE 634 646 SECRETOLYTIN.
FT DISULFID 36 57 BY SIMILARITY.
FT MOD_RES 158 158 SULFATATION (POTENTIAL).
FT MOD_RES 315 315 SULFATATION (BY SIMILARITY).
FT CONFLICT 64 64 N -> S (IN REF. 1).
FT CONFLICT 70 70 N -> D (IN REF. 2).
FT CONFLICT 93 98 SEAPGL -> FRSPRAS (IN REF. 3).
FT CONFLICT 181 181 T -> M (IN REF. 2).
FT CONFLICT 261 261 H -> R (IN REF. 2).
FT CONFLICT 386 386 P -> R (IN REF. 2).
FT CONFLICT 481 481 H -> L (IN REF. 3).

```



Db 345 E--GALLRRGRGFSSSSGGSDSLSPARSAPRAPAAAAARRSASS 391

## RESULT 13

ST13\_MOUSE  
ID ST13\_MOUSE STANDARD; PRT; 215 AA.  
AC Q60924;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE RETINOIC ACID-INDUCIBLE E3 PROTEIN (HEMATOPOIETIC-SPECIFIC PROTEIN  
E3).  
GN STRA13.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;

[1]

RN SEQUENCE FROM N.A.

RC STRAIN=MDF1;

RA MEDLINE=96437028; PubMed=8839844;

RT "E3, a hematopoietic-specific transcript directly regulated by the

retinoic acid receptor alpha."

RL Blood 88:2517-2530(1996).

CC -1- TISSUE SPECIFICITY: PRESENT IN THE MYELOID, B-LYMPHOID, AND

ERYTHROID LINEAGES. ABSENT IN NONHEMATOPOIETIC CELLS.

CC -1- INDUCTION: BY RETINOIC ACID.

CC -----

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CC -----

CC EMBL; U29539; AAB48193.1; -

DR MGD; MGI:894324; Stra13.

DR Repeat.

KW DOMAIN

FT 16 171 13 X 12 AA TANDEM REPEAT OF G-[AG]-P-P-T-

FT T-H-W-S-A-H-H.

FT SEQUENCE 215 AA; 23140 MW; 647CCB5FDA7BC73E CRC64;

SQ

## Query Match

Best Local Similarity 9.4%; Score 84.5; DB 1; Length 215;  
Matches 33; Conservative 7; Mismatches 76; Indels 11; Gaps 3;

QY 17 SAERGLGSPAGDGPSSG-----GKHHQAPGLLDASHQOEPTSSHHGGAGAVEIR 70

Db 72 SAHGCAPPTTHWSAHHCAPPTTHWSAHHCAPPTTHWSAHHCAPPTTHWSAHHCAPPTTHW 131

QY 71 SRHSYPAGTDEDDGMEEPSPFRGRSRAPPNL-WAAQRYGRELRLRMXDFVDSFKKGL 129

Db 132 SAHGCAPPTTHWSAHHCAPPTTHWSAHHCAPPTTHWSAHHCAPPTTHWSAHHCAPPTTHW 187

QY 130 PRPKSAG 136

Db 188 SNSLGAG 194

## RESULT 14

HXA5\_HUMAN  
ID HXA5\_HUMAN STANDARD; PRT; 270 AA.  
AC P20719; O43367;  
DT 01-FEB-1991 (Rel. 17, Created)  
DT 01-FEB-1991 (Rel. 17, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE HOMEBOX PROTEIN HOX-A5 (HOX-1C).  
GN HOXA5 OR HOXC1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=89313782; PubMed=2568583;  
RA Tournier-Lasserre E., Odenwald W.F., Garbern J., Trojanowski J.,  
Lazzarini R.A.;  
RT "Remarkable intron and exon sequence conservation in human and mouse  
homeobox Hox 1.3 genes."  
RL Mol. Cell. Biol. 9:2273-2278(1989).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Bradshaw H., Hinds K., Keppler D.;  
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE OF 195-260 FROM N.A.  
RX MEDLINE=90215236; PubMed=2576652;  
RA Boncinelli E., Acampora D., Pannese M., D'Esposito M., Somma R.,  
Gaudino G., Stornaiuolo A., Cafiero M., Faiella A., Simeone A.;  
RT "Organization of human class I homeobox genes."  
RL Genome 31:745-756(1989).  
CC -1- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF  
A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH  
SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.  
CC ALSO BINDS TO ITS OWN PROMOTER. BINDS SPECIFICALLY TO THE MOTIF:  
5'-CYNATTA(TG)Y-3'.  
CC -1- SUBCELLULAR LOCATION: NUCLEAR.  
CC -1- DEVELOPMENTAL STAGE: EXPRESSED DURING EMBRYOGENESIS AND IN ADULT  
KIDNEY.  
CC -1- SIMILARITY: BELONGS TO THE ANTP FAMILY OF HOMEBOX PROTEINS.  
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration  
between the Swiss Institute of Bioinformatics and the EMBL outstation -  
the European Bioinformatics Institute. There are no restrictions on its  
use by non-profit institutions as long as its content is in no way  
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entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC EMBL; M26679; AAA58663.1; -

DR EMBL; AC004080; AAB97946.1; -

DR PIR; A32799; WJHUIC.

DR HSP; P02833; ISAN.

DR TRANSFAC; T01702; -

DR TM; 142952; -

DR InterPro; IPR001356; -

DR InterPro; IPR001827; -

DR Pfam; PF00046; homeobox; 1.

DR PRINTS; PR00024; HOMEBOX.

DR PRINTS; PR00025; ANTENNAPEDIA.

DR PROSITE; PS00027; HOMEBOX 1; 1.

DR PROSITE; PS00032; ANTENNAPEDIA; 1.

DR PROSITE; PSS0071; HOMEBOX 2; 1.

KW Homeobox; DNA-binding; Developmental protein; Nuclear protein;

Transcription regulation.

FT DOMAIN 176 181 ANTP-TYPE HEXAPEPTIDE.

FT DNA\_BIND 195 254 HOMEBOX.

FT CONFLICT 114 114 T->S (IN REF. 2).

SQ SEQUENCE 270 AA; 29359 MW; 6583BF2562BC9AC CRC64;

Query Match 9.3%; Score 84; DB 1; Length 270;

Best Local Similarity 24.5%; Pred. No. 5.7;

Matches 49; Conservative 17; Mismatches 78; Indels 56; Gaps 8;

QY 10 SEQ-EDSSAERG-----LGPSPAGDGPSSGKHHQ--APGLLDASHQOEPT 56

Db 31 SEQFRDSASMSHSGRYGYGYNGMDLSVGRSGCHFGSRARSYAASAPAPRYSPA 90

QY 57 SS-----SHHG-----AGAVEIRSRHS-SYPACTE 81

Db 91 TSHSPQDPPLPCSAVAPSGSDTHHGKNSLSNSSGASADAGSTHTSSREGVGTASGA 150





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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 9, 2001, 15:58:15 ; Search time 35.13 seconds  
(without alignments)  
632.714 Million cell updates/sec

Title: 09-580523-la  
Perfect score: 902  
Sequence: 1 MFQIPFEPSEQEDSSAER.....RVFQSWDRNLGRGSSAPSQ 168

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues  
Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL\_16:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_unclassified:\*
- 13: sp\_vertebrate:\*
- 14: sp\_virus:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	901	99.9	168	014803	014803 homo sapien
2	632.5	70.1	205	11 035147	035147 rattus norv
3	632.5	70.1	205	11 070256	070256 rattus norv
4	442	49.0	220	11 09JHX1	09JHX1 rattus norv
5	203.5	22.6	95	13 0919N2	0919N2 brachydanio
6	100	11.1	608	14 09Q5K9	09Q5K9 herpesvirus
7	98.5	10.9	569	13 09DF20	09DF20 brachydanio
8	98	10.9	272	4 09NS37	09NS37 homo sapien
9	98	10.9	355	2 09RDL8	09RDL8 streptomyc
10	96.5	10.7	867	10 09FVZ6	09FVZ6 oryza sativ
11	95.5	10.6	980	4 095387	095387 homo sapien
12	95.5	10.6	2506	4 09NS88	09NS88 homo sapien
13	94.5	10.5	923	5 09NKN4	09NKN4 leishmania
14	94.5	10.5	1729	5 025734	025734 plasmodium
15	93.5	10.4	549	4 09H0B9	09H0B9 homo sapien
16	93.5	10.4	1203	4 09UPQ9	09UPQ9 homo sapien
17	93.5	10.4	1398	11 009000	009000 mus musculu
18	93	10.3	1146	5 09N809	09N809 trypanosoma
19	93	10.3	1300	14 036421	036421 alcelaphine

20	92.5	10.3	1082	11 09EPU2	09EPU2 rattus norv
21	92	10.2	2472	4 09NS89	09NS89 homo sapien
22	91	10.1	622	4 09NTE2	09NTE2 homo sapien
23	91	10.1	670	5 09NEL2	09NEL2 caenorhabdi
24	91	10.1	701	4 09NTP8	09NTP8 homo sapien
25	91	10.1	803	4 09ULK9	09ULK9 homo sapien
26	91	10.1	990	4 015206	015206 homo sapien
27	91	10.1	1218	4 005331	005331 homo sapien
28	90	10.0	414	11 09ERU8	09ERU8 mus musculu
29	90	10.0	474	5 09VA96	09VA96 drosophila
30	89.5	9.9	393	11 008719	008719 rattus norv
31	89.5	9.9	393	11 070429	070429 mus musculu
32	89.5	9.9	947	10 09LWJ9	09LWJ9 oryza sativ
33	89	9.9	903	4 09UPX1	09UPX1 homo sapien
34	88.5	9.8	336	14 098321	098321 molluscum c
35	88.5	9.8	809	5 09NAN8	09NAN8 caenorhabdi
36	88	9.8	362	4 095884	095884 homo sapien
37	88	9.8	416	4 09UI08	09UI08 homo sapien
38	88	9.8	418	4 09UIC2	09UIC2 homo sapien
39	88	9.8	462	6 097643	097643 lama glama
40	88	9.8	735	11 09JIG4	09JIG4 mus musculu
41	88	9.8	956	4 09UQ39	09UQ39 homo sapien
42	88	9.8	1262	4 09UQ40	09UQ40 homo sapien
43	88	9.8	2296	4 09UHA8	09UHA8 homo sapien
44	88	9.8	2752	4 09UQ35	09UQ35 homo sapien
45	87.5	9.7	510	5 09VAI8	09VAI8 drosophila

ALIGNMENTS

RESULT 1

014803

ID 014803 PRELIMINARY; PRT; 168 AA.

AC 014803;

DT 01-JAN-1998 (TReMBLrel. 05, Created)

DT 01-JAN-1998 (TReMBLrel. 05, Last sequence update)

DT 01-NOV-1998 (TReMBLrel. 08, Last annotation update)

DE BCL-X/BCL-2 BINDING PROTEIN (FRAGMENT).

GN BAD.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OC NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=97083574; PubMed=8929532;

RA Wang H.G., Rapp U.R., Reed J.C.;

RT "Bcl-2 targets the protein kinase Raf-1 to mitochondria.";

RL Cell 87:629-638(1996).

RN [2]

RP SEQUENCE FROM N.A.

RA Takayama S., Reed J.C.;

RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.

RN [3]

RP SEQUENCE FROM N.A.

RA Ottilie S., Diaz J.L., Horne W., Chang J., Wang Y., Wilson G.,

RA Weeks S., McConnell M., Chang S., Fritz L.C., Oltersdorf T.;

RA J. Biol. Chem. 0:0-0(1997).

DR EMBL; AF021792; AAB72092.1; -

DR EMBL; AF031523; AAB88124.1; -

FT NON\_TER 1

SQ SEQUENCE 168 AA; 18392 MW; 69FD8D27DDEE3241 CRC64;

Query Match 99.9%; Score 901; DB 4; Length 168;  
Best Local Similarity 99.4%; Pred. No. 2.2e-76;  
Matches 167; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MFQIPFEPSEQEDSSAERGLGSPAGDGSFGSGKHKHRQAPGLLWDASHQEQPTSSSH 60  
|||||  
Db 1 MFQIPFEPSEQEDSSAERGLGSPAGDGSFGSGKHKHRQAPGLLWDASHQEQPTSSSH 60

QY 61 HGGAGAVEIRSRHSSYPAGTDEDEGMEEPSPFRGRSRAPPNLWAAQRYGRELRMXDE 120  
DB 61 HGGAGAVEIRSRHSSYPAGTDEDEGMEEPSPFRGRSRAPPNLWAAQRYGRELRMSDE 120  
QY 121 FVDSFKKGLPRPKSAGTATQMRQSSWTRVFQSWWDRNLGRGSSAPSQ 168  
DB 121 FVDSFKKGLPRPKSAGTATQMRQSSWTRVFQSWWDRNLGRGSSAPSQ 168  
RESULT 2  
035147  
ID 035147 PRELIMINARY; PRT; 205 AA.  
AC 035147;  
DT 01-JAN-1998 (TremBLrel. 05, Created)  
DT 01-JAN-1998 (TremBLrel. 05, Last sequence update)  
DT 01-NOV-1998 (TremBLrel. 08, Last annotation update)  
DE BCL-2 ASSOCIATED DEATH PROMOTER.  
GN BAD.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=OVARY;  
RX MEDLINE=98034386; PubMed=9369453;  
RA Hsu S.Y., Hsueh A.J.W.;  
RT "Interference of BAD (Bcl-xL/Bcl-2-associated death promoter)-induced  
apoptosis in mammalian cells by 14-3-3 isoforms and P11.";  
RL Mol. Endocrinol. 11:1858-1867(1997).  
DR EMBL; AF003523; AAC53374.1; -;  
SQ SEQUENCE 205 AA; 22468 MW; 04DD3EBA03B11168 CRC64;

Query Match 70.1%; Score 632.5; DB 11; Length 205;  
Best Local Similarity 74.6%; Pred. No. 2.3e-51;  
Matches 126; Conservative 11; Mismatches 25; Indels 7; Gaps 4;  
QY 1 MFOIPEFEPSEQDSSAERGLGSPAGDPGSGGKHHRQAPGLLWDASHQOE-QPTSSS 59  
DB 43 MFOIPEFEPSEQDASTDRLGSLTEQDP---GPY--LAPGLGSIYQQPGQAANN 97  
QY 60 HGGAGAVEIRSRHSSYPAGTDEDEGMEEPSPFRGRSRAPPNLWAAQRYGRELRMXD 119  
DB 98 HGGAGTMTSRHSSYPAGTDEDEGMEELSPFRGRSRAPPNLWAAQRYGRELRMSD 157  
QY 120 EFVDSFKKGLPRPKSAGTATQMRQSSWTRVFQSWWDRNLGRGSSAPSQ 168  
DB 158 EFGESF-KGLPRPKSAGTATQMRQSSASWTRIIQSWWDRNLGRGGSTPSQ 205

RESULT 3  
070256  
ID 070256 PRELIMINARY; PRT; 205 AA.  
AC 070256;  
DT 01-AUG-1998 (TremBLrel. 07, Created)  
DT 01-AUG-1998 (TremBLrel. 07, Last sequence update)  
DT 01-OCT-2000 (TremBLrel. 15, Last annotation update)  
DE BCL-2 ASSOCIATED DEATH PROMOTER BAD (BCL-2 ASSOCIATED DEATH AGONIST  
ALPHA).  
GN BAD OR BAD-ALPHA.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=BRAIN;  
RX MEDLINE=98194755; PubMed=9535132;  
RA D'Agata V., Magro G., Travali S., Musco S., Cavallaro S.;  
RT "Cloning and expression of the programmed cell death regulator Bad in  
the rat brain";  
RL Neurosci. Lett. 243:137-140(1998).

RNA SEQUENCE FROM N.A.  
RA Hammer S., Arumne U., Li-Ying Y., Sun Y.-F., Saarma M., Lindholm D.;  
RT "Functional characterization of two splice variants of rat Bad and  
their interaction with bcl-w in sympathetic neurons.";  
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF031227; AAC15100.1; -;  
DR EMBL; AF279910; AAF91427.1; -;  
SQ SEQUENCE 205 AA; 22228 MW; 7AFA71DAE9CF4A81 CRC64;

Query Match 70.1%; Score 632.5; DB 11; Length 205;  
Best Local Similarity 74.6%; Pred. No. 2.3e-51;  
Matches 126; Conservative 11; Mismatches 25; Indels 7; Gaps 4;  
QY 1 MFOIPEFEPSEQDSSAERGLGSPAGDPGSGGKHHRQAPGLLWDASHQOE-QPTSSS 59  
DB 43 MFOIPEFEPSEQDASTDRLGSLTEQDP---GPY--LAPGLGSIYQQPGQAANN 97  
QY 60 HGGAGAVEIRSRHSSYPAGTDEDEGMEEPSPFRGRSRAPPNLWAAQRYGRELRMXD 119  
DB 98 HGGAGTMTSRHSSYPAGTDEDEGMEELSPFRGRSRAPPNLWAAQRYGRELRMSD 157  
QY 120 EFVDSFKKGLPRPKSAGTATQMRQSSWTRVFQSWWDRNLGRGSSAPSQ 168  
DB 158 EFGESF-KGLPRPKSAGTATQMRQSSASWTRIIQSWWDRNLGRGGSTPSQ 205

RESULT 4  
Q9JHX1  
ID Q9JHX1 PRELIMINARY; PRT; 220 AA.  
AC Q9JHX1;  
DT 01-OCT-2000 (TremBLrel. 15, Created)  
DT 01-OCT-2000 (TremBLrel. 15, Last sequence update)  
DT 01-OCT-2000 (TremBLrel. 15, Last annotation update)  
DE BCL-2 ASSOCIATED DEATH AGONIST BETA.  
GN BAD-BETA.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Hammer S., Arumne U., Li-Ying Y., Sun Y.-F., Saarma M., Lindholm D.;  
RT "Functional characterization of two splice variants of rat Bad and  
their interaction with bcl-w in sympathetic neurons.";  
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF279911; AAF91428.1; -;  
SQ SEQUENCE 220 AA; 24278 MW; E27BCDD7C969E90F CRC64;

Query Match 49.0%; Score 442; DB 11; Length 220;  
Best Local Similarity 71.7%; Pred. No. 1.2e-33;  
Matches 91; Conservative 8; Mismatches 22; Indels 6; Gaps 3;  
QY 1 MFOIPEFEPSEQDSSAERGLGSPAGDPGSGGKHHRQAPGLLWDASHQOE-QPTSSS 59  
DB 43 MFOIPEFEPSEQDASTDRLGSLTEQDP---GPY--LAPGLGSIYQQPGQAANN 97  
QY 60 HGGAGAVEIRSRHSSYPAGTDEDEGMEEPSPFRGRSRAPPNLWAAQRYGRELRMXD 119  
DB 98 HGGAGTMTSRHSSYPAGTDEDEGMEELSPFRGRSRAPPNLWAAQRYGRELRMSD 157  
QY 120 EFVDSFK 126  
DB 158 EFGESFK 164  
RESULT 5  
Q9I9N2  
ID Q9I9N2 PRELIMINARY; PRT; 95 AA.  
AC Q9I9N2;  
DT 01-OCT-2000 (TremBLrel. 15, Created)

DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)  
DE BAD (FRAGMENT).  
GN BAD.  
OS Brachydanio rerio (zebrafish) (Zebra danio).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;  
OC Cypriniformes; Cyprinidae; Rasbora; Danio.  
OX NCBI\_TaxID=7955;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20373792; PubMed=10917738;  
RA Inohara N., Nunez G.;  
RT "Genes with Homology to Mammalian Apoptosis Regulators Identified in  
RT zebrafish";  
RL Cell Death Differ. 7:509-510(2000).  
DR EMBL; AF231017; AAF66962.1; -  
FT NON\_CODING  
SQ SEQUENCE 95 AA; 10804 MW; 77F5CDE879E69FF7 CRC64;

Query Match 22.6%; Score 203.5; DB 13; Length 95;  
Best Local Similarity 48.9%; Pred. No. 7e-12; Length 95;  
Matches 44; Conservative 10; Mismatches 25; Indels 11; Gaps 3;  
Qy 83 DEGMEEP-SPFRGRSRAPNLAAQRYGRELRLRMXDFVDSFKKGLPRPKSAGTA 138  
Dy 13 ETGVAEDPHMLGDFRPRSRAPNLAAQRYGRELRLRMXDFVDSFKKGLPRPKSAGTA 68  
Qy 139 TOMROSSWTRVFSQSWMDRNLGRSSAPSQ 168  
Dy 69 ROMSQSPSWLAF---WSHKESDAESRAE 95

RESULT 6  
Q9Q5K9 ID Q9Q5K9 PRELIMINARY; PRT; 608 AA.  
AC Q9Q5K9;  
DT 01-MAY-2000 (TREMBlrel. 13, Created)  
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
DE 01-MAY-2000 (TREMBlrel. 13, Last annotation update)  
DE NTR.  
OS Herpesvirus papio.  
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
OC Gammaherpesvirinae; Lymphocryptovirus.  
OX NCBI\_TaxID=10394;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BABOON LYMPHOCRYPTOVIRUS BA65;  
RA Zong J.-C., Ryan J., Ling P.D., Loeb D.D., Pagano J.S., Hayward S.D.,  
RA Hayward G.S.;  
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF200364; AAF23950.1; -  
SQ SEQUENCE 608 AA; 60458 MW; 4BF82ACB0A029627 CRC64;

Query Match 11.1%; Score 100; DB 14; Length 608;  
Best Local Similarity 33.3%; Pred. No. 0.19; Length 608;  
Matches 37; Conservative 7; Mismatches 55; Indels 12; Gaps 3;

Qy 9 PSEQDSSAERGLGSPAGDPSGSGKHRRQAPGLLWDASHQEQPTSSSHHG---GA 64  
Dy 502 PRTERRRSAGRHPPPGAGQPSGTPGGHAPAGCPGPRSPRTERRRSAGRHPPPGGA 561  
Qy 65 GAVEIRSHSYPACTEDDEGMGEPPSPFRGRSRAPNLAAQRYGRELRL 115  
Dy 562 G-----QRPSTGTHPAAGPAGPPNPERGSGPADPP---AATRLPLEPR 604

RESULT 7  
Q9DF20 ID Q9DF20 PRELIMINARY; PRT; 569 AA.  
AC Q9DF20;

DT 01-MAR-2001 (TREMBlrel. 16, Created)  
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)  
DE KH DOMAIN CONTAINING RNA-BINDING PROTEIN FMRL.  
OS Brachydanio rerio (zebrafish) (Zebra danio).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;  
OC Cypriniformes; Cyprinidae; Rasbora; Danio.  
OX NCBI\_TaxID=7955;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20501263; PubMed=11046149;  
RA Wan L., Dockendorff T.C., Jongens T.A., Dreyfuss G.;  
RT "Characterization of dFMR1, a Drosophila melanogaster Homolog of the  
RT Fragile X Mental Retardation Protein";  
RL Mol. Cell. Biol. 20:8536-8547(2000).  
DR EMBL; AF305882; AAG22046.1; -  
SQ SEQUENCE 569 AA; 63906 MW; 2B66A0689F7EDFB5 CRC64;

Query Match 10.9%; Score 98.5; DB 13; Length 569;  
Best Local Similarity 32.3%; Pred. No. 0.24; Length 569;  
Matches 31; Conservative 8; Mismatches 42; Indels 15; Gaps 3;  
Qy 11 EQEDSSAERGLGSPAGDPSGSGKHRRQAP---GLLWDASHQEQPTSSSHHGAGA 66  
Dy 391 EKERSFMADNGMPSRGGKPGRGGRGPTLASGTNSENASE---TESDH----- 442  
Qy 67 VEIRSRHSYPAGTDEDEGMGEPPSPFRGRSRAP 102  
Dy 443 ---RDELDWSLAPTDEESMGYPKRAPDGRKRGGP 475

RESULT 8  
Q9NS37 ID Q9NS37 PRELIMINARY; PRT; 272 AA.  
AC Q9NS37;  
DT 01-OCT-2000 (TREMBlrel. 15, Created)  
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)  
DE HCF-BINDING TRANSCRIPTION FACTOR ZHANGFEI.  
DE ZF.  
GN Homo sapiens (Human).  
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20330366; PubMed=10871379;  
RA Lu R., Misra V.;  
RT "Zhangfei, a second cellular protein interacts with herpes simplex  
RT virus accessory factor HCF in a manner similar to Luman and VP16";  
RL Nucleic Acids Res. 28:2446-2454(2000).  
DR EMBL; AF039942; AAD28325.1; -  
DR InterPro; IPR001871; -  
DR Pfam; PF00170; bZIP; 1.  
DR SMART; SM00338; BRLZ; 1.  
SQ SEQUENCE 272 AA; 28859 MW; B1F94B438F0702BF CRC64;

Query Match 10.9%; Score 98; DB 4; Length 272;  
Best Local Similarity 28.2%; Pred. No. 0.13; Length 272;  
Matches 40; Conservative 13; Mismatches 69; Indels 20; Gaps 4;  
Qy 10 SEQEDSSAERGLGSPAGDPSGSGKHRRQAPGLLWDASHQEQPTSSSHHGAGAVEI 69  
Dy 92 SSSSDSGAERKRRKSPGGGGGGGNDNNQA-----ATKSPKAAAAAARL 138  
Qy 70 -RSRHSYPAGTDEDEGMGEPPSPFRGRSRAPNLAAQRYGRELRLRMXDFVDSFKK 127  
Dy 139 NRLKKKYYVGLSVRGVLAENQELRAENRELGRKRVQALQESRYLRA-----VLANET 193  
Qy 128 GLPRPKSAGTATQMRQSSWTR 149

Db 194 GLARLLSRLSGVGLRLTTSLFR 215

RESULTS

AC002118 5 Q9RDL8 PRELIMINARY; PRT; 355 AA.  
ID Q9RDL8;  
AC Q9RDL8;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
DE PUTATIVE DNA-BINDING PROTEIN.  
GN SCC123.06C.  
OS Streptomyces coelicolor.  
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
OC Actinomycetales; Streptomycetales; Streptomycetaceae; Streptomycetes.  
OX NCBI\_TaxID=1902;  
RN [1]  
RS SEQUENCE FROM N.A.  
RC STRAIN=A3(2);  
RA Brown S.P., Harris D.;  
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RS SEQUENCE FROM N.A.  
RC STRAIN=A3(2);  
RA Thomson N.R., Parkhill J., Barrell B.G., Rajandream M.A.;  
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RS SEQUENCE FROM N.A.  
RC STRAIN=A3(2);  
RX MEDLINE=97000351; PubMed=8843436;  
RA Redenbach M., Kieser H.M., Denapalte D., Eichner A., Cullum J.,  
R Kinashi H., Hopwood D.A.;  
RT "A set of ordered cosmids and a detailed genetic and physical map for  
RT the 8 Mb Streptomyces coelicolor A3(2) chromosome.";  
RT Mol. Microbiol. 21:77-96(1996).  
DR EMBL; AL136518; CAB66246.1; -;  
DR InterPro; IPR000445; -;  
DR InterPro; IPR003583; -;  
DR Pfam; PF00633; HHH; 1.  
DR SMART; SM00278; HHH1; 1.  
KW DNA-binding.  
SQ SEQUENCE 355 AA; 36853 MW; ELE9D0A574CCABDE CRC64;

```

Query Match      10.9%; Score 98; DB 2; Length 355;
Best Local Similarity 28.5%; Pred. No. 0.17;
Matches 43; Conservative 14; Mismatches 66; Indels 28; Gaps

QY      15  SSSAERCLGSPAGDPSGSKHHRAQPLLWDASHHQEQPTSSSHHG--GAGAVEIRSR 72
      : : | | : | | | | | | | | | | | | | | | | | | |
Db      9  TATAGTGGPRAPASDGLA----HREAPGSRTHARH-----SHARGRRHAAPEELRR 59

QY      73  -HSSYPAGTDEDDGMEGEEPSPPFGRGRSAP--PNLWAAQRYGRELRRMNXDFVDSFKGL 129
      : : : : : : : : : : : : : : : : : : : : : :
Db      60  AETLFAERAGYDHAGHEGA--HGCTGKGPPPLGLDAPARQGSPL-----PGL 105

QY      130  PRPKSAGTATQMRQSSSWTRVFQSWWDRNLG 160
      : | | | : | : | : | : | : | : | : | : | : | : |
Db      106  DAPTGPCTAWRRAGSALRERNPLWLQTRCG 136

```

## RESULT 10

Accession	Gene	Species	Accession	Gene	Species
Q9FVZ6	PRELIMINARY;	PRT.	867	AA.	
AD	Q9FVZ6				
AC	Q9FVZ6;				
DT	01-MAR-2001 (TRENBLrel. 16, Created)				
DT	01-MAR-2001 (TRENBLrel. 16, Last sequence update)				
DT	01-MAR-2001 (TRENBLrel. 16, Last annotation update)				
DE	PUTATIVE REPLICATION PROTEIN.				
OS	<i>Oryza sativa</i> (Rice).				
OC	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;				
OC	Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae;				
OC					

OC Oryza.  
OX NCBI TaxID=4530:

[1] SEQUENCE FROM N.A.  
RP STRAIN=CV. NIPPONARE;  
RA Buell C.R., Yuan Q., Moffat K.S., Hill J.N., Jenkins C.N., Burr P.C.,  
RA Hsiao J., Zismann V., Pai G., Bowman C.L., Fujii C.Y., VanAken S.E.,  
RA Bowman C.L., Craven B., Utterback T.R., Khalak H., Feldblyum T.V.,  
RA Quackenbush J., White O., Salzberg S.L., Fraser C.M.;  
RT "Oryza sativa chromosome 10 BAC OSUNBB0073N24 genomic sequence.";  
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AC078840; AAG13631.1; -  
SQ SEQUENCE 867 AA; 194083 MW; 4FEA69E1BFC0CB2C CRC64;

Query Match 10.7%; Score 96.5; DB 10; Length 867;  
Best Local Similarity 28.7%; Pred. No. 0.57;  
Matches 37; Conservative 9; Mismatches 44; Indels 39

Qy	13	EDSSASRGILGSPAG----	DGSGSGKHQAP-----	GLINDASHQOE----	53
Db	730	KEEAARAGGGPDL	SHSHLGGGGGTGKEAAAT	PTRGASRGGGGADADAGEQEDAA	799
Qy	54	-----OPTSSHHGGAGAVEIR	SHSSYPAGTDEDDGMEEPSP	FRGRSRAPPNLWAA	107
Db	790	AWGGGPDPLSHL	GGGG-----GTGKEA-	AAAPTPTRGASRGGGGGTGT	835
Qy	108	QRYGRELRR	116		
Db	836	RRERRLGR	844		

## RESULT 11

```

095387      PRELIMINARY;      PRT;      980 AA.
AC      095387;
DT      01-MAY-1999 (TREMBLrel. 10, Created)
DT      01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT      01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE      VOLTAGE-DEPENDENT P/O TYPE CALCIUM CHANNEL ALPHA 1A SUBUNIT
DE      (FRAGMENT).
OS      HOMO SAPIENS (Human).
OS      GACNAILA.
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX      NCBI_TaxID=9606;
[1]
RN      SEQUENCE FROM N.A.
RP      Black J.L., Snutch T.P., Lennon V.A.;
RA      "Partial sequence of Homo sapiens P/O-type voltage-gated calcium channel alpha 1 [alpha 1A] subunit: isolated from small cell carcinoma cell line, SCC 9, cDNA library.";
RT      Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
RL      EMBL; AF100774; AAC77460.1; -.
DR      InterPro; IPR000636; -.
DR      InterPro; IPR001682; -.
DR      InterPro; IPR002077; -.
DR      InterPro; IPR002111; -.
DR      Pfam; PF00520; Ion_trans; 1.
DR      PRINTS; PR00167; CACHANNEL.
FT      1
SQ      SEQUENCE      980 AA; 110251 MW; AF627D9F8BE16D43 CRC64;

```

Query Match 10.6%; Score 95.5; DB 4; Length 980;

	Best local similarity	23.1%, tied: NO: 0.0;	Matches 46;	Conservative	Mismatches 18;	Indels 50;	Gaps 69;	Gaps 10;
QY	15	SSSAERGLGSP----	AGDPGSGSKHHQAP-----					GLLWDS- 49
	:	:	:	:	:	:	:	:
	:	:	:	:	:	:	:	:
Db	809	TSGPRRYPTAEPLADRPPTTGGHSGSRSPMERRVPGPARSESPRACRHGGARWPASG	868					
QY	50	-HQOEOPTSSHHGGAGAVEIRSRHSSYPACTEDDE-----	GMCEE-----					PSPF- 94

```
*
Db 869 PHVSEGGPPRRHG-----YIRGSDYDEADPGSGGGEAMAGAYDAPPVVR 915
QY 95 -----GRS-----RSAPPNLWAAQRYGRELRRMXDEFVDSFKKGLPRPKSAGTATQMRQ 143
Db 916 HASSGATGRSPRTPRASGACASPSRHG---RRLPNGYYP--HGLARPGRPGSRKKGHLHE 970
QY 144 SSS 146
Db 971 PYS 973

RESULT 12
Q9NS88 PRELIMINARY; PRT; 2506 AA.
AC Q9NS88:
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE ALPHA1A-VOLTAGE-DEPENDENT CALCIUM CHANNEL.
GN CACNA1A.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=CREBELLUM;
RX MEDLINE=20219126; PubMed=10733886;
RA Toru S., Murakoshi T., Ishikawa K., Saegusa H., Fujigasaki H.,
RA Uchiwara T., Nagayama S., Osanai M., Mizusawa H., Tanabe T.;
RA "Spinocerebellar ataxia type 6 mutation alters P-type calcium channel
RT function."
RT J. Biol. Chem. 275:10893-10898(2000).
DR EMBL; AB035727; BAA94766.2; -.
DR InterPro; IPR000636; -.
DR InterPro; IPR000637; -.
DR InterPro; IPR001682; -.
DR InterPro; IPR002077; -.
DR InterPro; IPR002111; -.
DR Pfam; PF00520; Ion_trans; 4.
DR PRINTS; PR00167; CACHANNEL.
DR SMART; SM00384; AT_hook; 1.
DR SEQUENCE 2506 AA; 282580 MW; D64A6C75284A1B53 CRC64;

Query Match 10.68; Score 95.5; DB 4; Length 2506;
Best Local Similarity 25.1%; Pred. No. 2.1;
Matches 46; Conservative 18; Mismatches 50; Indels 69; Gaps 10;

QY 15 SSSAERGLGSPSP--AGDGPSSGKHHROAP-----GLLWDAS- 49
Db 2335 TSGPRPRPGPTAEPLAGDRPTTGHSSGRSPMERVRVPGPARSPRACRHGGARWPASG 2394
QY 50 -HOOEQPTSSSHHGAGAVEIRSRHSSYPAGTDEDE-----GMGEE-----PSPFR 94
Db 2395 PHVSEGGPPRRHG-----YIRGSDYDEADPGSGGGEAMAGAYDAPPVVR 2441
QY 95 -----GRS-----RSAPPNLWAAQRYGRELRRMXDEFVDSFKKGLPRPKSAGTATQMRQ 143
Db 2442 HASSGATGRSPRTPRASGACASPSRHG---RRLPNGYYP--HGLARPGRPGSRKKGHLHE 2496
QY 144 SSS 146
Db 2497 PYS 2499

RESULT 13
Q9KNM4 PRELIMINARY; PRT; 923 AA.
AC Q9KNM4:
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
```

```
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE L5204.2.
GN L5204.2.
OS Leishmania major.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID=5664;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FRIEDLIN;
RA Myler P.J., Sisk E., Hixson G., Kiser P., Rickel E., Hassebrock M.,
RA Cawthra J., Marsolini F., Sunkin S., Stuart K.D.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC005941; AAF34290.1; -.
DR InterPro; IPR000533; -.
DR PRINTS; PR00194; TROPOMYOSIN.
DR SEQUENCE 923 AA; 103964 MW; C229C15F6448F7C7 CRC64;

Query Match 10.5%; Score 94.5; DB 5; Length 923;
Best Local Similarity 26.4%; Pred. No. 0.93;
Matches 33; Conservative 20; Mismatches 45; Indels 27; Gaps 7;

QY 10 SEQEDSSAERGLGSPAGDGPSSGKHHROAPGLLWDASHQQEQPTSSSHHGAGAVEI 69
Db 802 AEQRTNTDDR-----SPSAGGPASADVEHSA-----SQPQPHS---HAGGSAI-V 845
QY 70 RSRHSSYPAGTDEDEGMGEEPPFRGR--SRSAPENLWAAQRYGRELRRMXDEFVDSFKK 127
Db 846 SNSHNGVQAAA---SGTGRMSAANSRGVNGSVPP-----RNGRRRAPLAAILDTLTA 896
QY 128 GLRPP 132
Db 897 GPPQP 901

RESULT 14
Q25734 PRELIMINARY; PRT; 1729 AA.
AC Q25734:
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE PFEMP1 VARIANT 2 OF STRAIN MC (FRAGMENT).
GN MCVAR-2 PFEMP1.
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MALAYAN CAMP (MC132 K+C+R+);
RX MEDLINE=95330812; PubMed=7541722;
RA Baruch D.I., Pasloske B.L., Singh H.B., Bi X., Ma X.C., Feldman M.,
RA Taraschi T.F., Howard R.J.;
RT "Cloning the P. falciparum gene encoding PFEMP1, a malarial variant
RT antigen and adhesion receptor on the surface of parasitized human
RT erythrocytes."
RL Cell 82:77-87(1995).
DR EMBL; U27339; AAA89134.1; -.
FT NONTER 1729 1729
SQ SEQUENCE 1729 AA; 195156 MW; 7BFEC2131FFBAll CRC64;

Query Match 10.5%; Score 94.5; DB 5; Length 1729;
Best Local Similarity 21.6%; Pred. No. 1.8;
Matches 42; Conservative 23; Mismatches 66; Indels 63; Gaps 8;

QY 9 SEQEDSSAERGLGSPSP--AGDGPSSGKHHROAPGLL-----WDASHHQEQPTSSSHH 61
Db 926 PSGNESSPEKLPGQPTPETTKETPESSILLHAFVSPPRLRRLPW---HKFKEQWKAOHG 982
QY 62 GGAGAVEIRSRHSSYPAGTDEDEGMGEEPPFRGRSRSAPPNLWAAQRY----- 110
Db 983 AGATGLQL-----PGVTVD-----SDPDQTLKRGNIPLNDFLRQMFYTLGIDYDICI 1031
```

Query Match	10.4%	Score 93.5;	DB 4;	Length 549;
Best Local Similarity	25.0%	Pred. No. 0.68;		
Matches	41;	Conservative	17;	Mismatches 57; Indels 49; Gaps 8;

  

Qy	9	PSEQEDSSAERGLGSPAGDGPSCGSKHHRQA-----PGLLWDASHQEQPTSSSH	60
	:		
Db	360	PAKPEQSSASR---VPVASRGGKTLCKDGRQAPPPARPRPIWASPPRAPRSSTPC	416
	:		
Qy	61	HGGAGAVEIRSHRSYYPAGTDEDCMGEEPPRGRSAPPNLNAAQRYGRELRLMXDE	120
Db	417	PGGA-----VREDTYPVGTQG-----VPSP--ALAGGGPQGSWRFLQW-----	452
Qy	121	FVDSFFKGLPRKSGATATMRQSSSTRVF---QSWDRNLGR	161
Db	453	-----NSMPR-----LPTDLDEGPPFRHYDFRQSCWRAISO	485

Search completed: October 9, 2001, 16:03:21  
Job time: 306 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 9, 2001, 15:57:35 ; Search time 33.29 seconds  
(without alignments)  
305.943 Million cell updates/sec

Title: 09-580523-1A

Perfect score: 902

Sequence: 1 MFQIPFEPSEQEDSSAER.....RVFQSWDRNLGRGSSAPSQ 168

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A\_Geneseq\_0601.\*  
1: /SID88/gcgdata/geneseq/geneseq/AA1980.DAT.\*  
2: /SID88/gcgdata/geneseq/geneseq/AA1981.DAT.\*  
3: /SID88/gcgdata/geneseq/geneseq/AA1982.DAT.\*  
4: /SID88/gcgdata/geneseq/geneseq/AA1983.DAT.\*  
5: /SID88/gcgdata/geneseq/geneseq/AA1984.DAT.\*  
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20: /SID88/gcgdata/geneseq/geneseq/AA1999.DAT.\*  
21: /SID88/gcgdata/geneseq/geneseq/AA2000.DAT.\*  
22: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	901	99.9	168	19	AAW55779 Human Bcl-xL/Bcl-2
2	901	99.9	168	21	AAB13512 Human cell prolif
3	901	99.9	168	22	AAB70368 Human BAD mutant a
4	901	99.9	168	22	AAB48287 Human BAD protein.
5	747	82.8	166	18	AAB32476 BBC6 protein for r
6	645	71.5	162	22	AAB70370 Shorter murine BAD
7	645	71.5	204	17	AAR95168 bcl-x(L)/bcl-2 ass
8	645	71.5	204	19	AAW61315 Murine BCL-XL/BCL-
9	645	71.5	204	19	AAW58832 Murine BAD protein
10	645	71.5	204	22	AAB70369 Longer murine BAD
11	642	71.2	204	19	AAW61317 Mutant BCL-XL/BCL-

12	639	70.8	204	19	AAW61316	Mutant BCL-XL/BCL-
13	639	70.8	204	19	AAW61318	Mutant BCL-XL/BCL-
14	310	34.4	59	19	AAW61319	Mutant BCL-XL/BCL-
15	310	34.4	59	19	AAW61320	Mutant BCL-XL/BCL-
16	307	34.0	59	19	AAW61321	Mutant BCL-XL/BCL-
17	304	33.7	59	19	AAW61322	Mutant BCL-XL/BCL-
18	159	17.6	56	21	AAW02251	Human secreted pro
19	129	14.3	26	21	AAW96321	Mammalian Bad Bcl-
20	129	14.3	26	22	AAB70371	BAD BH3 consensus
21	116.5	12.9	27	21	AAB37003	Bcl2 polypeptide B
22	112	12.4	23	17	AAR95166	bcl-x(L)/bcl-2 ass
23	110	12.2	26	21	AAB37001	Bcl2 polypeptide B
24	110	12.2	26	21	AAB37002	Bcl2 polypeptide B
25	110	12.2	27	21	AAB37056	Bcl2 polypeptide B
26	110	12.2	28	21	AAB37055	Bcl2 polypeptide B
27	96	10.6	2510	16	AAR71007	Human neuronal cal
28	96	10.6	2510	21	AAB10579	Human calcium chan
29	95.5	10.6	1182	20	AAB33496	Human SCA6 protein
30	94.5	10.5	395	21	AAW91951	Human cytoskeleton
31	94.5	10.5	1726	17	AAW00385	Truncated Plasmodi
32	94	10.4	1931	13	AAR27649	Human calcium chan
33	93.5	10.4	549	21	AAW84901	A human proliferat
34	93.5	10.4	1447	20	AAW81029	Murine pcip protei
35	90	10.0	434	17	AAR96420	Peptide fragment o
36	90	10.0	434	21	AAB12821	Human N-type calci
37	90	10.0	2237	16	AAR71006	Human neuronal cal
38	90	10.0	2237	19	AAB63142	Human calcium chan
39	90	10.0	2237	21	AAB10573	Human calcium chan
40	90	10.0	2337	19	AAW37878	Human calcium chan
41	90	10.0	2339	14	AAR33549	Sequence of the al
42	90	10.0	2339	16	AAR71005	Human neuronal cal
43	90	10.0	2339	19	AAW63141	Human calcium chan
44	90	10.0	2339	21	AAB10572	Human calcium chan
45	90	10.0	2343	20	AAW31809	N-type calcium cha

## ALIGNMENTS

RESULT 1

AAW55779 AAW55779 standard; Protein; 168 AA.

XX AC AAW55779;

XX DT 17-JUL-1998 (first entry)

XX DE Human Bcl-xL/Bcl-2 associated death promoting polypeptide.

XX KW Human; Bcl-xL/Bcl-2 associated death promoting polypeptide; Bad;

XX KW Programmed cell death; apoptosis.

XX OS Homo sapiens.

XX PN WO9812328-A2.

XX PD 26-MAR-1998.

XX PF 18-SEP-1997; 97WO-US16991.

XX PR 20-SEP-1996; 96US-0717123.

XX PA (IDUN-) IDUN PHARM INC.

XX PI Horne WA, Oltersdorf T;

XX DR BPC6 protein for r

XX DR N-PSDB; AAV25877.

XX PT Bad gene mediating apoptosis - used to develop products for treating

XX PT e.g. neurodegenerative disease, cancers or autoimmune disease

XX PS Claim 8; Fig 1; 41pp; English.

XX The present sequence is the human Bcl-XL/Bcl-2 associated  
 CC death promoting polypeptide, Bad, the binding of which to Bcl-XL  
 CC results in the induction of programmed cell death, i.e. apoptosis.  
 CC Bad can be used in screening assays for compounds to treat or  
 CC prevent diseases characterised by apoptotic cell death, such as  
 CC neurodegenerative disorders, e.g. Alzheimer's and Parkinson's  
 CC disease, amyotrophic lateral sclerosis, retinitis pigmentosa and  
 CC cerebellar degeneration, and myelodysplastic syndromes, e.g.  
 CC aplastic anaemia and ischaemic injury including myocardial  
 CC infarction, stroke and reperfusion injury. Assays can also be  
 CC used to obtain apoptosis enhancing compounds to treat or prevent  
 CC diseases characterised by the loss of apoptotic cell death, such as  
 CC cancers, e.g. lymphoma and hormone dependent tumours, autoimmune  
 CC diseases, e.g. systemic lupus erythematosus and immune-mediated  
 CC glomerulonephritis and viral infections, e.g. herpesvirus,  
 CC poxvirus or adenovirus infection. Bad can also be used for  
 CC detection and diagnosis.  
 XX Sequence 168 AA;

Query Match 99.9%; Score 901; DB 19; Length 168;  
 Best Local Similarity 99.4%; Pred. No. 3.4e-87;  
 Matches 167; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MFOIPEFEPSEQEDSSAERGLGSPAGDPSGSGKHHRQAPGLLWDASHQOQPTSSSH 60  
 DB 1 mfgipfepseqedsssaerglgsagdgpgsgkhrgapglldashqgeqptcssh 60  
 QY 61 HGGAGAVEIRSRHSSYPAGTDEDEGMGEPPSPFRGRSRAPPNLWAAQRYGRELRRMXDE 120  
 DB 61 hggagaveirsrhssypagteddegmggeppsfgrgrsappnlwaaqrygrellrmsde 120  
 QY 121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWMDNLRGSSAPSQ 168  
 DB 121 fvdskkglprpksgagtatqmrqssswtrvfqswmdnlgsgssapsq 168

RESULT 2  
 AAB13512  
 ID AAB13512 standard; protein; 168 AA.  
 AC AAB13512;  
 XX  
 XX  
 DT 02-NOV-2000 (first entry)  
 XX  
 XX Human cell proliferation protein APOP-1.  
 DE  
 XX Human; cell proliferation; APOP-1; cancer; inflammation; infection;  
 KW trauma; neurodegenerative disease; ischaemic injury; wasting disease.  
 KW Homo sapiens.  
 XX US6080847-A.  
 PN  
 XX 27-JUN-2000.  
 XX  
 XX 04-DEC-1997; 97US-0985335.  
 XX  
 XX 04-DEC-1997; 97US-0985335.  
 PR  
 XX (INCY-) INCYTE PHARM INC.  
 XX  
 XX Corley NC, Hillman JL, Yue H, Lal P, Shah P;  
 PI  
 XX WPI; 2000-451230/39.  
 DR N-PSDB; AAA63332.  
 XX  
 XX Novel polynucleotide and polypeptide sequences of proteins associated  
 PT with cell proliferation for diagnosis, prevention and treatment of e.g.  
 PT Cancer, acquired immunodeficiency syndrome, and Parkinson's disease -  
 XX

PS Example 8; Fig 1; 58pp; English.  
 XX The present sequence is the human APOP-1 protein. This protein, which  
 CC shares structural and chemical homology with Bcl-2, is involved in cell  
 CC proliferation. Its coding sequence was isolated by screening a synovial  
 CC tissue cDNA library using a computer search for amino acid sequence  
 CC alignments. The gene and protein can be used in the treatment of various  
 CC cancers, disorders with associated inflammation such as Addison's  
 CC disease, adult respiratory distress syndrome, allergies, anaemia, asthma,  
 CC atherosclerosis, Crohn's disease, ulcerative colitis, diabetes mellitus,  
 CC emphysema, glomerulonephritis, gout, Graves' disease, irritable bowel  
 CC syndrome, lupus erythematosus, multiple sclerosis, myasthenia gravis,  
 CC myocardial or pericardial inflammation, osteoporosis, rheumatoid  
 CC arthritis, Sjogren's syndrome and autoimmune thyroiditis, complications  
 CC of cancer, haemodialysis and extracorporeal circulation, infections,  
 CC trauma, disorders with associated apoptosis including AIDS and other  
 CC infectious and genetic immunodeficiencies, neurodegenerative diseases  
 CC such as Alzheimer's disease and Parkinson's disease, ischaemic injuries  
 CC such as myocardial infarction, and wasting diseases including cachexia.  
 XX Sequence 168 AA;

Query Match 99.9%; Score 901; DB 21; Length 168;  
 Best Local Similarity 99.4%; Pred. No. 3.4e-87;  
 Matches 167; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MFOIPEFEPSEQEDSSAERGLGSPAGDPSGSGKHHRQAPGLLWDASHQOQPTSSSH 60  
 DB 1 mfgipfepseqedsssaerglgsagdgpgsgkhrgapglldashqgeqptsssh 60  
 QY 61 HGGAGAVEIRSRHSSYPAGTDEDEGMGEPPSPFRGRSRAPPNLWAAQRYGRELRRMXDE 120  
 DB 61 hggagaveirsrhssypagteddegmggeppsfgrgrsappnlwaaqrygrellrmsde 120  
 QY 121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWMDNLRGSSAPSQ 168  
 DB 121 fvdskkglprpksgagtatqmrqssswtrvfqswmdnlgsgssapsq 168

RESULT 3  
 AAB70368  
 ID AAB70368 standard; protein; 168 AA.  
 AC AAB70368;  
 XX  
 XX  
 DT 02-MAY-2001 (first entry)  
 XX  
 XX Human BAD mutant amino acid sequence SEQ ID NO:1.  
 DE  
 XX Bcl-XL/Bcl-2 associated cell death regulator; BAD; mutant; apoptosis;  
 KW immunostimulant; neuroprotective; nootropic; antiischaemic; vulnerary;  
 KW cytostatic; antiviral; antiarthritic; antiinflammatory; wound healing;  
 KW immunosuppressive; apoptosis inducer; apoptosis inhibitor; cancer;  
 KW immunodeficiency disease; neurodegenerative disease; viral infection;  
 KW ischaemic cell death; reperfusion cell death; arthritis; infertility;  
 KW lymphoproliferative condition; inflammation; autoimmune disease.  
 XX Homo sapiens.  
 OS Synthetic.  
 XX WO200110888-A1.  
 PN  
 XX 15-FEB-2001.  
 PD  
 XX 30-MAY-2000; 2000WO-US11864.  
 PF  
 XX 28-MAY-1999; 99US-0136783.  
 PR  
 XX (APOP-) APOPTOSIS TECHNOLOGY INC.  
 PA  
 XX Zhou X;  
 PI  
 XX



DR WPI; 2001-138734/14.  
XX New mutant Bcl-XL/Bcl-2 Associated Cell Death Regulator polypeptide,  
PT useful for screening for candidate compounds which induce or inhibit  
PT apoptosis, comprises amino acid substitutions at Ser118, Ser155 or  
PT Ser113 -  
XX  
PS Claim 1; Page 147; 157pp; English.  
XX  
XX The present invention describes an isolated or synthetic polypeptide  
CC (I) comprising a less than full length amino acid sequence of a mutant  
CC Bcl-XL/Bcl-2 associated cell death regulator polypeptide (BAD) or its  
CC fragment, which contains amino acid substitutions at Ser118 of a human  
CC BAD, Ser155 of a murine BAD (longer murine BAD) or Ser113 of a murine  
CC BAD (shorter murine BAD). (I) has immunostimulant, neuroprotective,  
CC neurotropic, antiischaemic, vulnerary, cytostatic, antiviral,  
CC antiarthritic, antiinflammatory and immunosuppressive activities, and  
CC can be used as an apoptosis inducer or inhibitor. BAD polypeptides and  
CC polynucleotides can be used for screening candidate compounds and drugs  
CC for activity that promote cell survival or apoptosis. Other uses include  
CC inducing or inhibiting apoptosis in a cell. Candidate compounds  
CC identified and (mutant) BAD polypeptides are useful in treating  
CC immunodeficiency diseases, neurodegenerative diseases, ischaemic cell  
CC death, reperfusion cell death, wound healing, cancer, viral infections,  
CC lymphoproliferative conditions, arthritis, infertility, inflammation and  
CC autoimmune diseases. The present sequence represents a specifically  
CC claimed human BAD mutant amino acid sequence from the present invention.  
XX  
XX Sequence 168 AA;  
SQ

Query Match 99.9%; Score 901; DB 22; Length 168;  
Best Local Similarity 99.4%; Pred. No. 3.4e-87;  
Matches 167; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MFQIPFEPSEQEDSSAERGLGSPAGDGPSSGKHHRRQAPGLLWDASHQOQPTSSSH 60  
Db 1 mfiqipefepseqedsssaerglgpspadgpgsggkhhrrqapglldashhqqeqtsssh 60  
Qy 61 HGGAGAVIRSRHSSYPAGTDEDCMGEEPSFGRGRSRAPPNLWAAQRYGRELRRMXDE 120  
Db 61 hggagaveirsrhssypagtdedgmgeepsfgrgrsrappnlwaaqrygreilrmsde 120  
Qy 121 FVDSFKKGLPRPKSAGTATQMRQSSWTRVFQSWMDRLNLRGSSAPSQ 168  
Db 121 fvdskfkgllprpksgatqmrqsswtrvfgswmdrnlgrgssapsq 168

RESULT 4  
AAB48287  
ID AAB48287 standard; protein; 168 AA.  
XX  
AC AAB48287;  
XX  
DT 02-APR-2001 (first entry)  
XX  
DE Human Bad protein.  
XX

KW S-phase kinase associated protein; SKP1; SKP2; SKP2-like protein; ZF;  
KW CUL-1; cullin; CDC53; p27; cyclin E; Max; Mad; c-Myc; MDM2; p53; Bax;  
KW BAD; Bcl-2; tumour; cytostatic.  
XX  
OS Homo sapiens.  
XX  
FN WO200075184-A1.  
XX  
PD 14-DEC-2000.  
XX

PF 05-JUN-2000; 2000WO-US15449.  
XX  
PR 04-JUN-1999; 99US-0137494.  
XX  
PA (UYVA ) UNIV YALE.

XX Zhang H, Tsvetkov LM, Kondo T;  
PI WPI; 2001-061703/07.  
XX N-PSDB; AAC84599.  
XX  
PT Modulating polypeptide levels in a cell, diagnosing and treating tumor,  
PT involves altering levels of proteins such as S-phase kinase associated  
PT proteins 1, 2 and cullin/CDC53 proteins -  
XX  
PS Claim 5; Page 102-103; 162pp; English.  
XX  
XX The invention relates to methods of altering the polypeptide levels in a  
CC cell, using proteins selected from S-phase kinase associated proteins 1  
CC and 2 (SKP1, SKP2), SKP2-like proteins (ZF) and CUL-1 (a member of the  
CC cullin/CDC53 family of proteins). The method is useful for altering the  
CC level of p27, cyclin E, Max, Mad, c-Myc, MDM2, p53, Bax, Bad or Bcl-2  
CC polypeptide in a cell. SKP2 and SKP2-like protein levels are useful for  
CC detecting tumours, and in monitoring tumor treatment in a mammal. Agents  
CC that modulate interactions between Skp and target proteins are useful for  
CC treating tumours.  
XX  
SQ Sequence 168 AA;

Query Match 99.9%; Score 901; DB 22; Length 168;  
Best Local Similarity 99.4%; Pred. No. 3.4e-87;  
Matches 167; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MFQIPFEPSEQEDSSAERGLGSPAGDGPSSGKHHRRQAPGLLWDASHQOQPTSSSH 60  
Db 1 mfiqipefepseqedsssaerglgpspadgpgsggkhhrrqapglldashhqqeqtsssh 60  
Qy 61 HGGAGAVIRSRHSSYPAGTDEDCMGEEPSFGRGRSRAPPNLWAAQRYGRELRRMXDE 120  
Db 61 hggagaveirsrhssypagtdedgmgeepsfgrgrsrappnlwaaqrygreilrmsde 120  
Qy 121 FVDSFKKGLPRPKSAGTATQMRQSSWTRVFQSWMDRLNLRGSSAPSQ 168  
Db 121 fvdskfkgllprpksgatqmrqsswtrvfgswmdrnlgrgssapsq 168

RESULT 5  
AAW32476  
ID AAW32476 standard; Protein; 166 AA.  
XX  
AC AAW32476;  
XX  
DT 15-JAN-1998 (first entry)  
XX  
DE BBC6 protein for regulating cell death.  
XX  
KW BBC6 gene; cell death; cell cycle; Bcl2; human.  
XX  
OS Homo sapiens.  
XX  
FN US5663316-A.  
XX  
PD 02-SEP-1997.  
XX  
PF 18-JUN-1996; 96US-0665617.  
XX  
PR 18-JUN-1996; 96US-0665617.  
XX  
PA (CLON-) CLONTECH LAB INC.  
XX  
PI Xudong Y;  
XX  
DR WPI; 1997-447980/41.  
DR N-PSDB; AAT91561.  
XX  
PT Isolated BBC6 gene - encodes a protein that regulates cell death  
PT through interaction with Bcl-2





KW cancer, viral infection; lymphoproliferative condition; arthritis;  
 KW inflammation; autoimmune diseases.  
 XX Mus sp.  
 XX WO9809643-A1.  
 PN 12-MAR-1998.  
 PD 09-SEP-1997; 97WO-US15871.  
 PE 09-SEP-1996; 96US-0707868.  
 XX (UNIV ) UNIV WASHINGTON.  
 PA Korsmeyer SJ;  
 PI WPI; 1998-207049/18.  
 DR Serine-phosphorylated Bcl-X-L/Bcl-2 Associated cell Death regulator  
 XX polypeptide - useful for modulation of apoptosis associated with,  
 PT e.g. cancer and immunodeficiency diseases  
 PT Claim 3; Fig 8; 61pp; English.  
 PS This sequence represents a novel serine-phosphorylated protein, BAD  
 XX (Bcl-XL/Bcl-2 associated cell death regulator). The serine residue is  
 CC phosphorylated in a post-translational modification and allows binding  
 CC to the 14-3-3 protein which is a signal transduction regulator.  
 CC Modulators of phosphorylated BAD, which act through inhibition/activation  
 CC of a phosphoserine phosphatase, are useful for preventing/treating  
 CC increased/decreased apoptosis in a cell. The increased apoptosis may  
 CC result from immunodeficiency diseases, senescence, neurodegenerative  
 CC disease, ischaemic cell death, reperfusion cell death, infertility and  
 CC wound-healing. Decreased apoptosis may result from cancer, viral  
 CC infection, lymphoproliferative conditions, arthritis, infertility,  
 CC inflammation and autoimmune diseases. Measuring the amount of  
 CC phosphorylated compared to unphosphorylated BAD polypeptide and/or total  
 CC BAD in a cell is useful for determining the apoptotic state of a cell.  
 XX Sequence 204 AA;  
 SQ

Query Match 71.5%; Score 645; DB 19; Length 204;  
 Best Local Similarity 75.0%; Pred. No. 3.8e-60;  
 Matches 126; Conservative 12; Mismatches 24; Indels 6; Gaps 3;

QY 1 MFQIPFEPSEQEDSSAERGLGPGAGDGPSCGKHHRQAPGLLWDASHQEQPTSSSH 60  
 |||||:|||||:|||||:| | | : ||||| ||| : :||  
 Db 43 mfiqipefseqedasatdrglpsitedqp---gpy--lapglgslnhqggraatsnsh 97

QY 61 HGGAGAVEIRSRHSSYPAGTDEDEGMEEPSFGRSRSAPPNLMWAQRYGRELRRMXDE 120  
 |||||:|||||:|||||:|||||:| | | : ||||| ||| : :||  
 Db 98 hggagamestrsrhssypagteedegmeelspfgrsrsappnlwaaqrygreilrmsde 157

QY 121 FVDSFKKGLPRPKSAGTATQMRQSSWTRVFQSWDNLGRGSSAPSQ 168  
 | || |||||:|||||: |||: |||||: |||  
 Db 158 fegsf-kglprksagtatqmrqsagwtrliqswdnlrgkgstpsq 204

RESULT 10  
 AAB70369  
 ID AAB70369 standard; protein; 204 AA.  
 XX  
 AC AAB70369;  
 XX  
 XX 02-MAY-2001 (first entry)  
 DT Longer murine BAD mutant amino acid sequence SEQ ID NO:2.  
 XX  
 DE Bcl-XL/Bcl-2 associated cell death regulator; BAD; mutant; apoptosis;  
 KW immunostimulant; neuroprotective; nontropic; antiischaemic; vulnary;  
 KW cytostatic; antiviral; antiarthritic; antiinflammatory; wound healing;

KW immunosuppressive; apoptosis inducer; apoptosis inhibitor; cancer;  
 KW immunodeficiency disease; neurodegenerative disease; viral infection;  
 KW ischaemic cell death; reperfusion cell death; arthritis; infertility;  
 XX lymphoproliferative condition; inflammation; autoimmune disease.  
 OS Mus musculus.  
 OS Synthetic.  
 XX WO200110888-A1.  
 PN 15-FEB-2001.  
 PD 30-MAY-2000; 2000WO-US11864.  
 XX 28-MAY-1999; 99US-0136783.  
 XX (APOP-) APOPTOSIS TECHNOLOGY INC.  
 PA Zhou X;  
 PI WPI; 2001-138734/14.  
 DR New mutant Bcl-XL/Bcl-2 Associated Cell Death Regulator polypeptide,  
 XX useful for screening for candidate compounds which induce or inhibit  
 PT apoptosis, comprises amino acid substitutions at Ser118, Ser155 or  
 PT Ser113 -  
 PT Claim 4; Page 148; 157pp; English.  
 PS The present invention describes an isolated or synthetic polypeptide  
 XX (I) comprising a less than full length amino acid sequence of a mutant  
 CC Bcl-XL/Bcl-2 associated cell death regulator polypeptide (BAD) or its  
 CC fragment, which contains amino acid substitutions at Ser118 of a human  
 CC BAD, Ser155 of a murine BAD (longer murine BAD) or Ser113 of a murine  
 CC BAD (shorter murine BAD). (I) has immunostimulant, neuroprotective,  
 CC nontoxic, antiischaemic, vulnary, cytostatic, antiviral,  
 CC antiarthritic, antiinflammatory and immunosuppressive activities, and  
 CC can be used as an apoptosis inducer or inhibitor. BAD polypeptides and  
 CC polynucleotides can be used for screening candidate compounds and drugs  
 CC for activity that promote cell survival or apoptosis. Other uses include  
 CC inducing or inhibiting apoptosis in a cell. Candidate compounds  
 CC identified and (mutant) BAD polypeptides are useful in treating  
 CC immunodeficiency diseases, neurodegenerative diseases, ischaemic cell  
 CC death, reperfusion cell death, wound healing, cancer, viral infections,  
 CC lymphoproliferative conditions, arthritis, infertility, inflammation and  
 CC autoimmune diseases. The present sequence represents a specifically  
 CC claimed longer murine BAD mutant amino acid sequence from the present  
 CC invention.  
 XX Sequence 204 AA;  
 SQ

Query Match 71.5%; Score 645; DB 22; Length 204;  
 Best Local Similarity 75.0%; Pred. No. 3.8e-60;  
 Matches 126; Conservative 12; Mismatches 24; Indels 6; Gaps 3;

QY 1 MFOIPEFEPSEQEDSSAERGLGPGAGDGPSCGKHHRQAPGLLWDASHQEQPTSSSH 60  
 |||||:|||||:|||||:| | | : ||||| ||| : :||  
 Db 43 mfiqipefseqedasatdrglpsitedqp---gpy--lapglgslnhqggraatsnsh 97

QY 61 HGGAGAVEIRSRHSSYPAGTDEDEGMEEPSFGRSRSAPPNLMWAQRYGRELRRMXDE 120  
 |||||:|||||:|||||:|||||:| | | : ||||| ||| : :||  
 Db 98 hggagamestrsrhssypagteedegmeelspfgrsrsappnlwaaqrygreilrmsde 157

QY 121 FVDSFKKGLPRPKSAGTATQMRQSSWTRVFQSWDNLGRGSSAPSQ 168  
 | || |||||:|||||: |||: |||||: |||  
 Db 158 fegsf-kglprksagtatqmrqsagwtrliqswdnlrgkgstpsq 204

RESULT 11  
 AAW61317  
 ID AAW61317 standard; Protein; 204 AA.  
 XX

AC AAW61317;  
DT 07-OCT-1998 (first entry)  
DE Mutant BCL-XL/BCL-2 associated cell death regulator #2.  
XX Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein;  
KW serine substituted mutant; apoptosis; cancer; viral infection.  
XX Mus sp.  
OS Synthetic.  
XX WO9817682-A1.  
FN 30-APR-1998. 97WO-US19175.  
PD 17-OCT-1997; 97WO-US19175.  
XX 18-OCT-1996; 96US-0733505.  
PR (UNIW ) UNIV WASHINGTON.  
XX Korsmeyer SJ;  
XX WPI; 1998-261422/23.  
DR N-PSDB; AAV27835.  
XX New mutant BAD polypeptide with phosphorylatable serine replaced -  
PT useful for, e.g. treating reduced apoptosis such as in cancer or  
PT viral infection  
XX Claim 7; Page 60; 95pp; English.  
XX The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell  
CC death regulator) proteins, having an amino acid other than Ser at  
CC position 112 and/or 136, relative to the murine BAD 204 aa sequence. The  
CC present sequence represents a mutant BAD protein. Also described are: (1)  
CC fragments of mutant BAD protein able to decrease cell viability; (2)  
CC fusion proteins of mutant BAD with a heterologous polypeptide that  
CC increases intracellular delivery. Mutant BAD proteins are used to treat  
CC or prevent diseases associated with reduced apoptosis, e.g. cancer,  
CC viral infection, lymphoproliferation, arthritis, infertility,  
CC inflammation and autoimmune disease. Polynucleotide sequences encoding  
CC mutant BAD proteins can be used similarly by gene therapy or to produce  
CC transgenic animals for use as disease models or in drug screening. BAD  
CC proteins phosphorylated at specified Ser are used to screen for enhancers  
CC and inhibitors of serine-phosphatase. Inhibitors are potentially useful  
CC in treatment of excessive apoptosis such as AIDS, neurodegeneration,  
CC aging or ischaemic cell death. The apoptotic status of cells is  
CC determined by measuring relative amounts of phosphorylated and non-  
CC phosphorylated BAD, by usual immunoassays. Mutant BAD proteins have  
CC greater death-promoting activity than wild-type BAD which can become  
CC phosphorylated on the specified Ser, forming a product that does not  
CC heterodimerise with BCL-2 or BCL-XL but instead binds to 14-3-3 family  
CC proteins in the cytosol, thus promoting cell survival. The mutants with  
CC Ser substituted cannot bind 14-3-3.  
XX Sequence 204 AA;  
SQ  
Query Match 71.2%; Score 642; DB 19; Length 204;  
Best Local Similarity 74.4%; Pred. No. 7.9e-60;  
Matches 125; Conservative 13; Mismatches 24; Indels 6; Gaps 3;  
Qy 1 MFQIPEFPSEQEDSSAERGLGSPAGDGPSSGKGKHHRRQAPGLLWDASHHQEQPTSSSH 60  
DB 43 mfiqipepseqedasatdrglgspltdqp---gpy--lapglglnhbggraatnsh 97  
Qy 61 HGGAGAVIRSRHSSYPAGTDEGMEGPEPFRGSRSPAPNLWAAORYGRELRMXDE 120  
DB 98 hggagavetrshssypagtdeegmeelspfgrsraapnlwaaqrgygrelrmsde 157  
Qy 121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWMDRNLGRGSSAPSQ 168

DB 158 fegsf-kglprpksagtatmrqsagwtriiqswwdrnlkggstpsq 204  
RESULT 12  
AAW61316  
ID AAW61316 standard; Protein; 204 AA.  
XX AAW61316;  
XX 07-OCT-1998 (first entry)  
XX Mutant BCL-XL/BCL-2 associated cell death regulator #1.  
XX Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein;  
KW serine substituted mutant; apoptosis; cancer; viral infection.  
XX Mus sp.  
OS Synthetic.  
XX WO9817682-A1.  
XX 30-APR-1998.  
XX 17-OCT-1997; 97WO-US19175.  
XX 18-OCT-1996; 96US-0733505.  
XX (UNIW ) UNIV WASHINGTON.  
XX Korsmeyer SJ;  
XX WPI; 1998-261422/23.  
XX N-PSDB; AAV27834.  
XX New mutant BAD polypeptide with phosphorylatable serine replaced -  
PT useful for, e.g. treating reduced apoptosis such as in cancer or  
PT viral infection  
XX Claim 7; Page 59; 95pp; English.  
XX The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell  
CC death regulator) proteins, having an amino acid other than Ser at  
CC position 112 and/or 136, relative to the murine BAD 204 aa sequence. The  
CC present sequence represents a mutant BAD protein. Also described are: (1)  
CC fragments of mutant BAD protein able to decrease cell viability; (2)  
CC fusion proteins of mutant BAD with a heterologous polypeptide that  
CC increases intracellular delivery. Mutant BAD proteins are used to treat  
CC or prevent diseases associated with reduced apoptosis, e.g. cancer,  
CC viral infection, lymphoproliferation, arthritis, infertility,  
CC inflammation and autoimmune disease. Polynucleotide sequences encoding  
CC mutant BAD proteins can be used similarly by gene therapy or to produce  
CC transgenic animals for use as disease models or in drug screening. BAD  
CC proteins phosphorylated at specified Ser are used to screen for enhancers  
CC and inhibitors of serine-phosphatase. Inhibitors are potentially useful  
CC in treatment of excessive apoptosis such as AIDS, neurodegeneration,  
CC aging or ischaemic cell death. The apoptotic status of cells is  
CC determined by measuring relative amounts of phosphorylated and non-  
CC phosphorylated BAD, by usual immunoassays. Mutant BAD proteins have  
CC greater death-promoting activity than wild-type BAD which can become  
CC phosphorylated on the specified Ser, forming a product that does not  
CC heterodimerise with BCL-2 or BCL-XL but instead binds to 14-3-3 family  
CC proteins in the cytosol, thus promoting cell survival. The mutants with  
CC Ser substituted cannot bind 14-3-3.  
XX Sequence 204 AA;  
SQ  
Query Match 70.8%; Score 639; DB 19; Length 204;  
Best Local Similarity 73.8%; Pred. No. 1.6e-59;  
Matches 124; Conservative 14; Mismatches 24; Indels 6; Gaps 3;  
Qy 1 MFQIPEFPSEQEDSSAERGLGSPAGDGPSSGKGKHHRRQAPGLLWDASHHQEQPTSSSH 60

Db 43 mfgipefepsegedasatdrglgsitedqp---gpy--lapglgnsnhqggraatsnsh 97  
QY 61 HGGAGAVEIRSRHSSYPAGTDEDEGMEEPSPPRGSRSAAPPNLWAAQRYGRELRRMXDE 120  
Db 98 hggagamestrhsaypagteedegmeelspfgrsraappnlwaaqrygrelrrmsde 157  
QY 121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWMDRNLGRGSSAPSQ 168  
Db 158 fegsf-kglprksagtatqmrqsagwttriigswdwnlrgkgsstpsq 204

RESULT 13  
AAW61318  
ID AAW61318 standard; Protein; 204 AA.  
AC AAW61318;  
XX  
XX 07-OCT-1998 (first entry)  
DT  
XX Mutant BCL-XL/BCL-2 associated cell death regulator #3.  
DE  
XX Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein;  
KW serine substituted mutant; apoptosis; cancer; viral infection.  
XX  
OS Mus sp.  
XX Synthetic.  
XX WO9817682-Al.  
PN  
XX  
XX 30-APR-1998.  
PD  
XX  
XX 17-OCT-1997; 97WO-US19175.  
PF  
XX  
XX 18-OCT-1996; 96US-0733505.  
PR  
XX  
XX (UNIW ) UNIV WASHINGTON.  
PA  
XX  
XX Korsmeyer SJ;  
PI  
XX  
XX WPI; 1998-261422/23.  
DR  
XX N-PSDB; AAV27836.  
DR  
XX  
XX New mutant BAD polypeptide with phosphorylatable serine replaced -  
PT useful for, e.g. treating reduced apoptosis such as in cancer or  
PT viral infection  
XX  
XX Claim 7; Page 60-61; 95pp; English.  
PS  
XX  
XX The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell  
CC death regulator) proteins, having an amino acid other than Ser at  
CC position 112 and/or 136, relative to the murine BAD 204 aa sequence. The  
CC present sequence represents a mutant BAD protein. Also described are: (1)  
CC fragments of mutant BAD protein able to decrease cell viability; (2)  
CC fusion proteins of mutant BAD with a heterologous polypeptide that  
CC increases intracellular delivery. Mutant BAD proteins are used to treat  
CC or prevent diseases associated with reduced apoptosis, e.g. cancer,  
CC viral infection, lymphoproliferation, arthritis, infertility,  
CC inflammation and autoimmune disease. Polynucleotide sequences encoding  
CC mutant BAD proteins can be used similarly by gene therapy or to produce  
CC transgenic animals for use as disease models or in drug screening. BAD  
CC proteins phosphorylated at specified Ser are used to screen for enhancers  
CC and inhibitors of serine-phosphatase. Inhibitors are potentially useful  
CC in treatment of excessive apoptosis such as AIDS, neurodegeneration,  
CC aging or ischaemic cell death. The apoptotic status of cells is  
CC determined by measuring relative amounts of phosphorylated and non-  
CC phosphorylated BAD, by usual immunoassays. Mutant BAD proteins have  
CC greater death-promoting activity than wild-type BAD which can become  
CC phosphorylated on the specified Ser, forming a product that does not  
CC heterodimerise with BCL-2 or BCL-XL but instead binds to 14-3-3 family  
CC proteins in the cytosol, thus promoting cell survival. The mutants with  
CC Ser substituted cannot bind 14-3-3.  
XX

SQ Sequence 204 AA;  
Query Match 70.8%; Score 639; DB 19; Length 204;  
Best Local Similarity 73.8%; Pred. No. 1.6e-59;  
Matches 124; Conservative 14; Mismatches 24; Indels 6; Gaps 3;  
QY 1 MFOIPEFEPSEQEDSSAERGLGSPAGDPSGSGKHHRQAPGLLMDASHQEQPPTSSSH 60  
Db 43 mfgipefepsegedasatdrglgsitedqp---gpy--lapglgnsnhqggraatsnsh 97  
QY 61 HGGAGAVEIRSRHSSYPAGTDEDEGMEEPSPPRGSRSAAPPNLWAAQRYGRELRRMXDE 120  
Db 98 hggagamestrhsaypagteedegmeelspfgrsraappnlwaaqrygrelrrmsde 157  
QY 121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWMDRNLGRGSSAPSQ 168  
Db 158 fegsf-kglprksagtatqmrqsagwttriigswdwnlrgkgsstpsq 204

RESULT 14  
AAW61319  
ID AAW61319 standard; Protein; 59 AA.  
XX  
AC AAW61319;  
XX  
XX 07-OCT-1998 (first entry)  
DT  
XX  
XX Mutant BCL-XL/BCL-2 associated cell death regulator #4.  
DE  
XX  
XX Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein;  
KW serine substituted mutant; apoptosis; cancer; viral infection.  
XX  
XX Mus sp.  
OS Synthetic.  
XX  
XX WO9817682-Al.  
PN  
XX  
XX 30-APR-1998.  
PD  
XX  
XX 17-OCT-1997; 97WO-US19175.  
PF  
XX  
XX 18-OCT-1996; 96US-0733505.  
PR  
XX  
XX (UNIW ) UNIV WASHINGTON.  
PA  
XX  
XX Korsmeyer SJ;  
PI  
XX  
XX WPI; 1998-261422/23.  
DR  
XX N-PSDB; AAV27837.  
DR  
XX  
XX New mutant BAD polypeptide with phosphorylatable serine replaced -  
PT useful for, e.g. treating reduced apoptosis such as in cancer or  
PT viral infection  
XX  
XX Claim 8; Page 73; 95pp; English.  
PS  
XX  
XX The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell  
CC death regulator) proteins, having an amino acid other than Ser at  
CC position 112 and/or 136, relative to the murine BAD 204 aa sequence. The  
CC present sequence represents a mutant BAD protein. Also described are: (1)  
CC fragments of mutant BAD protein able to decrease cell viability; (2)  
CC fusion proteins of mutant BAD with a heterologous polypeptide that  
CC increases intracellular delivery. Mutant BAD proteins are used to treat  
CC or prevent diseases associated with reduced apoptosis, e.g. cancer,  
CC viral infection, lymphoproliferation, arthritis, infertility,  
CC inflammation and autoimmune disease. Polynucleotide sequences encoding  
CC mutant BAD proteins can be used similarly by gene therapy or to produce  
CC transgenic animals for use as disease models or in drug screening. BAD  
CC proteins phosphorylated at specified Ser are used to screen for enhancers  
CC and inhibitors of serine-phosphatase. Inhibitors are potentially useful  
CC in treatment of excessive apoptosis such as AIDS, neurodegeneration,  
CC aging or ischaemic cell death. The apoptotic status of cells is









QY 61 HGCAGAVEIRSRHSSYPAGTDEDEGMGEPPFRGRSRAPPNLMWAAQRYGRELRRMXDE 120  
|||||  
Db 61 HGCAGAVEIRSRHSSYPAGTDEDEGMGEPPFRGRSRAPPNLMWAAQRYGRELRRMSDE 120  
QY 121 FVDSFKKGLPRPKSAGTATQMROSSSWTRVFQSWWDRNLGRGSSAPSQ 168  
|||||  
Db 121 FVDSFKKGLPRPKSAGTATQMROSSSWTRVFQSWWDRNLGRGSSAPSQ 168

RESULT 2  
US-08-985-335-1  
; Sequence 1, Application US/08985335  
; Patent No. 6080847  
; GENERAL INFORMATION:  
; APPLICANT: Hillman, Jennifer L.  
; APPLICANT: Yue, Henry  
; APPLICANT: Lal, Preeti  
; APPLICANT: Shah, Purvi  
; APPLICANT: Corley, Neil C.  
; TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL  
; TITLE OF INVENTION: PROLIFERATION  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Dr.  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/985,335  
; FILING DATE: Filed Herewith  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Billings, Lucy J.  
; REGISTRATION NUMBER: 36,749  
; REFERENCE/DOCKET NUMBER: PF-0421 US  
; TELEPHONE: 650-855-0555  
; TELEFAX: 650-845-4166  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 168 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: SYNORAB01  
; CLONE: 358673  
US-08-985-335-1

Query Match 99.9%; Score 901; DB 3; Length 168;  
Best Local Similarity 99.4%; Pred. No. 3.7e-86;  
Matches 167; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MFOIPEFEPSEQEDSSAERGLGSPAGDGPSCGKHHRQAPGLLDASHHQOQPTSSSH 60  
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Db 1 MFOIPEFEPSEQEDSSAERGLGSPAGDGPSCGKHHRQAPGLLDASHHQOQPTSSSH 60  
QY 61 HGCAGAVEIRSRHSSYPAGTDEDEGMGEPPFRGRSRAPPNLMWAAQRYGRELRRMXDE 120  
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Db 61 HGCAGAVEIRSRHSSYPAGTDEDEGMGEPPFRGRSRAPPNLMWAAQRYGRELRRMSDE 120  
QY 121 FVDSFKKGLPRPKSAGTATQMROSSSWTRVFQSWWDRNLGRGSSAPSQ 168  
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Db 121 FVDSFKKGLPRPKSAGTATQMROSSSWTRVFQSWWDRNLGRGSSAPSQ 168

RESULT 3  
US-08-665-617-2  
; Sequence 2, Application US/08665617  
; Patent No. 5663316  
; GENERAL INFORMATION:  
; APPLICANT: Xudong, Yin  
; TITLE OF INVENTION: Gene and Protein for Regulation of Cell Death  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Saliwanchik & Saliwanchik  
; STREET: 2421 N.W. 41st Street, Suite A-1  
; CITY: Gainesville  
; STATE: Florida  
; COUNTRY: USA  
; ZIP: 32606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC Compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/665,617  
; FILING DATE:  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Saliwanchik, David R.  
; REGISTRATION NUMBER: 31,794  
; REFERENCE/DOCKET NUMBER: CL-8  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (352) 375-8100  
; TELEFAX: (352) 372-5800  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 166 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-665-617-2

Query Match 82.8%; Score 747; DB 1; Length 166;  
Best Local Similarity 83.4%; Pred. No. 3.3e-70;  
Matches 146; Conservative 3; Mismatches 10; Indels 16; Gaps 3;

QY 1 MFOIPEFEPSEQEDSSAERGLGSPAGDGPSCGKHHRQAPG-----LLWDASHQOE 53  
|||||  
Db 1 MFOIPEFEPSEQEDSSAERG-WRSPAGTGP-----QAPASIIARQVLDASHQOE 51  
QY 54 OPTSSSHHGGAGAVEIRSRHSSYPAGTDEDEGMGEPPFRGRSRAPPNLMWAAQRYGRE 113  
|||||  
Db 52 OPTSSSHHGGAGAVEIRSRHSSYPAGTDEDEGMGEPPFRGARARPPNLMWAAQRYGRE 111  
QY 114 LRRMXDEFVDSFKKGLPRPKSAGTATQMROSSSWTRVFQSWWDRNLGRGSSAPSQ 168  
|||||  
Db 112 LRRMXDEFVDSFKKGLPRPKSAGTATQMROSSSWTRVFQSWWDRNLGRGTAAPSQ 166

RESULT 4  
US-08-985-335-7  
; Sequence 7, Application US/08985335  
; Patent No. 6080847  
; GENERAL INFORMATION:  
; APPLICANT: Hillman, Jennifer L.  
; APPLICANT: Yue, Henry  
; APPLICANT: Lal, Preeti  
; APPLICANT: Shah, Purvi  
; APPLICANT: Corley, Neil C.  
; TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL  
; TITLE OF INVENTION: PROLIFERATION



;/ FILING DATE: 31-OCT-1994  
;/ ATTORNEY/AGENT INFORMATION:  
;/ NAME: Smith, William M  
;/ REGISTRATION NUMBER: 30,223  
;/ REFERENCE/DOCKET NUMBER: 15726A-000700  
;/ TELECOMMUNICATION INFORMATION:  
;/ TELEPHONE: (415) 326-2400  
;/ TELEFAX: (415) 326-2422  
;/ INFORMATION FOR SEQ ID NO: 2:  
;/ SEQUENCE CHARACTERISTICS:  
;/ LENGTH: 204 amino acids  
;/ TYPE: amino acid  
;/ STRANDEDNESS: single  
;/ TOPOLOGY: linear  
;/ MOLECULE TYPE: protein  
;/ FEATURE:  
;/ NAME/KEY: Protein  
;/ LOCATION: 1..204  
;/ OTHER INFORMATION: /note= "Deduced amino acid sequence  
;/ OTHER INFORMATION: of mouse BAD."  
US-08-661-479-2

Query Match 71.5%; Score 645; DB 2; Length 204;  
Best Local Similarity 75.0%; Pred. No. 1.6e-59;  
Matches 126; Conservative 12; Mismatches 24; Indels 6; Gaps 3;

QY 1 MFOIPEFSEQEDSSAERGLGSPAGDGPSCGSKHHRQAPGLLWDASHQOQPTSSSH 60  
Db 43 MFOIPEFSEQEDASATDRGLGSLTEQD---GPY--LAPGLLGSNHQOQRAATNSH 97  
QY 61 HGGAGAVEIRSRHSSYPAGTDEDDGMEGPEPSPRGRSRAPPNLWAAQRYGRELRRMXDE 120  
Db 98 HGGAGAMETRSRHSYPAGTDEDDGMEELSPRGRSRAPPNLWAAQRYGRELRRMSDE 157  
QY 121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWMDRNLGRGSSAPSQ 168  
Db 158 FEGSF-KGLPRPKSAGTATQMRQSGWTRIIQSWMDRNLGKGSTPSQ 204

RESULT 7  
US-08-733-505A-1  
;/ Sequence 1, Application US/08733505A  
;/ Patent No. 5856445  
;/ GENERAL INFORMATION:  
;/ APPLICANT: KORSMEYER, STANLEY J.  
;/ TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF  
;/ TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR  
;/ NUMBER OF SEQUENCES: 60  
;/ CORRESPONDENCE ADDRESS:  
;/ ADDRESSEE: HOWELL & HAERKAMP, L.C.  
;/ STREET: 7733 FORSYTH BLVD., SUITE 1400  
;/ CITY: ST. LOUIS  
;/ STATE: MISSOURI  
;/ COUNTRY: USA  
;/ ZIP: 63105  
;/ COMPUTER READABLE FORM:  
;/ MEDIUM TYPE: Floppy disk  
;/ COMPUTER: IBM PC compatible  
;/ OPERATING SYSTEM: PC-DOS/MS-DOS  
;/ SOFTWARE: Patent in Release #1.0, Version #1.30  
;/ CURRENT APPLICATION NUMBER: US/08/733,505A  
;/ FILING DATE:  
;/ CLASSIFICATION: 530  
;/ ATTORNEY/AGENT INFORMATION:  
;/ NAME: HOLLAND, DONALD R.  
;/ REGISTRATION NUMBER: 35,197  
;/ REFERENCE/DOCKET NUMBER: 965458  
;/ TELECOMMUNICATION INFORMATION:  
;/ TELEPHONE: (314) 727-5188  
;/ TELEFAX: (314) 727-6092  
;/ INFORMATION FOR SEQ ID NO: 1:  
;/

;/ SEQUENCE CHARACTERISTICS:  
;/ LENGTH: 204 amino acids  
;/ TYPE: amino acid  
;/ STRANDEDNESS:  
;/ TOPOLOGY: linear  
;/ MOLECULE TYPE: protein  
US-08-733-505A-1

Query Match 71.5%; Score 645; DB 2; Length 204;  
Best Local Similarity 75.0%; Pred. No. 1.6e-59;  
Matches 126; Conservative 12; Mismatches 24; Indels 6; Gaps 3;

QY 1 MFOIPEFSEQEDSSAERGLGSPAGDGPSCGSKHHRQAPGLLWDASHQOQPTSSSH 60  
Db 43 MFOIPEFSEQEDASATDRGLGSLTEQD---GPY--LAPGLLGSNHQOQRAATNSH 97  
QY 61 HGGAGAVEIRSRHSSYPAGTDEDDGMEGPEPSPRGRSRAPPNLWAAQRYGRELRRMXDE 120  
Db 98 HGGAGAMETRSRHSYPAGTDEDDGMEELSPRGRSRAPPNLWAAQRYGRELRRMSDE 157  
QY 121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWMDRNLGRGSSAPSQ 168  
Db 158 FEGSF-KGLPRPKSAGTATQMRQSGWTRIIQSWMDRNLGKGSTPSQ 204

RESULT 8  
US-08-717-123-3  
;/ Sequence 3, Application US/08717123  
;/ Patent No. 5965703  
;/ GENERAL INFORMATION:  
;/ APPLICANT: Horne, William A.  
;/ APPLICANT: Oltersdorf, Tilman  
;/ TITLE OF INVENTION: Human BAD Polypeptides, Encoding Nucleic  
;/ TITLE OF INVENTION: Acids and Methods of Use  
;/ NUMBER OF SEQUENCES: 15  
;/ CORRESPONDENCE ADDRESS:  
;/ ADDRESSEE: Campbell and Flores  
;/ STREET: 4370 La Jolla Village Drive, Suite 700  
;/ CITY: San Diego  
;/ STATE: California  
;/ COUNTRY: United States  
;/ ZIP: 92122  
;/ COMPUTER READABLE FORM:  
;/ MEDIUM TYPE: Floppy disk  
;/ COMPUTER: IBM PC compatible  
;/ OPERATING SYSTEM: PC-DOS/MS-DOS  
;/ SOFTWARE: Patent in Release #1.0, Version #1.25  
;/ CURRENT APPLICATION NUMBER: US/08/717,123  
;/ FILING DATE: 20-SEP-1996  
;/ CLASSIFICATION: 435  
;/ ATTORNEY/AGENT INFORMATION:  
;/ NAME: Campbell, Cathryn A.  
;/ REGISTRATION NUMBER: 31,815  
;/ REFERENCE/DOCKET NUMBER: P-ID 1929  
;/ TELECOMMUNICATION INFORMATION:  
;/ TELEPHONE: (619) 535-9001  
;/ TELEFAX: (619) 535-8949  
;/ INFORMATION FOR SEQ ID NO: 3:  
;/ SEQUENCE CHARACTERISTICS:  
;/ LENGTH: 204 amino acids  
;/ TYPE: amino acid  
;/ TOPOLOGY: linear  
US-08-717-123-3

Query Match 71.5%; Score 645; DB 2; Length 204;  
Best Local Similarity 75.0%; Pred. No. 1.6e-59;  
Matches 126; Conservative 12; Mismatches 24; Indels 6; Gaps 3;

QY 1 MFOIPEFSEQEDSSAERGLGSPAGDGPSCGSKHHRQAPGLLWDASHQOQPTSSSH 60  
Db 43 MFOIPEFSEQEDASATDRGLGSLTEQD---GPY--LAPGLLGSNHQOQRAATNSH 97

Db	43	MFQIPEEPEEQEDASNTDRGLPSLTEDP---GPY--LAPCLGSLNHQOGRAATNSH	97
QY	61	HGAGAVEISRHSSTPAGTTEDEGMCGEPPSPRGRSRSPAPNLMAAQRYGRELRMXDE	120
Db	98	HGAGAMETSRHSSTPAGTTEDEGMEELSPRGRSRSPAPNLMAAQRYGRELRMTEDE	157
QY	121	FVDSFKKGLPRPSAGTATQMRQSSSWTRVYFQSWDNRNLGRGSSAPSQ	168
Db	158	FECSF-KGLPRPSAGTATQMRQSGAGWTRIIQSWDNRNLCKGSTGPSQ	204

RESULT 9  
US-08-733-505A-12  
: Sequence 12, Application US/08733505A  
: Patent No. 5856445  
: GENERAL INFORMATION:  
: APPLICANT: KORSMEYER, STANLEY J.  
: TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF  
: TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR

RESULT 10  
US-08-733-505A-13  
: Sequence 13, Application US/087333505A

Patent No. 5856445  
GENERAL INFORMATION:  
APPLICANT: KORSMEYER, STANLEY J.  
TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF  
BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR  
NUMBER OF SEQUENCES: 60  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: HOWELL & HAFERKAMP, L.C.  
STREET: 7733 FORSYTH BLVD., SUITE 1400  
CITY: ST. LOUIS  
STATE: MISSOURI  
COUNTRY: USA  
ZTP: 63105

```

RESULT 11
US-08-733-505A-14
; Sequence 14, Application US/08733505A
; Patent No. 5856445
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, STANLEY J.
; TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
; TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWELL & HAFERKAMP, L.C.
; STREET: 7733 FORSYTH BLVD., SUITE 1400
; CITY: ST. LOUIS
; STATE: MISSOURI
; COUNTRY: USA
; ZIP: 63105
; COMPUTER READABLE FORM:

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Query Match      34.0%;   Score 307;   DB 2;   Length 59;
Best Local Similarity 90.6%;   Pred. No. 3.5e-25;
Matches 57;   Conservative 1;   Mismatches 1;   Indels 0;   Gaps 0;

Qy 63 GAGAVEIRSRHSSYPAGTDEGMEEPSPPRGSRSSAPPNLWAAQRYGRELRRMXDEF 121
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 GAGAVEIRSRHSAYPAGTDEGMEEPSPPRGSRSSAPPNLWAAQRYGRELRRMSDEF 59

RESULT 14
US-08-733-505A-57

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RESULT 15
US-08-733-505A-58
; Sequence 58, Application US/08733505A
; Patent No. 5856445
;
GENERAL INFORMATION:
;
; APPLICANT: KORSMEYER, STANLEY J
;
; TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
; BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
;
; NUMBER OF SEQUENCES: 60
;
; CORRESPONDENCE ADDRESS:
; ADDRESSER: HOWELL & HAFERKAMP, L.C.
; STREET: 7733 FORSYTH BLVD., SUITE 1400
; CITY: ST. LOUIS
; STATE: MISSOURI
; COUNTRY: USA
; ZIP: 63105
;
COMPUTER READABLE FORM:
;
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
;
CURRENT APPLICATION DATA:
;
; APPLICATION NUMBER: US/08/733,505A
; FILING DATE:

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Search completed: October 9, 2001, 15:58:34  
Job time: 59 sec

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GenCore version 4.5  
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## OM protein - protein search, using sw model

Run on: October 9, 2001, 15:58:09 ; Search time 24.69 seconds  
(without alignments)  
518.320 Million cell updates/sec

Title: 09-580523-lb

Perfect score: 905

Sequence: 1 MFQIPEFSPSEQEDSSAER.....RVFQSWDRNLGRGSSAPSQ 168

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

## Database :

PIR\_68: \*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	646	71.4	204	2 A55671	bad protein - mous
2	94.5	10.4	1729	2 T18396	erythrocyte membra
3	93	10.3	1300	2 T03166	probable immediate
4	92	10.2	834	2 T42702	hypothetical prote
5	90.5	10.0	393	2 JC5614	RNB6 protein - rat
6	90	9.9	2237	2 T45115	N-type calcium cha
7	90	9.9	2248	2 A35938	profilaggrin - hum
8	90	9.9	2339	2 A42566	omega-conotoxin-se
9	89.5	9.9	336	2 T30757	hypothetical prote
10	88.5	9.8	449	1 A41520	chromogranin A pre
11	88.5	9.8	2715	2 T13049	eyelid - fruit fly
12	88	9.7	222	2 T43500	hypothetical prote
13	87	9.6	646	1 S15901	chromogranin B pre
14	87	9.6	2023	2 T13134	polycomb protein e
15	86.5	9.6	1077	2 A44057	serine-rich protei
16	86.5	9.6	1647	2 S45252	SNF2beta protein -
17	86	9.5	343	2 T05221	hypothetical prote
18	86	9.5	420	2 B38104	LFY floral meriste
19	85.5	9.4	751	2 T02858	hypothetical prote
20	85.5	9.4	1159	2 T38465	probable potassium
21	85	9.4	270	1 WJMS13	homeotic protein H
22	84.5	9.3	134	2 T54810	pHL E1F1 - human
23	84.5	9.3	1323	2 T00037	hypothetical prote
24	84.5	9.3	1392	2 T51947	probable transcrip
25	84.5	9.3	1562	2 T29146	hypothetical prote
26	84	9.3	313	2 A28444	filaggrin precurs
27	84	9.3	380	2 S51797	vasodilator-stimul
28	84	9.3	381	2 S16506	hypothetical prote
29	84	9.3	542	2 A44358	zyxin - chicken

```
RESULT 1
A55671
bad protein - mouse
C:Species: Mus musculus (house mouse)
C:Date: 03-Mar-1995 #sequence_revision 03-Mar-1995 #text_change 05-Nov-1999
C:Accession: A55671
R:Yang, E.; Zha, J.; Jockel, J.; Boise, L.H.; Thompson, C.B.; Korsmeyer, S.J.
Cell 80, 285-291, 1995
A:Title: Bad, a heterodimeric partner for Bcl-x-L and Bcl-2, displaces Bax and promotes apoptosis
A:Reference number: A55671; MUID:95136361
A:Accession: A55671
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-204 <YAN>
A:Cross-references: GB:L37296; NID:g639778; PIDN:AAA64465.1; PID:g639779
C:Keywords: heterodimer

Query Match 71.4%; Score 646; DB 2; Length 204;
Best Local Similarity 75.0%; Pred. No. 3.le-45;
Matches 126; Conservative 13; Mismatches 23; Indels 6; Gaps 3;

Oy 1 MFQIPEFSPSEQEDSSAERGLGSPAGDGSGCKHHRQAPGLLDASHQEQPTSSSH 60
Db 43 MFQIPEFSPSEQEDSSAERGLGSPAGDGSGCKHHRQAPGLLDASHQEQPTSSSH 97
Oy 61 HGGAGAVEIRSHSSYPAGTEDECGEGEPPFRGSRSPAPNLWAAQRYGRELRRMADE 120
Db 98 HGGAGAVETRSRSHSSYPAGTEDECGEGEELSFPFRGSRSPAPNLWAAQRYGRELRRMSDE 157
Oy 121 FVDSFKGLPRPKSAGTATQMRQSSWTRVFQSWDRNLGRGSSAPSQ 168
Db 158 FEGSP-KGLPRPKSAGTATQMRQSSWTRVFQSWDRNLGRGSSAPSQ 204

RESULT 2
T18396
erythrocyte membrane protein variant 2 - malaria parasite (Plasmodium falciparum) (fr
C:Species: Plasmodium falciparum
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jun-2000
C:Accession: T18396
R:Baruch, D.I.; Pasloske, B.L.; Singh, H.B.; Bi, X.; Ma, X.C.; Feldman, M.; Taraschi,
Cell 82, 77-87, 1995
A:Title: Cloning the P. falciparum gene encoding PfEMP1, a malarial variant antigen a
A:Reference number: T18396; MUID:95330812
A:Accession: T18396
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1729 <BAR>
A:Cross-references: EMBL:U27339; NID:g914920; PID:g914921; PIDN:AAA89134.1
C:Genetics:
A:Gene: EMP1
```

## ALIGNMENTS

A;Note: var-2

Query Match 10.4%; Score 94.5; DB 2; Length 1729;  
Best Local Similarity 21.6%; Pred. No. 8.3;  
Matches 42; Conservative 23; Mismatches 66; Indels 63; Gaps 8;

QY 9 PSQEDSSAERGLGSP--AGDGPSCGSKHHRQAPGLL-----WDASHQEQPTSSSHH 61  
DB 926 PSQEDSSAERGLGSP--AGDGPSCGSKHHRQAPGLL-----WDASHQEQPTSSSHH 982

QY 62 GGAGVEIKRHSYPAGTDEDEGMGEESPFRGRSRAPPNLWAAQRY----- 110  
DB 983 AGATGLQL-----SDPDQQLKRGNIPLDFRQMFYTLGDYRDICI 1031

QY 111 -----GRELRRMADEFVDSFKKGLPRPKSAGTATOMROSSWTRVF--- 151  
DB 1032 GGDROIVGDTIVITGEGSTKKISKIIEGFLK-----KQTVTSPSPRDTSSRTVPHPQT 1086

QY 152 -----QSWDRN 158  
DB 1087 SVEKTPQTWWEAN 1100

RESULT 3  
T03166  
probable immediate early protein - alcelaphine herpesvirus 1  
C:Species: alcelaphine herpesvirus 1  
C:Date: 24-Mar-1999 #sequence\_revision 24-Mar-1999 #text\_change 24-Nov-1999  
C:Accession: T03166  
R:Enser, A.; Pfanz, R.; Fleckenstein, B.  
J. Virol. 71, 6517-6525, 1997  
A:Title: Primary structure of the alcelaphine herpesvirus 1 genome.  
A:Reference number: 214840; MUID:97404659  
A:Accession: T03166  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-1300 <ENS>  
A:Cross-references: EMBL:AF005370; NID:g2337967; PIDN:AAC58118.1; PID:g2338034  
C:Superfamily: collagen alpha 2(I) chain; fibrillar collagen carboxyl-terminal homology

Query Match 10.3%; Score 93; DB 2; Length 1300;  
Best Local Similarity 29.0%; Pred. No. 8;  
Matches 31; Conservative 6; Mismatches 56; Indels 14; Gaps 3;

QY 5 PEPESEQEDSSAERGLG-SPAGDGPSCGSKHHRQAPGLLWDASHQEQPTSSSHHG 63  
DB 466 PEGEPERPEGPEGPEGPEGPEGPEGPEGPEGPEGPEGPEGPEGPEGPEG 521

QY 64 AGAVEIRSRHSYPAGTDEDEGMGE-----PSPRGRSRAP 101  
DB 522 EGPEGLEGPEGPEGPEGPEGPEGPEGPEGPEGPEGPEGPEGPEGPEG 568

RESULT 4  
T42702  
hypothetical protein DKFZp434F117.1 - human (fragment)  
N:Alternate names: hypothetical protein DKFZp434B239.1  
C:Species: Homo sapiens (man)  
C:Date: 11-Jan-2000 #sequence\_revision 11-Jan-2000 #text\_change 02-Jun-2000  
C:Accession: T42702; T46502  
R:Koehler, K.; Beyer, A.; Meves, H.W.; Gassenhuber, J.; Wiemann, S.  
submitted to the Protein Sequence Database, November 1999  
A:Reference number: 222234  
A:Accession: T42702  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-834 <AAA>  
A:Cross-references: EMBL:AL133028  
A:Experimental source: adult testis; clone DKFZp434F117  
R:Poustka, A.; Klein, M.; Meves, H.W.; Gassenhuber, J.; Wiemann, S.  
submitted to the Protein Sequence Database, January 2000

A:Reference number: 223029  
A:Accession: T46502  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 213-834 <AA2>  
A:Cross-references: EMBL:AL137336  
A:Experimental source: adult testis; clone DKFZp434B239  
C:Genetics:  
A:Note: DKFZp434F117.1; DKFZp434B239.1

Query Match 10.2%; Score 92; DB 2; Length 834;  
Best Local Similarity 27.1%; Pred. No. 6;  
Matches 49; Conservative 18; Mismatches 50; Indels 64; Gaps 11;

QY 13 EDSSAERGLGSP--AGDGPSCGSKHHRQAPGLLWDASHQEQPTSSSHHGAGAVEI 69  
DB 226 EKKHAEAPAGPPRPGDARAGSK-----AKPQESPSSAS--ALAEMASI 272

QY 70 RSR-----HSSYPAGTDEDE-GMGEESP-----FRGRSRAPP-----NLMAAQRY--- 110  
DB 273 RSRILKNAESDPRSSERDQLRPGDESTPRGRCDSRGNQRKTPPVNAKFSIMPWQKESDG 332

QY 111 GRELRMADEFVDSFKK-----GLPRPKSAGTATOMROSSWTRVFQSWDRNLGR 161  
DB 333 GTETSKQSTE-AESIRKRPMLGPSEETAPQPPAGV-----RELK 372

QY 162 G 162  
DB 373 G 373

RESULT 5  
JC5614  
RNB6 protein - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 23-Sep-1997 #sequence\_revision 17-Oct-1997 #text\_change 05-Nov-1999  
C:Accession: JC5614  
R:Ohta, S.; Mineta, T.; Kimoto, M.; Tabuchi, K.  
Biochem. Biophys. Res. Commun. 237, 307-312, 1997  
A:Title: Differential display cloning of a novel rat cDNA (RNB6) that shows high expr  
A:Reference number: JC5614; MUID:97415794  
A:Accession: JC5614  
A:Molecule type: mRNA  
A:Residues: 1-393 <OHT>  
A:Cross-references: GB:U70211; NID:g2058461; PIDN:AAC53322.1; PID:g2058462  
A:Experimental source: brain  
C:Comment: This protein belongs to Ena/VASP family member, and is involved in the dev  
ion.

Query Match 10.0%; Score 90.5; DB 2; Length 393;  
Best Local Similarity 28.2%; Pred. No. 3.5;  
Matches 40; Conservative 16; Mismatches 45; Indels 41; Gaps 7;

QY 13 EDSSAERGLGSPAGDGPSCGSKHHRQAPGLLWDASHQEQPTSSSHHGAGAVEIRSR 72  
DB 237 EDAS-----GGSPSGTSSK-----DANR-----ASSGGGGGLMEEMNK 271

QY 73 -----HSSYPAGTDEDEGMGEESP-----SPPRG-RSRAPPNLWAAQRYGRELRMAD 119  
DB 272 LLAKRKAASQTDKPADRKEDENQEDPTSPSPGRATSPQPPNSSEAGRPWERSNSVE 331

QY 120 EFVDSFKKGLPRPKSAGTATOM 141  
DB 332 KPVSSL---LSRVKPGAGVNDV 350

RESULT 6  
T45115  
N-type calcium channel alpha-1 chain, omega-conotoxin-sensitive [imported] - human  
C:Species: Homo sapiens (man)  
C:Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 21-Jul-2000



b 150 --RYHADPNMDPYRYGQPLP--GGKPPQQQQ 176





GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: October 9, 2001, 16:03:43 ; Search time 15.11 Seconds  
(without alignments)  
380.868 Million cell updates/sec

Title: 09-580523-lb  
Perfect score: 905  
Sequence: 1 MFQIPEFPESEQEDSSAER.....RVFQSWDRNLGRGSSAPSQ 168

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	741	81.9	168	1	BAD_HUMAN
2	646	71.4	204	1	BAD_MOUSE
3	97	10.7	2505	1	CCAA_HUMAN
4	91.5	10.1	2300	1	CYAA_NEUCR
5	90	9.9	2339	1	CCAB_HUMAN
6	87.5	9.7	449	1	CNCA_BOVIN
7	87	9.6	646	1	SGI_BOVIN
8	87	9.6	962	1	ARVC_HUMAN
9	86.5	9.6	1077	1	HLES_DROME
10	86.5	9.6	1461	1	IE18_PRTIF
11	86.5	9.6	1647	1	SN24_HUMAN
12	85.5	9.4	510	1	DMPL_BOVIN
13	85.5	9.4	1159	1	HERG_HUMAN
14	85	9.4	270	1	HXA5_MOUSE
15	84.5	9.3	215	1	ST13_MOUSE
16	84	9.3	380	1	VASP_HUMAN
17	84	9.3	542	1	2YX_CHICK
18	83.5	9.2	1453	1	NKCR_MOUSE
19	83	9.2	263	1	PENK_BOVIN
20	83	9.2	270	1	HXA5_HUMAN
21	83	9.2	591	1	PAK4_HUMAN
22	82.5	9.1	558	1	ROL_HUMAN
23	82.5	9.1	1097	1	CCT_DROME
24	82.5	9.1	1191	1	NKCL_SQUAC
25	82	9.1	336	1	FILA_MOUSE
26	82	9.1	424	1	LFY_ARATH
27	82	9.1	1021	1	MANA_RHOMR
28	82	9.1	1081	1	SPS2_CRAPRL
29	82	9.1	1089	1	Y553_HUMAN
30	81.5	9.0	407	1	Z174_HUMAN
31	81.5	9.0	841	1	IE63_MCMVS
32	81	9.0	559	1	PAXI_CHICK
33	80.5	8.9	1411	1	TCOF_HUMAN

ALIGNMENTS

RESULT 1

ID	BAD_HUMAN	STANDARD;	PRT;	168 AA.
AC	Q92934;			
DT	01-NOV-1997 (Rel. 35, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DE	01-OCT-2000 (Rel. 40, Last annotation update)			
DE	BAD PROTEIN (BCL-2 BINDING COMPONENT 6).			
GN	BAD OR BBC6 OR BCL2L8.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Yin D.X., Li Z., Huang B., Chen S., Zhou H.;			
RL	Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.			
CC	-!- FUNCTION: PROMOTES CELL DEATH. SUCCESSFULLY COMPETES FOR THE BINDING TO BCL-X(L) AND BCL-2, THEREBY AFFECTING THE LEVEL HETERODIMERIZATION OF BOTH THESE PROTEINS WITH BAX. CAN REVERSE THE DEATH REPRESSOR ACTIVITY OF BCL-X(L), BUT NOT THAT OF BCL-2 (BY SIMILARITY).			
CC	-!- SUBUNIT: FORMS HETERODIMERS WITH BCL-X(L) AND BCL-2, BUT NOT WITH BAX, MCL-1, AL, OR BCL-X(S) (BY SIMILARITY).			
CC	-!- TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES.			
CC	-!- SIMILARITY: CONTAINS A BCL-2 HOMOLOG DOMAIN 1 (BH1).			
CC	-!- SIMILARITY: CONTAINS A BCL-2 HOMOLOG DOMAIN 2 (BH2).			
CC	-!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.			
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CC	EMBL; U66879; AAB36516.1; -.			
DR	MIN; 603167; -.			
KW	Apoptosis.			
FT	DOMAIN 101 121 BH1.			
FT	DOMAIN 146 163 BH2.			
SQ	SEQUENCE 168 AA; 18408 MW; BDF3D99587C222BE CRC64;			

Query Match	81.9%;	Score 741;	DB 1;	Length 168;
Best Local Similarity	84.5%;	Pred. No. 1.4e-49;		
Matches 142;	Conservative 1;	Mismatches 25;	Indels 0;	Gaps 0;
Qy	1	MFQIPEFPESEQEDSSAERGLGSPAGDPSGSGKHRRQAPGLLWDASHQEQPTSSSH 60		
Db	1	MFQIPEFPESEQEDSSAERGLGSPAGDPSGSGKHRRQAPGLLWDASHQEQPTSSSH 60		
Qy	61	HGGAGAVEIRSHSYYPAGTDEDCMGEEPPSPFRGSRSPAPNLWAAQRYGRELRLMADE 120		
Db	61	HGGRWGCGDPESPQLLPRGDGRRRDGGGAQPFGRGSRSPAPNLWAAQRYGRELRLMSDE 120		

QY 121 FVDSFKGLPRKSAGTATQMRSSSWTRVFQSWDRNLGRSSAPSQ 168  
 |||||  
 Db 121 FVDSFKGLPRKSAGTATQMRSSSWTRVFQSWDRNLGRSSAPSQ 168

## RESULT 2

BAD\_MOUSE  
 ID BAD\_MOUSE STANDARD; PRT; 204 AA.  
 AC 061337;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE BAD PROTEIN (BCL-2 BINDING COMPONENT 6).  
 GN BAD OR BBC6.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain, and Thymus;  
 RX MEDLINE=95136361; PubMed=7834748;  
 RA Yang E., Zha J., Jockel J., Boise L.H., Thompson C.B., Korsmeyer S.J.;  
 RT "Bad, a heterodimeric partner for Bcl-XL and Bcl-2, displaces Bax and  
 RT promotes cell death.";  
 RL Cell 80:285-291(1995).  
 CC -I- FUNCTION: PROMOTES CELL DEATH. SUCCESSFULLY COMPETES FOR THE  
 CC BINDING TO BCL-X(L) AND BCL-2, THEREBY AFFECTING THE LEVEL  
 CC HETERODIMERIZATION OF BOTH THESE PROTEINS WITH BAX. CAN REVERSE  
 CC THE DEATH REPRESSOR ACTIVITY OF BCL-X(L), BUT NOT THAT OF BCL-2.  
 CC -I- SUBUNIT: FORMS HETERODIMERS WITH BCL-X(L) AND BCL-2, BUT NOT WITH  
 CC BAX, MCL-1, AL, OR BCL-X(S).  
 CC -I- SIMILARITY: CONTAINS A BCL-2 HOMOLOG DOMAIN 1 (BH1).  
 CC -I- SIMILARITY: CONTAINS A BCL-2 HOMOLOG DOMAIN 2 (BH2).  
 CC -I- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.  
 -----  
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 -----  
 CC EMBL; L37296; AAA64465.1; -;  
 CC MGD; MGI:1096330; Bad.  
 KW Apoptosis. 138 158 BH1.  
 FT DOMAIN 182 199 BH2.  
 FT DOMAIN 204 AA; 22080 MW; 6C2BA910205053F7 CRC64;  
 SQ SEQUENCE 204 AA; 22080 MW; 6C2BA910205053F7 CRC64;

Query Match 71.4%; Score 646; DB 1; Length 204;

Best Local Similarity 75.0%; Pred. No. 2.4e-42;  
 Matches 126; Conservative 13; Mismatches 23; Indels 6; Gaps 3;

QY 1 MFQIPEPESEDESSAERGLGSPAGDGPFGSGKHHRQAPGLLMDASHQEQPQSSSH 60  
 |||||  
 Db 43 MFQIPEPESEDESSAERGLGSPAGDGPFGSGKHHRQAPGLLMDASHQEQPQSSSH 97  
 |||||  
 QY 61 HGGAGAVEIRSRHSSYPAGTDEGMEGEPSPFGKRSRAPPNLWAAQRYGRELRRMADE 120  
 |||||  
 Db 98 HGGAGAVETRSHSSYPAGTDEGMEGEPSPFGKRSRAPPNLWAAQRYGRELRRMSDE 157  
 |||||  
 QY 121 FVDSFKGLPRKSAGTATQMRSSSWTRVFQSWDRNLGRSSAPSQ 168  
 |||||  
 Db 158 FEGSF-KGLPRKSAGTATQMRSSAGWTRIIQSWDRNLGRSGSTPSQ 204  
 |||||

## RESULT 3

CCAA\_HUMAN STANDARD; PRT; 2505 AA.  
 ID CCAA\_HUMAN

AC 000555; Q92690; Q16290; Q99790; Q99791; Q99792; Q99793; P78510;  
 AC P78511;  
 DT 15-JUL-1999 (Rel. 38, Created)  
 DT 15-JUL-1999 (Rel. 38, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE VOLTAGE-DEPENDENT P/Q-TYPE CALCIUM CHANNEL ALPHA-1A SUBUNIT (CALCIUM  
 DE CHANNEL, L TYPE, ALPHA-1 POLYPEPTIDE ISOFORM 4) (BRAIN CALCIUM CHANNEL  
 DE I) (BI).  
 GN CACNALA OR CACNL1A4 OR CACH4 OR CACN3.  
 OS Homo sapiens (Human)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORMS BI-1-GGCAG/1A-1 AND BI-1/1A-2).  
 RC TISSUE=Neuron;  
 RX MEDLINE=99158614; PubMed=10049321;  
 RA Hans M., Urrutia A., Deal C., Brust P.F., Stauderman K., Ellis S.B.,  
 RA Harpold M.M., Johnson E.C., Williams M.E.;  
 RT "Structural elements in domain IV that influence biophysical and  
 RT pharmacological properties of human alpha1A-containing  
 RT high-voltage-activated calcium channels.";  
 RL Biophys. J. 76:1384-1400(1999).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORM BI-1(VI)), AND VARIANTS FHM.  
 RC TISSUE=Cerebellum;  
 RX MEDLINE=97053792; PubMed=8898206;  
 RA Ophoff R.A., Terwindt G.M., Vergouwe M.N., van Eijk R., Oefner P.J.,  
 RA Hoffman S.M.G., Lamerding J.E., Mohrenweiser H.W., Bulman D.E.,  
 RA Ferrari M., Haan J., Lindhout D., van Ommen G.-J.B., Hofker M.H.,  
 RA Ferrari M.D., Frants R.R.;  
 RT "Familial hemiplegic migraine and episodic ataxia type-2 are caused by  
 RT mutations in the Ca2+ channel gene CACNL1A4.";  
 RL Cell 87:543-552(1996).  
 RN [3]  
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.  
 RC TISSUE=Brain;  
 RX MEDLINE=97141920; PubMed=8988170;  
 RA Zhuchenko O., Bailey J., Bonnen P.E., Ashizawa T., Stockton D.W.,  
 RA Amos C., Dobyns W.B., Subramony S.H., Zoghbi H.Y., Lee C.C.;  
 RT "Autosomal dominant cerebellar ataxia (SCA6) associated with small  
 RT polyglutamine expansions in the alpha 1A-voltage-dependent calcium  
 RT channel.";  
 RL Nat. Genet. 15:62-69(1997).  
 RN [4]  
 RP SEQUENCE OF 1693-1807 FROM N.A.  
 RC TISSUE=Lung carcinoma;  
 RX MEDLINE=95123449; PubMed=7823133;  
 RA Barry E.L.R., Viglione M.P., Kim Y.I., Froehner S.C.;  
 RT "Expression and antibody inhibition of P-type calcium channels in  
 RT human small-cell lung carcinoma cells.";  
 RL J. Neurosci. 15:274-283(1995).  
 RN [5]  
 RP SEQUENCE OF 2038-2258 FROM N.A.  
 RC TISSUE=Frontal cortex;  
 RX MEDLINE=96102310; PubMed=8525433;  
 RA Margolis R.L., Rosschel T.S., Li S.H., Kidwai A.S., Antonarakis S.E.,  
 RA McInnis M.G., Bress C.A.;  
 RT "Characterization of cDNA clones containing CCA trinucleotide repeats  
 RT derived from human brain.";  
 RL Somat. Cell Mol. Genet. 21:279-284(1995).  
 CC -I- FUNCTION: VOLTAGE-SENSITIVE CALCIUM CHANNELS (VSCC) MEDIATE THE  
 CC ENTRY OF CALCIUM IONS INTO EXCITABLE CELLS AND ARE ALSO INVOLVED  
 CC IN A VARIETY OF CALCIUM-DEPENDENT PROCESSES, INCLUDING MUSCLE  
 CC CONTRACTION, HORMONE OR NEUROTRANSMITTER RELEASE, GENE EXPRESSION,  
 CC CELL MOTILITY, CELL DIVISION AND CELL DEATH. THE ISOFORM ALPHA-1A  
 CC GIVES RISE TO P AND/OR Q-TYPE CALCIUM CURRENTS. P/Q-TYPE CALCIUM  
 CC CHANNELS BELONG TO THE "HIGH-VOLTAGE ACTIVATED" (HVA) GROUP AND  
 CC ARE BLOCKED BY THE FUNNEL TOXIN (FTX) AND BY THE OMEGA-AGATOXIN-  
 CC IVA (OMEGA-AGA-IVA). THEY ARE HOWEVER INSENSITIVE TO  
 CC DIHYDROPYRIDINES (DHP), AND OMEGA-CONOTOXIN-GVIA (OMEGA-CTX-  
 CC GVIA).  
 CC -I- SUBUNIT: VOLTAGE-DEPENDENT CALCIUM CHANNELS ARE MULTISUBUNIT





```

RESULT 4
CYAA_NEUCR
ID CYAA_NEUCR STANDARD; PRT; 2300 AA.
AC Q01631;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE ADENYLATE CYCLASE (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (ADENYLYL
DE CYCLASE).
GN CR-1 OR NAC.
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=92000795; PubMed=16803356;
RA Kore-Eda S., Murayama T., Uno I.;
RT "Isolation and characterization of the adenylate cyclase structural
RT gene of Neurospora crassa";
RL Jpn. J. Genet. 66:317-334(1991).
CC -!- FUNCTION: PLAYS ESSENTIAL ROLES IN REGULATION OF CELLULAR
CC METABOLISM BY CATALYSING THE SYNTHESIS OF A SECOND MESSENGER,
CC CAMP.
CC -!- CATALYTIC ACTIVITY: ATP = 3',5'-CYCLIC AMP + PYROPHOSPHATE.
CC -!- SIMILARITY: BELONGS TO ADENYLYL CYCLASE CLASS-3 FAMILY.
CC -!- SIMILARITY: CONTAINS 23 LEUCINE-RICH REPEATS (LRR).
CC -!- SIMILARITY: CONTAINS A PP2C-LIKE DOMAIN.
CC -----
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CC -----
CC EMBL: D00909; BAA0755.1; -
CC InterPro: IPR001611; -
CC InterPro: IPR001932; -
CC Pfam: PF00560; LRR; 13.
CC Pfam: PF00481; PP2C; 1.
CC PROSITE: PR00019; LEUZYCHRP.
CC PROSITE: PS00125; GUANYLATE CYCLASES_2; 1.
KW Lyase; Repeat; Leucine-rich repeat; CAMP synthesis; Magnesium.
FT REPEAT 867 890
FT REPEAT 892 914
FT REPEAT 915 938
FT REPEAT 938 961
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FT REPEAT 1
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CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
 CC -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS: ALPHA-1B-1 (SHOWN HERE) AND  
 CC ALPHA-1B-2; ARE PRODUCED BY ALTERNATIVE SPLICING.  
 CC -!- TISSUE SPECIFICITY: ALPHA-1B-1 AND ALPHA-1B-2 ARE EXPRESSED IN THE  
 CC CENTRAL NERVOUS SYSTEM, BUT NOT IN SKELETAL MUSCLE OR AORTA.  
 CC -!- DOMAIN: EACH OF THE FOUR INTERNAL REPEATS CONTAINS FIVE  
 CC HYDROPHOBIC TRANSMEMBRANE SEGMENTS (S1, S2, S3, S5, S6) AND ONE  
 CC POSITIVELY CHARGED TRANSMEMBRANE SEGMENT (S4). S4 SEGMENTS  
 CC PROBABLY REPRESENT THE VOLTAGE-SENSOR AND ARE CHARACTERIZED BY A  
 CC SERIES OF POSITIVELY CHARGED AMINO ACIDS AT EVERY THIRD POSITION.  
 CC -!- PTM: PHOSPHORYLATED IN VITRO BY CAM-KINASE II, CAPK, PKC AND GPK  
 CC (BY SIMILARITY).  
 CC -!- SIMILARITY: BELONGS TO THE CALCIUM CHANNEL ALPHA-1 SUBUNITS  
 CC FAMILY.  
 CC  
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 CC -----  
 CC EMBL; M94172; AAA51897.1; -;  
 CC DR EMBL; M94173; AAA51898.1; -;  
 CC DR EMBL; U76666; AAC51138.1; -;  
 CC DR MIM; 601012; -;  
 CC DR InterPro; IPR000636; -;  
 CC DR InterPro; IPR002077; -;  
 CC DR Pfam; PF00520; Ion\_trans; 4;  
 CC DR PRINTS; PR00167; CACHANNEL.  
 CC KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;  
 CC Calcium channel; Glycoprotein; Repeat; Multigene family;  
 CC KW Calcium-binding; Phosphorylation; ATP-binding; Alternative splicing.  
 CC FT REPEAT 82 359 I.  
 CC FT REPEAT 468 712 II.  
 CC FT REPEAT 1137 1419 III.  
 CC FT REPEAT 1456 1711 IV.  
 CC FT DOMAIN 1 95  
 CC FT TRANSMEM 96 114 CYTOPLASMIC (POTENTIAL).  
 CC FT DOMAIN 115 132 S1 OF REPEAT I (POTENTIAL).  
 CC FT TRANSMEM 133 152 EXTRACELLULAR (POTENTIAL).  
 CC FT DOMAIN 153 163 S2 OF REPEAT I (POTENTIAL).  
 CC FT TRANSMEM 164 183 CYTOPLASMIC (POTENTIAL).  
 CC FT DOMAIN 184 187 S3 OF REPEAT I (POTENTIAL).  
 CC FT TRANSMEM 188 206 EXTRACELLULAR (POTENTIAL).  
 CC FT DOMAIN 207 225 S4 OF REPEAT I (POTENTIAL).  
 CC FT TRANSMEM 226 245 CYTOPLASMIC (POTENTIAL).  
 CC FT DOMAIN 246 331 S5 OF REPEAT I (POTENTIAL).  
 CC FT TRANSMEM 332 356 EXTRACELLULAR (POTENTIAL).  
 CC FT DOMAIN 357 482 S6 OF REPEAT I (POTENTIAL).  
 CC FT TRANSMEM 483 501 CYTOPLASMIC (POTENTIAL).  
 CC FT DOMAIN 502 516 S1 OF REPEAT II (POTENTIAL).  
 CC FT TRANSMEM 517 536 EXTRACELLULAR (POTENTIAL).  
 CC FT DOMAIN 537 544 S2 OF REPEAT II (POTENTIAL).  
 CC FT TRANSMEM 545 562 CYTOPLASMIC (POTENTIAL).  
 CC FT DOMAIN 563 573 S3 OF REPEAT II (POTENTIAL).  
 CC FT TRANSMEM 574 592 EXTRACELLULAR (POTENTIAL).  
 CC FT DOMAIN 593 611 S4 OF REPEAT II (POTENTIAL).  
 CC FT TRANSMEM 612 631 CYTOPLASMIC (POTENTIAL).  
 CC FT DOMAIN 632 684 S5 OF REPEAT II (POTENTIAL).  
 CC FT TRANSMEM 685 709 EXTRACELLULAR (POTENTIAL).  
 CC FT DOMAIN 710 1151 S6 OF REPEAT II (POTENTIAL).  
 CC FT TRANSMEM 1152 1169 CYTOPLASMIC (POTENTIAL).  
 CC FT DOMAIN 1170 1185 S1 OF REPEAT III (POTENTIAL).  
 CC FT TRANSMEM 1186 1205 EXTRACELLULAR (POTENTIAL).  
 CC FT DOMAIN 1206 1217 S2 OF REPEAT III (POTENTIAL).  
 CC FT TRANSMEM 1218 1236 CYTOPLASMIC (POTENTIAL).  
 CC FT DOMAIN 1237 1246 S3 OF REPEAT III (POTENTIAL).  
 CC FT TRANSMEM 1247 1265 EXTRACELLULAR (POTENTIAL).  
 CC FT DOMAIN 1266 1284 S4 OF REPEAT III (POTENTIAL).  
 CC FT TRANSMEM 1285 1304 CYTOPLASMIC (POTENTIAL).  
 CC FT DOMAIN 1305 1391 S5 OF REPEAT III (POTENTIAL).  
 CC FT DOMAIN 1392 1416 EXTRACELLULAR (POTENTIAL).  
 CC FT TRANSMEM 1417 1471 S6 OF REPEAT III (POTENTIAL).  
 CC FT DOMAIN 1472 1490 CYTOPLASMIC (POTENTIAL).  
 CC FT TRANSMEM 1491 1505 EXTRACELLULAR (POTENTIAL).  
 CC FT DOMAIN 1506 1525 S1 OF REPEAT IV (POTENTIAL).  
 CC FT TRANSMEM 1526 1533 CYTOPLASMIC (POTENTIAL).  
 CC FT DOMAIN 1534 1552 S2 OF REPEAT IV (POTENTIAL).  
 CC FT TRANSMEM 1553 1563 EXTRACELLULAR (POTENTIAL).  
 CC FT DOMAIN 1564 1582 S3 OF REPEAT IV (POTENTIAL).  
 CC FT TRANSMEM 1583 1601 EXTRACELLULAR (POTENTIAL).  
 CC FT DOMAIN 1602 1621 S4 OF REPEAT IV (POTENTIAL).  
 CC FT TRANSMEM 1622 1683 CYTOPLASMIC (POTENTIAL).  
 CC FT DOMAIN 1684 1708 EXTRACELLULAR (POTENTIAL).  
 CC FT TRANSMEM 1709 2339 S5 OF REPEAT IV (POTENTIAL).  
 CC FT DOMAIN 2050 2054 S6 OF REPEAT IV (POTENTIAL).  
 CC FT DOMAIN 2118 2122 CYTOPLASMIC (POTENTIAL).  
 CC FT DOMAIN 379 396 POLY-HIS.  
 CC FT NP\_BIND 451 BINDING TO THE BETA SUBUNIT (BY  
 CC FT SITE 314 SIMILARITY).  
 CC FT SITE 663 ATP (POTENTIAL).  
 CC FT SITE 1365 CALCIUM ION SELECTIVITY AND PERMEABILITY  
 CC FT SITE 1655 (BY SIMILARITY).  
 CC FT MOD\_RES 1719 CALCIUM ION SELECTIVITY AND PERMEABILITY  
 CC FT CA\_BIND 1737 (BY SIMILARITY).  
 CC FT CARBOHYD 256 PHOSPHORYLATION (BY CAPK) (POTENTIAL).  
 CC FT CARBOHYD 1563 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC FT CARBOHYD 1675 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC FT VARSPLIC 2164 GSGVNGSPLLSTSCASTPGGRRGLPOTPLTPRPSTTYK  
 CC FT TANSPPHFAQAQSLPAPSGRSLRGLSENNALLQRPDLS  
 CC FT QPLAPSGRIGSDPYLQRLDSEASVHALPDTLTFEEAVT  
 CC FT NSGRSSSTSYSSLTSGSHLRVPNGYHCTGLSSGGRAR  
 CC FT HSYHHPDQDHWC -> AGSAVGFPNTPCCRETPTSPSPPL  
 CC FT ALELALTLTGWGVTVPRLSTPCLTRSLRSLRLMPPTRAAP  
 CC FT PGLPTCPP (IN ISOFORM ALPHA-1B-2).  
 CC SQ SEQUENCE 2339 AA; 262494 MW; 1745C6D1E76B39D CRC64;

Query Match 9.9%; Score 90; DB 1; Length 2339;  
 Best Local Similarity 30.8%; Pred. No. 22;

Matches 36; Conservative 16; Mismatches 35; Indels 30; Gaps 9;

QY 8 EPSEQED-----SSSAERGLGPSA-----GDGSGSGKHRRQAPGLLWDA----- 48

DB 878 EPGAEEERPRPHRSHSKAAGPEARSERGRGPGEGRRHRR--GSPPEAAERPRRH 935

QY 49 -SHQEQPTSSHHGGAGAV-EIRSRHSYP-AGTDDDEGMGEPS-PFRGRSRAP 101

DB 936 RAHRHQDSKEC-----ACAKGERRARHRRGGPRAGPREAES-GEEPARRHRRKAP 987

RESULT 6

CMGA\_BOVIN STANDARD; PRT; 449 AA.

AC P05059; P79392;

DT 13-AUG-1987 (Rel. 05, Created)

DT 01-NOV-1988 (Rel. 09, Last sequence update)

DT 01-OCT-2000 (Rel. 40, Last annotation update)

DE CHROMOGRANIN A PRECURSOR (CGA) (PITUITARY SECRETORY PROTEIN 1) (SP-1)

DE [CONTAINS: VASOSTATIN-1; CHROMOSTATIN; CHROMACIN; PANCREASTATIN; WE-

DE 14; CATESTATIN].

GN CHGA.

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;

OC Bovidae; Bovinae; Bos.

OX NCBI\_TaxID=9913;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE-92140395; PubMed-1779968;  
RA Tacangelo A.L., Grimes M., Eiden L.E.;  
RT "The bovine chromogranin A gene: structural basis for hormone  
RL regulation and generation of biologically active peptides.";  
RL Mol. Endocrinol. 5:1651-1660(1991).  
RN [2]  
RN  
RP SEQUENCE FROM N.A.  
RX MEDLINE-86300648; PubMed-3755681;  
RA Benedet U.M., Baeuerle P.A., Konecki D.S., Frank R., Powell J.,  
RA Mallet J., Huttner W.B.;  
RT "The primary structure of bovine chromogranin A: a representative of  
RT a class of acidic secretory proteins common to a variety of  
RT peptidergic cells.";  
RL EMBO J. 5:1495-1502(1986).  
RN [3]  
RN  
RP SEQUENCE FROM N.A.  
RX MEDLINE-86311345; PubMed-3018587;  
RA Tacangelo A., Affolter H.-U., Eiden L.E., Herbert E., Grimes M.;  
RT "Bovine chromogranin A sequence and distribution of its messenger RNA  
RT in endocrine tissues.";  
RL Nature 323:82-86(1986).  
RN [4]  
RN  
RP SEQUENCE FROM N.A.  
RX MEDLINE-87260925; PubMed-3474638;  
RA Ahn T.G., Cohn D.V., Gorr S.U., Ornstein D.L., Kashdan M.A.,  
RA Levine M.A.;  
RT "Primary structure of bovine pituitary secretory protein I  
RT (chromogranin A) deduced from the cDNA sequence.";  
RL Proc. Natl. Acad. Sci. U.S.A. 84:5043-5047(1987).  
RN [5]  
RN  
RP SEQUENCE FROM N.A.  
RX MEDLINE-97228583; PubMed-9074643;  
RA Kang Y.K., Yoo S.H.;  
RT "Identification of the secretory vesicle membrane binding region of  
RT chromogranin A.";  
RL FEBS Lett. 404:87-90(1997).  
RN [6]  
RN  
RP SEQUENCE OF 19-45, AND CALCIUM-BINDING.  
RX MEDLINE-90354431; PubMed-2387861;  
RA Yoo S.H., Albanesi J.P.;  
RT "Ca2(+)-induced conformational change and aggregation of chromogranin  
RT A.";  
RL J. Biol. Chem. 265:14414-14421(1990).  
RN [7]  
RN  
RP SEQUENCE OF 142-161, AND SYNTHESIS OF CHROMOSTATIN.  
RX MEDLINE-91142185; PubMed-1996343;  
RA Gallardo E., Rill A., Bader M.-F., Aunis D.;  
RT "Chromostatin, a 20-amino acid peptide derived from chromogranin A,  
RT inhibits chromaffin cell secretion.";  
RL Proc. Natl. Acad. Sci. U.S.A. 88:1426-1430(1991).  
RN [8]  
RN  
RP ERRATUM.  
RA Gallardo E., Rill A., Bader M.-F., Aunis D.;  
RL Proc. Natl. Acad. Sci. U.S.A. 91:832-832(1994).  
RN [9]  
RN  
RP SEQUENCE OF 266-312.  
RX MEDLINE-89331945; PubMed-2756155;  
RA Nakano I., Funakoshi A., Miyasaka K., Ishida K., Makk G., Angwin P.,  
RA Chang D., Tatemoto K.;  
RT "Isolation and characterization of bovine pancreastatin.";  
RL Regul. Pept. 25:207-213(1989).  
RN [10]  
RN  
RP SEQUENCE OF 191-212 (CHROMACIN).  
RC TISSUE-Chromaffin granules;  
RX MEDLINE-97067080; PubMed-8910482;  
RA Strub J.-M., Goumon Y., Lagardon K., Capon C., Lopez M., Moniatte M.,  
RA van Dorsselaer A., Aunis D., Metz-Boutigue M.-H.;  
RT "Antibacterial activity of glycosylated and phosphorylated  
RT chromogranin A-derived peptide 173-194 from bovine adrenal medullary  
RT chromaffin granules.";  
RL J. Biol. Chem. 271:28533-28540(1996).  
RN [11]  
RN  
RP CHARACTERIZATION OF CATESTATIN.  
RX MEDLINE-97439785; PubMed-9294131;  
RA Mahata S.K., O'Connor D.T., Mahata M., Yoo S.H., Taupenot L., Wu H.,  
RA Gill B.M., Parmer R.J.;  
RT "Novel autocrine feedback control of catecholamine release. A discrete  
RT chromogranin A fragment is a noncompetitive nicotinic cholinergic  
RT antagonist.";  
RL J. Clin. Invest. 100:1623-1633(1997).  
RN [12]  
RN  
RP CHARACTERIZATION OF CATESTATIN.  
RX MEDLINE-99000113; PubMed-9786174;  
RA Kennedy B.P., Mahata S.K., O'Connor D.T., Ziegler M.G.;  
RT "Mechanism of cardiovascular actions of the chromogranin A fragment  
RT catestatin in vivo.";  
RL Peptides 19:1241-1248(1998).  
RN [13]  
RN  
RP 3D-STRUCTURE MODELING OF CATESTATIN.  
RX MEDLINE-99025667; PubMed-9809795;  
RA Tsigelny I., Mahata S.K., Taupenot L., Preece N.E., Mahata M.,  
RA Khan I., Parmer R.J., O'Connor D.T.;  
RT "Mechanism of action of chromogranin A on catecholamine release:  
RT molecular modeling of the catestatin region reveals a beta-  
RT strand/loop/beta-strand structure secured by hydrophobic interactions  
RT and predictive of activity.";  
RL Regul. Pept. 77:43-53(1998).  
RN [14]  
RN  
RP CHARACTERIZATION OF VASOSTATIN-1.  
RX MEDLINE-20219105; PubMed-10753865;  
RA Lagardon K., Raffner R., Goumon Y., Corti A., Delmas A., Bulet P.,  
RA Aunis D., Metz-Boutigue M.-H.;  
RT "Antibacterial and antifungal activities of vasostatin-1, the N-  
RT terminal fragment of chromogranin A.";  
RL J. Biol. Chem. 275:10745-10753(2000).  
RN [15]  
RN  
RP CARBOHYDRATE-BINDING SITES, PHOSPHORYLATION, AND DISULFIDE BOND.  
RX MEDLINE-99459228; PubMed-10527498;  
RA Bauer S.H., Zhang X.Y., Van Dongen W., Claeys M., Przybylski M.;  
RT "Chromogranin A from bovine adrenal medulla: molecular  
RT characterization of glycosylations, phosphorylations, and sequence  
RT heterogeneities by mass spectrometry.";  
RL Anal. Biochem. 274:69-80(1999).  
CC -!- FUNCTION: PANCREASTATIN STRONGLY INHIBITS GLUCOSE INDUCED INSULIN  
CC RELEASE FROM THE PANCREAS.  
CC -!- FUNCTION: CHROMOSTATIN COMPLETELY INHIBITS CATECHOLAMINE RELEASE  
CC FROM CHROMAFFIN CELLS.  
CC -!- FUNCTION: CHROMACIN HAS ANTIBACTERIAL ACTIVITY AGAINST MICROCOCCUS  
CC LUTEUS.  
CC -!- FUNCTION: CATESTATIN INHIBITS CATECHOLAMINE RELEASE FROM  
CC CHROMAFFIN CELLS AND NORADRENERGIC NEURONS BY ACTING AS A NON-  
CC COMPETITIVE NICOTINIC CHOLINERGIC ANTAGONIST.  
CC -!- FUNCTION: VASOSTATIN-1 HAS ANTIBACTERIAL ACTIVITY AGAINST GRAM-  
CC POSITIVE BACTERIA M.LUTEUS, B.MEGATERIUM, NOT ACTIVE AGAINST GRAM-  
CC POSITIVE BACTERIA B.CEREUS, B.SUBTILIS, S.PYROGENES, M.FORTUITUM,  
CC S.AUREUS AND L.MONOCYTOGENES AND AGAINST GRAM-NEGATIVE BACTERIA  
CC E.COLI, E.CLOACAE, S.TYPHIMURUM, K.PNEUMONIAE AND P.AURUGINOSA.  
CC POSSESSES ANTIFUNGAL ACTIVITY AGAINST N.CRASSA, A.FUMIGATUS,  
CC A.BRASSICOLA, N.HEMATOCOCCA, F.CULMORUM AND F.OXYSPORUM AND  
CC AGAINST S.CEREVISIAE AND C.ALBICANS YEAST. INACTIVE AGAINST  
CC T.MENTAGROPHYTES.  
CC -!- SUBCELLULAR LOCATION: NEUROENDOCRINE AND ENDOCRINE SECRETORY  
CC GRANULES.  
CC -!- MASS SPECTROMETRY: MW=8584.9; METHOD=MALDI; RANGE=19-94.  
CC -!- MISCELLANEOUS: BINDS CALCIUM WITH A LOW-AFFINITY.  
CC -!- SIMILARITY: BELONGS TO THE CHROMOGRANIN / SECRETOGRANIN PROTEIN  
CC FAMILY.  
CC -----  
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CC



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FT MOD_RES 315 315 SULFATATION (BY SIMILARITY).
FT CONFLICT 64 64 N -> S (IN REF. 1).
FT CONFLICT 70 70 N -> D (IN REF. 2).
FT CONFLICT 93 98 SEAPGL -> FRSPRAS (IN REF. 3).
FT CONFLICT 181 181 T -> M (IN REF. 2).
FT CONFLICT 261 261 H -> R (IN REF. 2).
FT CONFLICT 386 386 P -> R (IN REF. 2).
FT CONFLICT 481 481 H -> L (IN REF. 3).
FT CONFLICT 597 597 M -> V (IN REF. 2).
FT SEQUENCE 646 AA; 73339 MW; 420DB1178FD9E415 CRC64;

Query Match 9.6%; Score 87; DB 1; Length 646;
Best Local Similarity 27.9%; Pred. No. 9.6;
Matches 36; Conservative 17; Mismatches 52; Indels 24; Gaps 6;

QY 9 PSQEDSSSNERGLGSPAGDGGSGKHH--RQAGLLWDASHQEQP--TSSSHHGGA 64
DB 246 PGSEEDA-----SPEYDKRHSRPHHGRSRP---DRSSQGNPPLEESHVGTG 293
QY 65 GAVEIRSHSSYPAGTDEDEGMGEPPFRGSRSPAPNLAQAQRYGR-----ELRRMA 118
DB 294 NSDEKARHPAHFRALEAGNEYGEVVR--RHSAAQAPGDLOGARFGGRGEGHQAALRRPS 351
QY 119 DEFVDSFKK 127
DB 352 EESLEQENK 360
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RESULT 8
ARVC_HUMAN STANDARD; PRT; 962 AA.
AC 000192;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE ARMADILLO REPEAT PROTEIN DELETED IN VELO-CARDIO-FACIAL SYNDROME.
GN Arvcf.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A. (SHORT AND LONG ISOFORMS).
RX MEDLINE=97271559; PubMed=9126485;
RA Sirotkin H., O'Donnell H., DasGupta R., Halford S., St Jore B.,
RA Puech A., Parimoo S., Morrow S., Skoultschi A., Weissman S.,
RA Scambler P., Kucherlapati R.;
RT "Identification of a new human catenin gene family member (ARVCF) from
RT the region deleted in velo-cardio-facial syndrome.";
RL Genomics 41:75-83(1997).
CC -!- FUNCTION: INVOLVED IN PROTEIN-PROTEIN INTERACTIONS AT ADHERENS
CC JUNCTIONS.
CC -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A SHORT FORM AND A LONG FORM
CC (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -!- TISSUE SPECIFICITY: FOUND IN ALL THE EXAMINED TISSUES INCLUDING
CC HEART BRAIN, LIVER AND KIDNEY. FOUND AT LOW LEVEL IN LUNG.
CC -!- DISEASE: GENE DELETED IN VELO-CARDIO-FACIAL SYNDROME (VCFS) AND IS
CC HEMIZYGOUS IN ALL VCFS PATIENTS WITH INTERSTITIAL DELETIONS. THIS
CC PHENOTYPES ASSOCIATED WITH VCFS CHARACTERIZED BY A WIDE SPECTRUM
CC OF FACIAL DYSMORPHOLOGY.
CC -!- SIMILARITY: BELONGS TO THE BETA-CATENIN FAMILY.
CC -!- SIMILARITY: CONTAINS 10 ARM REPEATS.
CC
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CC EMBL; U51269; AAC51202.1; --
DR HSP; 002248; 2BCT.
DR MIM; 602269; --
DR MIM; 192430; --
DR InterPro; IPR000225; --
DR Pfam; PF00514; Armadillo_seg. 4.
DR PROSITE; PS0176; ARM_REPEAT; 3.
KW Repeat; Coiled coil; Alternative splicing.
FT DOMAIN 8 46 COILED COIL (POTENTIAL).
FT DOMAIN 607 623 NUCLEAR LOCALIZATION (POTENTIAL).
FT DOMAIN 608 611 POLY-ARG.
FT REPEAT 348 387 ARM 1.
FT REPEAT 390 429 ARM 2.
FT REPEAT 433 473 ARM 3.
FT REPEAT 468 508 ARM 4.
FT REPEAT 526 565 ARM 5.
FT REPEAT 575 622 ARM 6.
FT REPEAT 646 686 ARM 7.
FT REPEAT 699 738 ARM 8.
FT REPEAT 739 781 ARM 9.
FT REPEAT 782 826 ARM 10.
FT VARSPIC 1 69 MEDCNVHSAASILASVKEQEARFERLTRALEQERRHVALQL
FT ERAQQPGMVSGMGSGQPLPMWQQLVL -> MPALER
FT (IN SHORT ISOFORM).
SQ SEQUENCE 962 AA; 104641 MW; 74A1814A022FF2B1 CRC64;
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Query Match 9.6%; Score 87; DB 1; Length 962;
Best Local Similarity 25.2%; Pred. No. 15;
Matches 39; Conservative 13; Mismatches 55; Indels 48; Gaps 7;

QY 8 EPSEQEDSSSNERGLGSPAGDGGSGKHHRQAGLLWDASHQEQPTSSSHHGAGAV 67
DB 194 EPRDPSYGLSLRGLGNRPFRAGPLGPGP-----GDGCF 227
QY 68 EIRSHSSYPAGTDEDEGMGEPPFRGSRSPAPNLAQAQRYGR--LRRMADEFVDSF 125
DB 228 TLPGRHRAFP-----VGPEPPGGRSL---PERQAEPYGLDDTRSLAAD----- 271
QY 126 KKGKLPK-PRKAGTATQNRQSSS---WTRVFQSWWD 156
DB 272 DEGGPELEPDYGTATRRRRCGRLHTRAYEDTAD 306
```

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RESULT 9
HLES_DROME STANDARD; PRT; 1077 AA.
AC 002308;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE HAIRLESS PROTEIN.
GN H.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92387549; PubMed=1516831;
RA Bang A.G., Posakony J.W.;
RT "The Drosophila gene Hairless encodes a novel basic protein that
RT controls alternative cell fates in adult sensory organ development.";
RL Genes Dev. 6:1752-1769(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=93041287; PubMed=1419850;
RA Maier D., Stumm G., Kuhn K., Preiss A.;
RT "Hairless, a Drosophila gene involved in neural development, encodes
RT a novel, serine rich protein.";
RL Mech. Dev. 38:143-156(1992).
```





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RL Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE-9426802; PubMed-8208605;
RA Chiba H., Muramatsu M., Nomoto A., Kato H.;
RT "Two human homologues of Saccharomyces cerevisiae SWI2/SNF2 and
RT Drosophila brhma are transcriptional coactivators cooperating with
RT the estrogen receptor and the retinoic acid receptor.";
RL Nucleic Acids Res. 22:1815-1820(1994).
RN [4]
RP SEQUENCE OF 814-1474 FROM N.A.
RA Lamerdin J.E., McCreedy P.M., Skowronski E., Viswanathan V.,
RA Burkhardt-Schultz K., Gordon L., Dias J., Brower A., Stilwagen S.,
RA Phan H., Velasco N., Do L., Regala W., Terry A., Garnes J.,
RA Danganan L., Erler A., Christensen M., Georgescu A., Avila J., Liu S.,
RA Attix C., Andreise T., Trankheim M., Amico-Keller G., Coefield J.,
RA Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Kronmiller B.,
RA Arellano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A.,
RA Olsen A.S., Carrano A.V.;
RL Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
CC -1- FUNCTION: TRANSCRIPTIONAL COACTIVATOR COOPERATING WITH NUCLEAR
CC HORMONE RECEPTORS TO POTENTIATE TRANSCRIPTIONAL ACTIVATION.
CC -1- SUBCELLULAR LOCATION: NUCLEAR.
CC -1- SIMILARITY: CONTAINS 1 BROMODOMAIN.
CC -1- SIMILARITY: BELONGS TO THE SNF2/RAD54 HELICASE FAMILY.
CC -----
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CC -----
DR EMBL; U29175; AAB40977.1; -
DR EMBL; D26156; BAA05143.1; -
DR EMBL; AC006127; AAC97987.1; -
DR MIM; 603254; -
DR InterPro; IPR000330; -
DR InterPro; IPR001487; -
DR InterPro; IPR001650; -
DR Pfam; PF00176; SNF2_N; 1
DR Pfam; PF00439; bromodomain; 1.
DR Pfam; PF00271; helicase_C; 1.
DR PRINTS; PR00503; BROMODOMAIN.
DR PROSITE; PS00633; BROMODOMAIN_1; 1.
DR PROSITE; PS50014; BROMODOMAIN_2; 1.
KW Transcription regulation; Nuclear protein; Activator; Bromodomain;
KW ATP-binding; Helicase.
FT DOMAIN 578 588 POLY-LYS.
FT DOMAIN 663 672 POLY-GLU.
FT NP_BIND 779 786 ATP (POTENTIAL).
FT SITE 881 884 DEGH BOX.
FT DOMAIN 1360 1364 POLY-GLU.
FT DOMAIN 1477 1547 BROMODOMAIN.
FT DOMAIN 1571 1584 POLY-GLU.
SQ SEQUENCE 1647 AA; 184585 MW; 7B785E7953277F1D CRC64;

Query Match 9.6%; Score 86.5; DB 1; Length 1647;
Best Local Similarity 29.8%; Pred. No. 28;
Matches 31; Conservative 9; Mismatches 55; Indels 9; Gaps 4;

QY 9 PSEQDSSAERGLGSPAGDGGSGKHH---RQAP-GLLWDASHQEQPTSSSHHGCA 64
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 30 PSPGPGSAHSMWGSP---GPPSAG--HPPTQCGPGYPQDNMQMKPMESMEKCM 84
::: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 65 GAVEIRSHSSYPAGTDEDDGMEEPSPFRGRSRAPNLWAAQ 108
::: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 85 SDDPRYNQMKGMGRSGGHAGMPFPSPMDQHSQGYPSPLGGSE 128
::: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 12
```

```
DMPL_BOVIN .STANDARD; PRT; 510 AA.
ID DMPL_BOVIN AC Q95120;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE DENTIN MATRIX ACIDIC PHOSPHOPROTEIN 1 PRECURSOR (DENTIN MATRIX
DE PROTEIN-1) (DMP-1).
GN DMPL.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Tooth;
RX MEDLINE-97263352; PubMed-9109824;
RA Hirst K.L., Ibaraki-O'Connor K., Young M.F., Dixon M.J.;
RT "Cloning and expression analysis of the bovine dentin matrix acidic
RT phosphoprotein gene.";
RL J. Dent. Res. 76:754-760(1997).
CC -1- FUNCTION: COULD BE INVOLVED IN THE INDUCTION OF MINERALIZATION OF
CC EXTRACELLULAR MATRIX AND IN DENTINOGENESIS.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN FETAL BRAIN, BONE AND TOOTH
CC PARTICULARLY IN ODONTOBLAST, BUT NOT IN AMELOBLAST. NOT EXPRESSED
CC IN LIVER AND SKIN.
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CC -----
DR EMBL; U47636; AAB09412.1; -
KW Extracellular matrix; Signal.
FT SIGNAL 1 16 POTENTIAL.
FT CHAIN 17 510 DENTIN MATRIX ACIDIC PHOSPHOPROTEIN 1.
FT CARBOHYD 351 351 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 370 370 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 427 427 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 464 464 N-LINKED (GLCNAC. .) (POTENTIAL).
FT SITE 364 366 CELL ATTACHMENT SITE (POTENTIAL).
SQ SEQUENCE 510 AA; 55491 MW; 9BFA9A74F6450865 CRC64;

Query Match 9.4%; Score 85.5; DB 1; Length 510;
Best Local Similarity 25.2%; Pred. No. 9.7;
Matches 29; Conservative 12; Mismatches 35; Indels 39; Gaps 5;

QY 9 PSEQEDSSAERGLGSPAGDGGSGKHHRQAPGLLWDASHQ-----HOADESSEEDVLDKPSDS 51
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 347 PSQENSESQEALHES-RGDNPDNATSHRE-----HOADESSEEDVLDKPSDS 396
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 52 -----QEQTPTSSHHGGAGAVEIRSHSSYPAGTDEDDGMEEPSPFRGRSRAP 101
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 397 ESTSTEQADSESHE-----SLRSSEES-PESTEQNSSSQEGAQTSRSQSP 444
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 13
HERG_HUMAN .STANDARD; PRT; 1159 AA.
ID HERG_HUMAN AC Q12809;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE VOLTAGE-GATED POTASSIUM CHANNEL HERG (POTASSIUM CHANNEL, VOLTAGE-GATED
DE SUBFAMILY H MEMBER 2) (ETHER-A-GO-GO-RELATED PROTEIN).
GN KCNH2 OR HERG
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```



CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 RN NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Hippocampus;  
 RX MEDLINE=942111879; PubMed=8159766;  
 RA Warmke J.W., Ganetzky B.;  
 RT "A family of potassium channel genes related to eag in Drosophila and  
 RT mammals.";  
 RL Hum. Genet. 102:435-439(1998).  
 RN [2]  
 RP Proc. Natl. Acad. Sci. U.S.A. 91:3438-3442(1994).  
 RN [3]  
 RP SEQUENCE FROM N.A., AND VARIANT LQT2 CYS-534.  
 RX MEDLINE=98260867; PubMed=9600240;  
 RA Itoh T., Tanaka T., Nagai R., Kamiya T., Sawayama T., Nakayama T.,  
 RA Tomoike H., Sakurada H., Yazaki Y., Nakamura Y.;  
 RT "Genomic organization and mutational analysis of HERG, a gene  
 RT responsible for familial long QT syndrome.";  
 RL Hum. Genet. 102:435-439(1998).  
 RN [3]  
 RP SEQUENCE OF 27-1159 FROM N.A.  
 RA Yang P., Paulussen A., Verhasselt P., Crabbe R., Luyten W.,  
 RA Armstrong M.;  
 RT "Analysis of the human HERG gene: intron localisation and  
 RT identification of a novel inherited mutation associated with long  
 RT QT.";  
 RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP VARIANTS LQT2 ASP-470; VAL-561; SER-628 AND 500-ILE--PHE-508 DEL.  
 RX MEDLINE=95196272; PubMed=7889573;  
 RA Curran M.E., Splawski J., Timothy K.W., Vincent G.M., Green E.D.,  
 RA Keating M.T.;  
 RT "A molecular basis for cardiac arrhythmia: HERG mutations cause long  
 RT QT syndrome.";  
 RL Cell 80:795-803(1995).  
 RN [5]  
 RP VARIANT LQT2 MET-822.  
 RX MEDLINE=97071892; PubMed=9914737;  
 RA Satler C.A., Walsh E.P., Vesely M.R., Plummer M.H., Ginsburg G.S.,  
 RA Jacob H.J.;  
 RT "Novel missense mutation in the cyclic nucleotide-binding domain of  
 RT HERG causes long QT syndrome.";  
 RL Am. J. Med. Genet. 65:27-35(1996).  
 RN [6]  
 RP VARIANT LQT2 ARG-593.  
 RX MEDLINE=96259954; PubMed=8635257;  
 RA Benson D.W., MacRae C.A., Vesely M.R., Walsh E.P., Seidman J.G.,  
 RA Seidman C.E., Satler C.A.;  
 RT "Missense mutation in the pore region of HERG causes familial long QT  
 RT syndrome.";  
 RL Circulation 93:1791-1795(1996).  
 RN [7]  
 RP VARIANTS LQT2 ILE-474; VAL-561; HIS-611; VAL-614 AND ALA-630.  
 RX MEDLINE=97176600; PubMed=9024139;  
 RA Tanaka T., Nagai R., Tomoike H., Takata S., Yano K., Yabuta K.,  
 RA Haneda N., Nakano O., Shibata A., Sawayama T., Kasai H., Yazaki Y.,  
 RA Nakamura Y.;  
 RT "Four novel KVLQT1 and four novel HERG mutations in familial long-QT  
 RT syndrome.";  
 RL Circulation 95:565-567(1997).  
 RN [8]  
 RP VARIANTS LQT2 CYS-572; ASP-588; VAL-614 AND ALA-630.  
 RX MEDLINE=98360095; PubMed=9693036;  
 RA Splawski J., Shen J., Timothy K.W., Vincent G.M., Lehmann M.H.,  
 RA Keating M.T.;  
 RT "Genomic structure of three long QT syndrome genes: KVLQT1, HERG, and  
 RT KCNE1.";  
 RL Genomics 51:86-97(1998).  
 RN [9]  
 RP VARIANTS LQT2 LEU-612; VAL-614; ASP-629; SER-629 AND SER-633.  
 RX MEDLINE=98204397; PubMed=9544837;  
 RA Satler C.A., Vesely M.R., Duggal P., Ginsburg G.S., Beggs A.H.;  
 RT "Multiple different missense mutations in the pore region of HERG in  
 RT patients with long QT syndrome.";

RL Hum. Genet. 102:265-272(1998).  
 RN [10]  
 RP VARIANTS LQT2 SER-601.  
 RX MEDLINE=98112459; PubMed=9452080;  
 RA Akimoto K., Furutani M., Imamura S.-I., Furutani Y., Kasanuki H.,  
 RA Takao A., Momma K., Matsuoka R.;  
 RT "Novel missense mutation (G601S) of HERG in a Japanese long QT  
 RT syndrome family.";  
 RL Hum. Mutat. Suppl. 1:S184-S186(1998).  
 RN [11]  
 RP VARIANTS LQT2 PRO-558; CYS-582; SER-604; MET-613 AND LEU-640.  
 RX MEDLINE=99235550; PubMed=10220144;  
 RA Jongbloed R.J.E., Wilde A.A.M., Geelen J.L.M.C., Doevendans P.,  
 RA Schaap C., Van Langen I., van Tintelen J.P., Cobben J.M.,  
 RA Beaufort-Krol G.C.M., Geraedts J.P.M., Smeets H.J.M.;  
 RT "Novel KCNQ1 and HERG missense mutations in Dutch long-QT families.";  
 RL Hum. Mutat. 13:301-310(1999).  
 RN [12]  
 RP VARIANT LQT2 ARG-572.  
 RX MEDLINE=99235552; PubMed=10220146;  
 RA Larsen L.A., Christiansen M., Vuust J., Andersen P.S.;  
 RT "High-throughput single-strand conformation polymorphism analysis by  
 RT automated capillary electrophoresis: robust multiplex analysis and  
 RT pattern-based identification of allelic variants.";  
 RL Hum. Mutat. 13:318-327(1999).  
 RN [13]  
 RP VARIANTS LQT2 L-29; T-33; R-53; Q-56; G-66; R-70; P-78 AND R-86.  
 RX MEDLINE=99214568; PubMed=10187793;  
 RA Chen J., Zou A., Splawski J., Keating M.T., Sanguinetti M.C.;  
 RT "Long QT syndrome-associated mutations in the Per-Arnt-Sim (PAS)  
 RT domain of HERG potassium channels accelerate channel deactivation.";  
 RL J. Biol. Chem. 274:10113-10118(1999).  
 RN [14]  
 RP VARIANT LQT2 LYS-629.  
 RX MEDLINE=9945248; PubMed=10517660;  
 RA Yoshida H., Horie M., Otani H., Takano M., Tsuji K., Kubota T.,  
 RA Fukunami M., Saseyama S.;  
 RT "Characterization of a novel missense mutation in the pore of HERG in  
 RT a patient with long QT syndrome.";  
 RL J. Cardiovasc. Electrophysiol. 10:1262-1270(1999).  
 RN [15]  
 RP VARIANT LQT2 ARG-572.  
 RX MEDLINE=20197680; PubMed=10735633;  
 RA Larsen L.A., Svendsen I.H., Jensen A.M., Kanters J.K., Andersen P.S.,  
 RA Moller M., Sorensen S.A., Sandoe E., Jacobsen J.R., Vuust J.,  
 RA Christiansen M.;  
 RT "Long QT syndrome with a high mortality rate caused by a novel G572R  
 RT missense mutation in KCNH2.";  
 RL Clin. Genet. 57:125-130(2000).  
 RN [16]  
 RP VARIANTS LQT2.  
 RX MEDLINE=20432616; PubMed=10973849;  
 RA Splawski J., Shen J., Timothy K.W., Lehmann M.H., Priori S.,  
 RA Robinson J.L., Moss A.J., Schwartz P.J., Towbin J.A., Vincent G.M.,  
 RA Keating M.T.;  
 RT "Spectrum of mutations in long-QT syndrome genes. KVLQT1, HERG, SCN5A,  
 RT KCNE1, and KCNE2.";  
 RL Circulation 102:1178-1185(2000).  
 CC -1- FUNCTION: INWARDLY RECTIFYING CARDIAC POTASSIUM (IKR) CHANNEL.  
 CC -1- SUBUNIT: MAY ASSEMBLE WITH EITHER MIRP1 OR MINK. COMPLEXES WITH  
 CC MIRP1 ARE MORE STABLE.  
 CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN HEART.  
 CC -1- DISEASE: DEFECTS IN KCNH2 IS ASSOCIATED WITH LONG QT SYNDROME TYPE  
 CC 2 (LQT2). THIS DISEASE IS CHARACTERIZED BY A PROLONGED QT SEGMENT  
 CC ON THE ECG AND POLYMORPHIC VENTRICULAR ARRHYTHMIAS KNOWN AS  
 CC TORSADES DE POINTES. THESE ARRHYTHMIAS OFTEN OCCUR IN RELATION TO  
 CC EXERCISE OR EMOTIONAL STRESS AND MAY RESULT IN RECURRENT SYNCOPE,  
 CC SEIZURES, OR SUDDEN CARDIAC DEATH. DEAFNESS IS OFTEN ASSOCIATED TO  
 CC THE SYNDROME.  
 CC -1- MISCELLANEOUS: IT HAS THE ARCHITECTURAL PLAN OF THE  
 CC DEPOLARIZATION-ACTIVATED POTASSIUM CHANNEL FAMILY (6 PUTATIVE  
 CC TRANSMEMBRANE SEGMENTS), YET IT EXHIBITS RECTIFICATION LIKE THAT  
 CC OF THE INWARD-RECTIFYING POTASSIUM CHANNELS.



Best Local Similarity 25.8%; Pred. No. 5.5;  
Matches 55; Conservative 13; Mismatches 63; Indels 82; Gaps 11;

Qy 10 SEQ-EDSSAERG-----LGPSPAGDPSGKGHHQ-----APCLLDASHQ 51  
Db 31 SEQFDSASMHSGRYGYNGMDLSVGRSGHFGSGGERARSYAAGASAAAP-----AEFR 85  
Qy 52 QEQPTSS-----SHGG-----AGAVEIRSR----- 72  
Db 86 YSOPATSTHSPDPLPCSAVAPSGSDSHGGKNSLGNSSCASANAGSTHSSREGVGT 145  
Qy 73 -----HSSYPAGTEDEGMEGPEPFRGRSRAPPNLWAAQRYGRELRMADEFVDSFKKG 128  
Db 146 ASAAEEDAPASSE-QAGAQSESP-----APPAQPOIYPMWRKLHSHDNI-----G 191  
Qy 129 LPRPKSAGTATOMROSSWTRVFSQWDRNLGR 161  
Db 192 GPEGKARTATRYQTLEKEFH--FNRYLTR 222

RESULT 15

ST13\_MOUSE  
ID ST13\_MOUSE STANDARD; PRT: 215 AA.  
AC Q60924;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE RETINOIC ACID-INDUCIBLE E3 PROTEIN (HEMATOPOIETIC-SPECIFIC PROTEIN  
DE E3).  
GN STRA13.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=MDP1;  
RA MEDLINE=96437028; PubMed=8839844;  
RX Scott L.M., Mueller L., Collins S.J.;  
RT "E3, a hematopoietic-specific transcript directly regulated by the  
RT retinoic acid receptor alpha";  
RL Blood 88:2517-2530(1996).  
CC -!- TISSUE SPECIFICITY: PRESENT IN THE MYELOID, B-LYMPHOID, AND  
CC ERYTHROID LINEAGES, ABSENT IN NONHEMATOPOIETIC CELLS.  
CC -!- INDUCTION: BY RETINOIC ACID.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; U29539; AAB48193.1; -;  
DR MGD; MGI:894324; STRA13.  
KW Repeat.  
FT DOMAIN 16 171 13 X 12 AA TANDEM REPEAT OF G-[AG]-P-P-T-  
FT T-H-W-S-A-H-H  
SQ SEQUENCE 215 AA; 23140 MW; 647CCB5FDA7BC73E CRC64;

Query Match 9.3%; Score 84.5; DB 1; Length 215;  
Best Local Similarity 26.0%; Pred. No. 4.7;  
Matches 33; Conservative 7; Mismatches 76; Indels 11; Gaps 3;

Qy 17 SAERGLGSPAGDPSGS-----GKHHQAPGLWDASHQEQPTSSSHHGGAGAVEIR 70  
Db 72 SAHHCAPPTTHWSAHHGAPPTTHWSAHHGAPPTTHWSAHHGAPPTTHWSAHHGAPPTTHW 131  
Qy 71 SRHSYPAGTEDEGMEGPEPFRGRSRAPPNLWAAQRYGRELRMADEFVDSFKKGL 129  
Db 132 SAHHCAPPTTHWSAHHGAPPTTHWSAHHGAPPTTHWSAHHGAQALL-----EFLQHLEGGK 187

Qy 130 PRPKSAG 136  
Db 188 SNSLGAG 194

Search completed: October 9, 2001, 16:03:44  
Job time: 309 sec





QY 61 HGGAGAVEIRSRHSSYPAGTDEGMEEPSPFRGRSRAPPNLWAAORYGRELRMADE 120  
|||||  
Db 61 HGGAGAVEIRSRHSSYPAGTDEGMEEPSPFRGRSRAPPNLWAAORYGRELRMSDE 120  
|||||  
QY 121 FVDSFKKGLPRPKSAGTATQMRQSSWTRVFQSWDRNLGRGSSAPSQ 168  
|||||  
Db 121 FVDSFKKGLPRPKSAGTATQMRQSSWTRVFQSWDRNLGRGSSAPSQ 168  
|||||  
RESULT 2  
O35147 PRELIMINARY; PRT; 205 AA.  
AC O35147;  
DT 01-JAN-1998 (TREMBLrel. 05, Created)  
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)  
DE BCL-2 ASSOCIATED DEATH PROMOTER.  
GN BAD.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=OVARY;  
RX MEDLINE=98034386; PubMed=9369453;  
RA Hsu S.Y., Hsueh A.J.W.;  
RT "Interference of BAD (Bcl-xL/Bcl-2-associated death promoter)-induced  
apoptosis in mammalian cells by 14-3-3 isoforms and P11";  
RL Mol. Endocrinol. 11:1858-1867(1997).  
DR EMBL; AF003523; AAC53374.1; -.  
SQ SEQUENCE 205 AA; 22468 MW; 04DD3EBA03B11168 CRC64;

Query Match 70.0%; Score 633.5; DB 11; Length 205;  
Best Local Similarity 74.6%; Pred. No. 2.3e-50;  
Matches 126; Conservative 12; Mismatches 24; Indels 7; Gaps 4;  
QY 1 MFQIPEFESEQEDSSAERGLGSPAGDGPSSGKHHRQAPGLLWDASHQOE-QPTSSS 59  
|||||  
Db 43 MFQIPEFESEQEDASTDRGLGSLTEDEP---GPY--LAPGLLGSIVQQQPGQAANN 97  
|||||  
QY 60 HGGAGAVEIRSRHSSYPAGTDEGMEEPSPFRGRSRAPPNLWAAORYGRELRMADE 119  
|||||  
Db 98 HGGAGCTMETRSHSSYPAGTDEGMEELSPFRGRSRAPPNLWAAORYGRELRMSD 157  
|||||  
QY 120 EFVDSFKKGLPRPKSAGTATQMRQSSWTRVFQSWDRNLGRGSSAPSQ 168  
|||||  
Db 158 EFGSP-KGLPRPKSAGTATQMRQSSWTRVFQSWDRNLGRGSSAPSQ 205  
|||||

RESULT 3  
O70256 PRELIMINARY; PRT; 205 AA.  
AC O70256;  
DT 01-AUG-1998 (TREMBLrel. 07, Created)  
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)  
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)  
DE BCL-2 ASSOCIATED DEATH PROMOTER BAD (BCL-2 ASSOCIATED DEATH AGONIST  
ALPHA).  
GN BAD OR BAD-ALPHA.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=BRAIN;  
RX MEDLINE=98194755; PubMed=9535132;  
RA D'Agata V., Magro G., Travali S., Musco S., Cavallaro S.;  
RT "Cloning and expression of the programmed cell death regulator Bad in  
the rat brain.";  
RL Neurosci. Lett. 243:137-140(1998).

RN [2]  
RP SEQUENCE FROM N.A.  
RA Hamner S., Arumne U., Li-Ying Y., Sun Y.-F., Saarma M., Lindholm D.;  
RT "Functional characterization of two splice variants of rat bad and  
their interaction with bcl-w in sympathetic neurons.";  
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF031227; AAC15100.1; -.  
DR EMBL; AF279910; AAF91427.1; -.  
SQ SEQUENCE 205 AA; 22228 MW; 7AFA71DAE9CF4A81 CRC64;

Query Match 70.0%; Score 633.5; DB 11; Length 205;  
Best Local Similarity 74.6%; Pred. No. 2.3e-50;  
Matches 126; Conservative 12; Mismatches 24; Indels 7; Gaps 4;  
QY 1 MFQIPEFESEQEDSSAERGLGSPAGDGPSSGKHHRQAPGLLWDASHQOE-QPTSSS 59  
|||||  
Db 43 MFQIPEFESEQEDASTDRGLGSLTEDEP---GPY--LAPGLLGSIVQQQPGQAANN 97  
|||||  
QY 60 HGGAGAVEIRSRHSSYPAGTDEGMEEPSPFRGRSRAPPNLWAAORYGRELRMADE 119  
|||||  
Db 98 HGGAGCTMETRSHSSYPAGTDEGMEELSPFRGRSRAPPNLWAAORYGRELRMSD 157  
|||||  
QY 120 EFVDSFKKGLPRPKSAGTATQMRQSSWTRVFQSWDRNLGRGSSAPSQ 168  
|||||  
Db 158 EFGSP-KGLPRPKSAGTATQMRQSSWTRVFQSWDRNLGRGSSAPSQ 205  
|||||

RESULT 4  
Q9JHX1 PRELIMINARY; PRT; 220 AA.  
AC Q9JHX1;  
DT 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)  
DE BCL-2 ASSOCIATED DEATH AGONIST BETA.  
GN BAD-BETA.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Hamner S., Arumne U., Li-Ying Y., Sun Y.-F., Saarma M., Lindholm D.;  
RT "Functional characterization of two splice variants of rat bad and  
their interaction with bcl-w in sympathetic neurons.";  
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF279911; AAF91428.1; -.  
SQ SEQUENCE 220 AA; 24278 MW; E27BCD7C969E90F CRC64;

Query Match 49.0%; Score 443; DB 11; Length 220;  
Best Local Similarity 71.7%; Pred. No. 5.5e-33;  
Matches 91; Conservative 9; Mismatches 21; Indels 6; Gaps 3;  
QY 1 MFQIPEFESEQEDSSAERGLGSPAGDGPSSGKHHRQAPGLLWDASHQOE-QPTSSS 59  
|||||  
Db 43 MFQIPEFESEQEDASTDRGLGSLTEDEP---GPY--LAPGLLGSIVQQQPGQAANN 97  
|||||  
QY 60 HGGAGAVEIRSRHSSYPAGTDEGMEEPSPFRGRSRAPPNLWAAORYGRELRMADE 119  
|||||  
Db 98 HGGAGCTMETRSHSSYPAGTDEGMEELSPFRGRSRAPPNLWAAORYGRELRMSD 157  
|||||  
QY 120 EFVDSFK 126  
Db 158 EFGSPK 164  
|||||  
RESULT 5  
Q9I9N2 PRELIMINARY; PRT; 95 AA.  
ID Q9I9N2  
AC Q9I9N2;  
DT 01-OCT-2000 (TREMBLrel. 15, Created)

01-OCT-2000 (TReMBLrel. 15, Last sequence update)  
01-MAR-2001 (TReMBLrel. 16, Last annotation update)  
DE BAD (FRAGMENT).  
GN BAD.  
OS Brachydanio rerio (Zebrafish) (Zebra danio).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;  
OC Cypriniformes; Cyprinidae; Rasbora; Danio.  
OX NCBI\_TaxID=7955;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20337392; PubMed=10917738;  
RA Inohara N., Nunez G.;  
RT "Genes with Homology to Mammalian Apoptosis Regulators Identified in  
RT Zebrafish";  
RL Cell Death Differ. 7:509-510(2000).  
DR EMBL: AF231017; AAF66962.1; -;  
FT NON\_TER 1  
SQ SEQUENCE 95 AA; 10804 MW; 77F5CDE879E69FF7 CRC64;  
  
Query Match 22.6%; Score 204.5; DB 13; Length 95;  
Best Local Similarity 48.9%; Pred. No. 1.2e-11;  
Matches 44; Conservative 11; Mismatches 24; Indels 11; Gaps 3;  
  
Qy 83 DEGMGEPP-----SPFRGSRSPAPNLWAAQRYGRELRRMADEFVDSFKKGLPRPKSAGTA 138  
Db 13 ETGVAEPHMLGDFRPRRSAPPALWAAKKYGGQLRRMSDE----FDKMKRVKSAGTA 68  
Qy 139 TOMROSSSWTRVFSQWDRNLGRGSSAPSQ 168  
Db 69 ROMSQSPSWLAFL---WSHKESDAESRPAE 95  
  
RESULT 6  
Q9NS37 ID Q9NS37 PRELIMINARY; PRT; 272 AA.  
AC Q9NS37;  
DT 01-OCT-2000 (TReMBLrel. 15, Created)  
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)  
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)  
DE HCF-BINDING TRANSCRIPTION FACTOR ZHANGFEI.  
GN ZF.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20330366; PubMed=10871379;  
RA Lu R., Misra V.;  
RT "Zhangfei: a second cellular protein interacts with herpes simplex  
RT virus accessory factor HCF in a manner similar to Human and VP16";  
RL Nucleic Acids Res. 28:2446-2454(2000).  
DR EMBL: AF039942; AAD28325.1; -;  
DR InterPro: IPR001871; -;  
DR Pfam: PF00170; bZIP: 1.  
DR SMART: SM00338; BRLZ: 1.  
SQ SEQUENCE 272 AA; 28859 MW; B1F94B438F0702BF CRC64;  
  
Query Match 11.0%; Score 100; DB 4; Length 272;  
Best Local Similarity 28.7%; Pred. No. 0.12;  
Matches 41; Conservative 13; Mismatches 67; Indels 22; Gaps 5;  
  
Qy 10 SEQEDSSAERGLGSPAGDPGSGGKHRRQAPGLLWDASHQOQPTSSSHHGAGAVEI 69  
Db 92 SSSDSSGAERKRKRKSGGGGGGGGNDNQA-----ATKSPKRAAAAAARL 138  
Qy 70 -RSRSHSSYPACTEDD-EGMGEEPPFRGRSRSAPPNLWAAQRYGRELRR-MADEFVDSFK 126  
Db 139 NLRKKKEYVMGLSRVGLAAENQELRAENRELKRVQALQESRYLRAVLANE----- 192

Qy 127 KGLPRPKSAGTATQMRSSSWTR 149  
Db 193 TGLARLLSRLSGVGLRLTSLFR 215  
  
RESULT 7  
Q9Q5K9 ID Q9Q5K9 PRELIMINARY; PRT; 608 AA.  
AC Q9Q5K9;  
DT 01-MAY-2000 (TReMBLrel. 13, Created)  
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
DT 01-MAY-2000 (TReMBLrel. 13, Last annotation update)  
DE NTR.  
OS Herpesvirus papio.  
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
OC Gammaherpesvirinae; Lymphocryptovirus.  
OX NCBI\_TaxID=10394;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BABOON LYMPHOCRYPTOVIRUS BA65;  
RA Zong J.-C., Ryan J., Ling P.D., Loeb D.D., Pagano J.S., Hayward S.D.,  
RA Hayward G.S.;  
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF200364; AAF23950.1; -;  
SQ SEQUENCE 608 AA; 60458 MW; 4BF82ACB0A029627 CRC64;  
  
Query Match 11.0%; Score 100; DB 14; Length 608;  
Best Local Similarity 33.3%; Pred. No. 0.27;  
Matches 37; Conservative 7; Mismatches 55; Indels 12; Gaps 3;  
  
Qy 9 PSEQEDSSAERGLGSPAGDPGSGGKHRRQAPGLLWDASHQOQPTSSSHHG----GA 64  
Db 502 PTERRRCSAQRGHPGAGORPSGPTGGHAAACGAPCRPRTERRRCSAQRGHPGGA 561  
Qy 65 GAVEIRSRHSSYPAGTEDEGMGEPPSPFRGRSRSAPPNLWAAQRYGRELRR 115  
Db 562 G-----QRPSGTGGHAAACGAPGPPNPERGSGPADPP---AATRLPLEPR 604  
  
RESULT 8  
Q9DF20 ID Q9DF20 PRELIMINARY; PRT; 569 AA.  
AC Q9DF20;  
DT 01-MAR-2001 (TReMBLrel. 16, Created)  
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)  
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)  
DE KH DOMAIN CONTAINING RNA-BINDING PROTEIN FMRI.  
OS Brachydanio rerio (Zebrafish) (Zebra danio).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;  
OC Cypriniformes; Cyprinidae; Rasbora; Danio.  
OX NCBI\_TaxID=7955;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20501263; PubMed=11046149;  
RA Wan L., Dockendorff T.C., Jongens T.A., Dreyfuss G.;  
RT "Characterization of dFMR1, a Drosophila melanogaster Homolog of the  
RT Fragile X Mental Retardation Protein";  
RL Mol. Cell. Biol. 20:8536-8547(2000).  
DR EMBL: AF305882; AAG22046.1; -;  
SQ SEQUENCE 569 AA; 63906 MW; 2E66A0689F7EDFB5 CRC64;  
  
Query Match 10.9%; Score 98.5; DB 13; Length 569;  
Best Local Similarity 32.3%; Pred. No. 0.34;  
Matches 31; Conservative 8; Mismatches 42; Indels 15; Gaps 3;  
  
Qy 11 EQEDSSAERGLGSPAGDPGSGGKHRRQAP---GLLWDASHQOQPTSSSHHGAGAGA 66  
Db 391 EKESFMADNMGSPRGSGGKPFGRGRRRGPTLASGNTSEASNASE--TESDH----- 442  
Qy 67 VEIRSRHSSYPAGTEDEGMGEPPSPFRGRSRSAPP 102







RESULT 15

003000  
ID\* 009000  
PRELIMINARY:  
PRT: 1398 AA.

DT 01-JUL-1997 (TREMBLrel. 04, Created)

DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)

GN NCOA3.

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi  
OC Mammalia; Eutheria; Podontia; Sciurognathi; Muridae; Murinae; Mur

```

OX
RN
NCBI_TaxID=10090;
[]

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RX MEDLINE=97336097: PubMed=9192892:  
SEQUENCE FROM N.R.

RA Rosenfeld M.G.;

RT nuclear-receptor function." ;

RN [2] RN

RA Torchia J., Rosenfeld M.G.;  
 PL Submitted /APP-1997\ to the EXPD/COMPACT/DBPT databases

AN  
[3]  
RP  
SEQUENCE FROM N.A.

RL Submitted (MAR-1998) to the EMBL/GenBank/DBDJ databases.

DR MGD; MGI:1276535; Ncoa3.

DR Pfam; PF00989; PAS; 1.

SQ SEQUENCE I398 AA; I515/3 MW; EF44E92735816C24 CRC64;

Best Local Similarity 25.9%; Pred. No. 2;

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[illegible]

1291 MGOPPEPAFCRG-SSPPSAMSSPMGPSONAMVCH-----POP-----TPMY

146 SWTRVFSWWDRLGRGSSAPSO 168

1335 D---MKGWPSGNLARNGSFPQQ 1353

Search completed: October 9, 2001, 16:03:21  
Job time: 306 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 9, 2001, 15:59:14 ; Search time 33.29 Seconds  
(without alignments)  
305.943 Million cell updates/sec

Title: 09-580523-lb  
Perfect score: 905  
Sequence: 1 MFQIFEPFSEQEDSSAER.....RVFQSWDRNLGRGSSAPSQ 168

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues  
Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_0601.\*  
1: /SID88/gcgdata/geneseq/geneseq/AA1980.DAT.\*  
2: /SID88/gcgdata/geneseq/geneseq/AA1981.DAT.\*  
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4: /SID88/gcgdata/geneseq/geneseq/AA1983.DAT.\*  
5: /SID88/gcgdata/geneseq/geneseq/AA1984.DAT.\*  
6: /SID88/gcgdata/geneseq/geneseq/AA1985.DAT.\*  
7: /SID88/gcgdata/geneseq/geneseq/AA1986.DAT.\*  
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9: /SID88/gcgdata/geneseq/geneseq/AA1988.DAT.\*  
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12: /SID88/gcgdata/geneseq/geneseq/AA1991.DAT.\*  
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14: /SID88/gcgdata/geneseq/geneseq/AA1993.DAT.\*  
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19: /SID88/gcgdata/geneseq/geneseq/AA1998.DAT.\*  
20: /SID88/gcgdata/geneseq/geneseq/AA1999.DAT.\*  
21: /SID88/gcgdata/geneseq/geneseq/AA2000.DAT.\*  
22: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	902	99.7	168	19	AAW5779 Human Bcl-xL/Bcl-2
2	902	99.7	168	21	AAW13512 Human cell prolif
3	902	99.7	168	22	AAW70368 Human BAD mutant a
4	902	99.7	168	22	AAW48287 Human BAD protein.
5	748	82.7	166	18	AAW32476 BBC6 protein for r
6	646	71.4	162	22	AAW70370 Shorter murine BAD
7	646	71.4	204	17	AAW95168 bcl-x(L)/bcl-2 ass
8	646	71.4	204	19	AAW61315 Murine BCL-XL/BCL-
9	646	71.4	204	19	AAW58832 Murine BAD protein
10	646	71.4	204	22	AAW70369 Longer murine BAD
11	643	71.0	204	19	AAW61317 Mutant BCL-XL/BCL-

12	640	70.7	204	19	AAW61316	Mutant BCL-XL/BCL-
13	640	70.7	204	19	AAW61318	Mutant BCL-XL/BCL-
14	311	34.4	59	19	AAW61319	Mutant BCL-XL/BCL-
15	311	34.4	59	19	AAW61320	Mutant BCL-XL/BCL-
16	308	34.0	59	19	AAW61321	Mutant BCL-XL/BCL-
17	305	33.7	59	19	AAW61322	Mutant BCL-XL/BCL-
18	159	17.6	56	21	AAW61322	Mutant BCL-XL/BCL-
19	130	14.4	26	21	AAW96321	Mammalian Bad Bcl-
20	130	14.4	26	22	AAW70371	BAD BH3 consensus
21	117.5	13.0	27	21	AAW70371	Bcl2 polypeptide B
22	113	12.5	23	17	AAW95166	bcl-x(L)/bcl-2 ass
23	111	12.3	26	21	AAW37001	Bcl2 polypeptide B
24	111	12.3	26	21	AAW37002	Bcl2 polypeptide B
25	111	12.3	27	21	AAW37056	Bcl2 polypeptide B
26	111	12.3	28	21	AAW37055	Bcl2 polypeptide B
27	97	10.7	2510	16	AAW71007	Human neuronal cal
28	97	10.7	2510	21	AAW10579	Human calcium chan
29	96.5	10.7	1182	20	AAW33496	Human SCA6 protein
30	95.5	10.6	395	21	AAW91951	Human cytoskeleton
31	94.5	10.4	1447	20	AAW81029	Murine PCIP protei
32	94.5	10.4	1726	17	AAW00385	Truncated Plasmodi
33	94	10.4	1931	13	AAW27649	Human calcium chan
34	93.5	10.3	549	21	AAW84901	A human proliferat
35	90.5	10.0	393	19	AAW37149	Murine Ena-Vasp li
36	90	9.9	434	17	AAW96420	Peptide fragment o
37	90	9.9	434	21	AAW12821	Human N-type calci
38	90	9.9	2237	16	AAW71006	Human neuronal cal
39	90	9.9	2237	19	AAW63142	Human calcium chan
40	90	9.9	2237	21	AAW10573	Human calcium chan
41	90	9.9	2337	19	AAW37878	Human calcium chan
42	90	9.9	2339	14	AAW33549	Sequence of the al
43	90	9.9	2339	16	AAW71005	Human neuronal cal
44	90	9.9	2339	19	AAW63141	Human calcium chan
45	90	9.9	2339	21	AAW10572	Human calcium chan

ALIGNMENTS

RESULT 1  
AAW5779 AAW55779 standard; Protein: 168 AA.  
XX  
AC AAW5779;  
XX  
DT 17-JUL-1998 (first entry)  
XX  
DE Human Bcl-xL/Bcl-2 associated death promoting polypeptide.  
XX  
KW Human; Bcl-xL/Bcl-2 associated death promoting polypeptide; Bad;  
KW programmed cell death; apoptosis.  
XX  
OS Homo sapiens.  
XX  
PN WO9812328-A2.  
XX  
PD 26-MAR-1998.  
XX  
PF 18-SEP-1997; 97WO-US16991.  
XX  
PR 20-SEP-1996; 96US-0717123.  
XX  
PA (IDUN-) IDUN PHARM INC.  
XX  
PI Horne WA, Oltersdorf T;  
XX  
DR WPI; 1998-217267/19.  
DR N-PSDB; AAW25877.  
XX  
PT Bad gene mediating apoptosis - used to develop products for treating  
PT e.g. neurodegenerative disease, cancers or autoimmune disease  
XX  
PS Claim 8; Fig 1; 41pp; English.

XX The present sequence is the human Bcl-XL/Bcl-2 associated  
 CC death promoting polypeptide, Bad, the binding of which to Bcl-XL  
 CC results in the induction of programmed cell death, i.e. apoptosis.  
 CC Bad can be used in screening assays for compounds to treat or  
 CC prevent diseases characterised by apoptotic cell death, such as  
 CC neurodegenerative disorders, e.g. Alzheimer's and Parkinson's  
 CC disease, amyotrophic lateral sclerosis, retinitis pigmentosa and  
 CC cerebellar degeneration, and myelodysplastic syndromes, e.g.  
 CC aplastic anaemia and ischaemic injury including myocardial  
 CC infarction, stroke and reperfusion injury. Assays can also be  
 CC used to obtain apoptosis enhancing compounds to treat or prevent  
 CC diseases characterised by the loss of apoptotic cell death, such as  
 CC cancers, e.g. lymphoma and hormone dependent tumours, autoimmune  
 CC diseases, e.g. systemic lupus erythematosus and immune-mediated  
 CC glomerulonephritis and viral infections, e.g. herpesvirus,  
 CC poxvirus or adenovirus infection. Bad can also be used for  
 CC detection and diagnosis.  
 XX  
 SQ Sequence 168 AA;

Query Match 99.7%; Score 902; DB 19; Length 168;  
 Best Local Similarity 99.4%; Pred. No. 7.2e-88;  
 Matches 167; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFQIPFEPSEQEDSSAERGLGSPAGDPSGSGKHHRQAPGLLDASHHQEQPTSSSH 60  
 |||  
 DB 1 mfiqipefepseqedsssaerglpspagdpsgskhhrqapglldashhqeqptsssh 60  
 |||

QY 61 HGAGAGAVEIRSRHSSYPAGTDEDEGMGEPPSPRGRSRAPPNLWAAQRYGRELRMADE 120  
 |||  
 DB 61 hgagagaveirsrhssypagteddegmgeepsprgrsrsappnlwaaqrygrelrmsde 120  
 |||

QY 121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWDRNLGRGSSAPSQ 168  
 |||  
 DB 121 fvdskkglprpksgatqmrqssswtrvfqswdrnlgrgssapsq 168  
 |||

RESULT 2  
 AAB13512  
 ID AAB13512 standard; protein; 168 AA.  
 XX  
 AC AAB13512;  
 XX  
 XX  
 DT 02-NOV-2000 (first entry)  
 XX  
 XX Human cell proliferation protein APOP-1.  
 XX  
 XX Human; cell proliferation; APOP-1; cancer; inflammation; infection;  
 KW trauma; neurodegenerative disease; ischaemic injury; wasting disease.  
 KW  
 XX Homo sapiens.  
 XX  
 XX US6080847-A.  
 XX  
 XX 27-JUN-2000.  
 XX  
 XX 04-DEC-1997; 97US-0985335.  
 XX  
 XX 04-DEC-1997; 97US-0985335.  
 XX  
 XX (INCY-) INCYTE PHARM INC.  
 XX  
 XX Corley NC, Hillman JL, Yue H, Lal P, Shah P;  
 XX  
 XX WPI; 2000-451230/39.  
 DR N-PSDB; AAA63332.  
 XX  
 XX Novel polynucleotide and polypeptide sequences of proteins associated  
 PT with cell proliferation for diagnosis, prevention and treatment of e.g.  
 PT cancer, acquired immunodeficiency syndrome, and Parkinson's disease.  
 XX

PS Example 8; Fig 1; 58pp; English.  
 XX

The present sequence is the human APOP-1 protein. This protein, which  
 CC shares structural and chemical homology with Bcl-2, is involved in cell  
 CC proliferation. Its coding sequence was isolated by screening a synovial  
 CC tissue cDNA library using a computer search for amino acid sequence  
 CC alignments. The gene and protein can be used in the treatment of various  
 CC cancers, disorders with associated inflammation such as Addison's  
 CC disease, adult respiratory distress syndrome, allergies, anaemia, asthma,  
 CC atherosclerosis, Crohn's disease, ulcerative colitis, diabetes mellitus,  
 CC emphysema, glomerulonephritis, gout, Graves' disease, irritable bowel  
 CC syndrome, lupus erythematosus, multiple sclerosis, myasthenia gravis,  
 CC myocardial or pericardial inflammation, osteoporosis, rheumatoid  
 CC arthritis, Sjogren's syndrome and autoimmune thyroiditis, complications  
 CC of cancer, haemodialysis and extracorporeal circulation, infections,  
 CC trauma, disorders with associated apoptosis including AIDS and other  
 CC infectious and genetic immunodeficiencies, neurodegenerative diseases  
 CC such as Alzheimer's disease and Parkinson's disease, ischaemic injuries  
 CC such as myocardial infarction, and wasting diseases including cachexia.  
 XX  
 SQ Sequence 168 AA;

Query Match 99.7%; Score 902; DB 21; Length 168;  
 Best Local Similarity 99.4%; Pred. No. 7.2e-88;  
 Matches 167; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFQIPFEPSEQEDSSAERGLGSPAGDPSGSGKHHRQAPGLLDASHHQEQPTSSSH 60  
 |||  
 DB 1 mfiqipefepseqedsssaerglpspagdpsgskhhrqapglldashhqeqptsssh 60  
 |||

QY 61 HGAGAGAVEIRSRHSSYPAGTDEDEGMGEPPSPRGRSRAPPNLWAAQRYGRELRMADE 120  
 |||  
 DB 61 hgagagaveirsrhssypagteddegmgeepsprgrsrsappnlwaaqrygrelrmsde 120  
 |||

QY 121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWDRNLGRGSSAPSQ 168  
 |||  
 DB 121 fvdskkglprpksgatqmrqssswtrvfqswdrnlgrgssapsq 168  
 |||

RESULT 3  
 AAB70368  
 ID AAB70368 standard; protein; 168 AA.  
 XX  
 AC AAB70368;  
 XX  
 DT 02-MAY-2001 (first entry)  
 XX  
 XX Human BAD mutant amino acid sequence SEQ ID NO:1.  
 DE  
 XX Bcl-XL/Bcl-2 associated cell death regulator; BAD; mutant; apoptosis;  
 KW immunostimulant; neuroprotective; nootropic; antiischaemic; vulnerability;  
 KW cytostatic; antiviral; antiarthritic; antiinflammatory; wound healing;  
 KW immunosuppressive; apoptosis inducer; apoptosis inhibitor; cancer;  
 KW immunodeficiency disease; neurodegenerative disease; viral infection;  
 KW ischaemic cell death; reperfusion cell death; arthritis; infertility;  
 KW lymphoproliferative condition; inflammation; autoimmune disease.  
 XX  
 XX Homo sapiens.  
 OS  
 OS Synthetic.  
 XX  
 XX WO200110888-A1.  
 XX  
 XX 15-FEB-2001.  
 XX  
 XX 30-MAY-2000; 2000WO-US11864.  
 PF  
 XX 28-MAY-1999; 99US-0136783.  
 PR  
 XX (APOP-) APOPTOSIS TECHNOLOGY INC.  
 XX  
 XX Zhou X;  
 PI  
 XX

DR WPI; 2001-138734/14.  
 XX New mutant Bcl-XL/Bcl-2 Associated Cell Death Regulator polypeptide,  
 PT useful for screening for candidate compounds which induce or inhibit  
 PT apoptosis, comprises amino acid substitutions at Ser118, Ser155 or  
 PT Ser113 -  
 XX  
 PS Claim 1; Page 147; 157pp; English.  
 XX  
 CC The present invention describes an isolated or synthetic polypeptide  
 CC (I) comprising a less than full length amino acid sequence of a mutant  
 CC Bcl-XL/Bcl-2 associated cell death regulator polypeptide (BAD) or its  
 CC fragment, which contains amino acid substitutions at Ser118 of a human  
 CC BAD, Ser155 of a murine BAD (longer murine BAD) or Ser113 of a murine  
 CC BAD (shorter murine BAD). (I) has immunostimulant, neuroprotective,  
 CC neurotropic, antiischaemic, vulnerary, cytostatic, antiviral,  
 CC antiarthritic, antiinflammatory and immunosuppressive activities, and  
 CC can be used as an apoptosis inducer or inhibitor. BAD polypeptides and  
 CC polynucleotides can be used for screening candidate compounds and drugs  
 CC for activity that promote cell survival or apoptosis. Other uses include  
 CC inducing or inhibiting apoptosis in a cell. Candidate compounds  
 CC identified and (mutant) BAD polypeptides are useful in treating  
 CC immunodeficiency diseases, neurodegenerative diseases, ischaemic cell  
 CC death, reperfusion cell death, wound healing, cancer, viral infections,  
 CC lymphoproliferative conditions, arthritis, infertility, inflammation and  
 CC autoimmune diseases. The present sequence represents a specifically  
 CC claimed human BAD mutant amino acid sequence from the present invention.  
 XX  
 SQ Sequence 168 AA;

Query Match 99.7%; Score 902; DB 22; Length 168;  
 Best Local Similarity 99.4%; Pred. No. 7.2e-88;  
 Matches 167; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 MFQIPEFPEPSEQEDSSAERGLGSPAGDGFSGGKHHRQAPGLLWDASHQOQPTSSSH 60  
 Db 1 mfiqipefepseqedsssaerglgpspagdgpsgkhhrrqapglldashhqeptsssh 60  
 Qy 61 HGGAGAVIRSRHSSYPAGTDEGCMGEEPSPFRCGRSRAPPNLWAAQRYGRELRRMADE 120  
 Db 61 hggagavairsrhssypagtdedgmgeepspfrgrsrappnlwaaqrygrellrmsde 120  
 Qy 121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWMDRNLGRGSSAPSQ 168  
 Db 121 fvdskfkgllprpkasagtatmrqssswtrvfgswdrnlgrgssapsq 168

RESULT 4  
 AAB48287  
 ID AAB48287 standard; protein; 168 AA.  
 AC AAB48287;  
 XX  
 DT 02-APR-2001 (first entry)  
 XX Human Bad protein.  
 DE  
 KW S-phase kinase associated protein; SKP1; SKP2; SKP2-like protein; ZF;  
 KW CUL-1; cullin; CDC53; p27; cyclin E; Max; Mad; c-Myc; MDM2; p53; Bax;  
 KW Bad; Bcl-2; tumour; cytostatic.  
 XX  
 OS Homo sapiens.  
 XX WO200075184-A1.  
 PN 14-DEC-2000.  
 XX  
 PF 05-JUN-2000; 2000WO-USI5449.  
 XX  
 PR 04-JUN-1999; 99US-0137494.  
 XX  
 PA (UYVA ) UNIV YALE.

XX Zhang H, Tsvetkov LM, Kondo T;  
 PI WPI; 2001-061703/07.  
 DR N-PSDB; AAC84599.  
 DR  
 XX Modulating polypeptide levels in a cell, diagnosing and treating tumor,  
 PT involves altering levels of proteins such as S-phase kinase associated  
 PT proteins 1, 2 and cullin/CDC53 proteins -  
 XX  
 PS Claim 5; Page 102-103; 162pp; English.  
 XX  
 CC The invention relates to methods of altering the polypeptide levels in a  
 CC cell, using proteins selected from S-phase kinase associated proteins 1  
 CC and 2 (SKP1, SKP2), SKP2-like proteins (ZF) and CUL-1 (a member of the  
 CC cullin/CDC53 family of proteins). The method is useful for altering the  
 CC level of p27, cyclin E, Max, Mad, c-Myc, MDM2, p53, Bax, Bad or Bcl-2  
 CC polypeptide in a cell. SKP2 and SKP2-like protein levels are useful for  
 CC detecting tumours, and in monitoring tumor treatment in a mammal. Agents  
 CC that modulate interactions between SKP and target proteins are useful for  
 CC treating tumours.  
 XX  
 SQ Sequence 168 AA;  
 Query Match 99.7%; Score 902; DB 22; Length 168;  
 Best Local Similarity 99.4%; Pred. No. 7.2e-88;  
 Matches 167; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 MFQIPEFPEPSEQEDSSAERGLGSPAGDGFSGGKHHRQAPGLLWDASHQOQPTSSSH 60  
 Db 1 mfiqipefepseqedsssaerglgpspagdgpsgkhhrrqapglldashhqeptsssh 60  
 Qy 61 HGGAGAVIRSRHSSYPAGTDEGCMGEEPSPFRCGRSRAPPNLWAAQRYGRELRRMADE 120  
 Db 61 hggagavairsrhssypagtdedgmgeepspfrgrsrappnlwaaqrygrellrmsde 120  
 Qy 121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWMDRNLGRGSSAPSQ 168  
 Db 121 fvdskfkgllprpkasagtatmrqssswtrvfgswdrnlgrgssapsq 168

RESULT 5  
 AAW32476  
 ID AAW32476 standard; Protein; 166 AA.  
 XX  
 AC AAW32476;  
 XX  
 DT 15-JAN-1998 (first entry)  
 XX BBC6 protein for regulating cell death.  
 DE  
 DE BBC6 gene; cell death; cell cycle; Bcl2; human.  
 KW  
 XX Homo sapiens.  
 OS  
 XX US5663316-A.  
 PN  
 XX 02-SEP-1997.  
 PD  
 XX 18-JUN-1996; 96US-0665617.  
 PF  
 XX 18-JUN-1996; 96US-0665617.  
 PR  
 XX (CLON-) CLONTECH LAB INC.  
 PA  
 XX Xudong Y;  
 PI  
 XX WPI; 1997-447980/41.  
 DR N-PSDB; AAT91561.  
 DR  
 XX Isolated BBC6 gene - encodes a protein that regulates cell death  
 PT through interaction with Bcl-2  
 PT

XX PS Claim 1; Column 11-12; 7pp; English.

XX CC The present sequence represents a protein of 166 amino acids. The

CC sequence is disclosed as being a protein called BBC6 which regulates

CC cell death through interaction with Bcl-2. The DNA may be used for the

CC production of the recombinant protein, which can be used in unspecified

CC therapeutic or diagnostic procedures, as a molecular weight marker, and

CC to raise antibodies that can be used in unspecified diagnostic or

CC therapeutic applications and to reduce or eliminate the biological

CC activity of the BBC6 protein in vivo.

XX SQ Sequence 166 AA;

Query Match 82.7%; Score 748; DB 18; Length 166;

Best Local Similarity 83.4%; Pred. No. 1.5e-71;

Matches 146; Conservative 4; Mismatches 9; Indels 16; Gaps 3;

QY 1 MFQIPFEPSEQEDSSAERGLGSPAGDPSGSGKHHRQAPG-----LLWDASHQOE 53

DB 1 mfgipefepseqedsssaerg-wrspagtp-----qapasliarpqvlwdashqge 51

QY 54 OPTSSSHHGAGAVEIRSRHSSYPAGTDEDEGMGEPSFRCGRSAPPNLWAAQRYGRE 113

DB 52 qptssshhgagaveirsrhssypagtdedegmgeepsfrcgrarpppnlwaaqrygre 111

QY 114 LRRMADEFVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWMDNLGRGSSAPSQ 168

DB 112 lrmsdefvdsfkkgprpksagatqmrqssswtrvfqswmdnlgrgtaapsg 166

RESULT 6

AAB70370

ID AAB70370 standard; protein; 162 AA.

XX AC AAB70370;

XX DT 02-MAY-2001 (first entry)

XX DE Shorter murine BAD mutant amino acid sequence SEQ ID NO:3.

XX KW Bcl-XL/Bcl-2 associated cell death regulator; BAD; mutant; apoptosis;

XX KW immunostimulant; neuroprotective; nontropic; antiischaemic; vulnary;

XX KW cytostatic; antiviral; antiarthritic; antiinflammatory; wound healing;

XX KW immunosuppressive; apoptosis inducer; apoptosis inhibitor; cancer;

XX KW immunodeficiency disease; neurodegenerative disease; viral infection;

XX KW ischaemic cell death; reperfusion cell death; arthritis; infertility;

XX KW lymphoproliferative condition; inflammation; autoimmune disease.

XX OS Mus musculus.

XX OS Synthetic.

XX PN WO200110888-A1.

XX PD 15-FEB-2001.

XX PF 30-MAY-2000; 2000WO-US11864.

XX PR 28-MAY-1999; 99US-0136783.

XX PA (APOB-) APOPTOSIS TECHNOLOGY INC.

XX PI Zhou X;

XX DR WPI; 2001-138734/14.

XX PT New mutant Bcl-XL/Bcl-2 Associated Cell Death Regulator polypeptide,

XX PT useful for screening for candidate compounds which induce or inhibit

XX PT apoptosis, comprises amino acid substitutions at Ser118, Ser155 or

XX PT Ser113 -

XX PS Claim 7; Page 148-149; 157pp; English.

XX CC The present invention describes an isolated or synthetic polypeptide

CC (I) comprising a less than full length amino acid sequence of a mutant

CC Bcl-XL/Bcl-2 associated cell death regulator polypeptide (BAD) or its

CC fragment, which contains amino acid substitutions at Ser118 of a human

CC BAD, Ser155 of a murine BAD (longer murine BAD) or Ser113 of a murine

CC BAD (shorter murine BAD). (I) has immunostimulant, neuroprotective,

CC nontropic, antiischaemic, vulnary, cytostatic, antiviral,

CC antiarthritic, antiinflammatory and immunosuppressive activities, and

CC can be used as an apoptosis inducer or inhibitor. BAD polypeptides and

CC polynucleotides can be used for screening candidate compounds and drugs

CC for activity that promote cell survival or apoptosis. Other uses include

CC inducing or inhibiting apoptosis in a cell. Candidate compounds

CC identified and (mutant) BAD polypeptides are useful in treating

CC immunodeficiency diseases, neurodegenerative diseases, ischaemic cell

CC death, reperfusion cell death, wound healing, cancer, viral infections,

CC lymphoproliferative conditions, arthritis, infertility, inflammation and

CC autoimmune diseases. The present sequence represents a specifically

CC claimed shorter murine BAD mutant amino acid sequence from the present

CC invention.

XX SQ Sequence 162 AA;

Query Match 71.4%; Score 646; DB 22; Length 162;

Best Local Similarity 75.0%; Pred. No. 9e-61;

Matches 126; Conservative 13; Mismatches 23; Indels 6; Gaps 3;

QY 1 MFQIPFEPSEQEDSSAERGLGSPAGDPSGSGKHHRQAPGLWDASHQOEQPTSSSH 60

DB 1 mfgipefepseqedssatdrglpsitedqp---gpy---lapglgsnhqggraatnsh 55

QY 61 HGCAGAVEIRSRHSSYPAGTDEDEGMGEPSFRCGRSAPPNLWAAQRYGRELRMADE 120

DB 56 hggagameitrshssypagteedegmeeisfgrsrsappnlwaaqrygrelrmsde 115

QY 121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWMDNLGRGSSAPSQ 168

DB 116 fegsf-kglprpksagatqmrqsgwtrliqswdnlgrkggstpsq 162

RESULT 7

AAR95168

ID AAR95168 standard; Protein; 204 AA.

XX AC AAR95168;

XX DT 06-JAN-1997 (first entry)

XX DE bcl-x(L)/bcl-2 associated death promoter protein.

XX KW Epitope; murine; bcl-x(L)/bcl-2 associated death promoter; Bad; stroke;

XX KW polypeptide; bcl-x; cell death; regulate; BH1; BH2; apoptotic cell death;

XX KW cytokine deprivation; IL-3 dependent cell line; immunodeficiency; AIDS;

XX KW neurodegenerative disease; senescence; ischaemia; neoplasia.

XX OS Mus musculus.

XX FH Location/Qualifiers

XX FT 147..149

XX FT /note= "BH1 conserved amino acids"

XX FT 191..192

XX FT /note= "BH2 conserved amino acids"

XX FT 38..61

XX FT /note= "PEST sequence"

XX FT 111..130

XX FT /note= "PEST sequence"

XX PN WO9613614-A1.

XX PD 09-MAY-1996.

XX PF 31-OCT-1995; 95WO-US14246.

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XX PR 31-OCT-1994;    94US-0333565.
XX PA (UNIW ) UNIV WASHINGTON.
XX PI Korsmeyer SJ;
XX DR WPI; 1996-251465/25.
XX DR N-PSDB; AAT29479.
XX PT Polynucleotide encoding bcl-x(L)/bcl-2 associated death promoter -
XX PT useful to treat neoplasia and apoptosis and to identify agents
XX PT inhibiting its binding to bcl-2 or bcl-x(L) to form heterodimers
XX PS Claim 3; Fig 1; 130pp; English.
XX CC This sequence represents the murine bcl-x(L)/bcl-2 associated death
XX CC promoter (Bad) gene. Bad is a 22.1 kD protein which interacts with
XX CC bcl-2 and bcl-x proteins and regulates cell death. It has homology
XX CC to the bcl-2-related family clustered in the BHI and BH2 domain. Bad
XX CC has been found to hybridise to bcl-x(L) and bcl-2 in yeast two-hybrid
XX CC assays and in vivo in mammalian cells. Overexpressed Bad counters the
XX CC death inhibitory activity of bcl-x(L), but is much less effective at
XX CC countering the death inhibitory activity of bcl-2. Bad expression can
XX CC accelerate apoptotic cell death induced by cytokine deprivation in an
XX CC IL-3 dependent cell line expressing bcl-x(L), and its also counters the
XX CC death repressor activity of bcl-x(L). Bad competes with Bax for binding
XX CC to bcl-x(L). Bad may be used to identify agents which inhibit its
XX CC binding to bcl-2 or bcl-x(L) to form heterodimers. Such agents may be
XX CC used to treat neurodegenerative diseases, immunodeficiency diseases,
XX CC e.g. AIDS, senescence or ischaemia.
XX SQ Sequence      204 AA;

Query Match          71.4%; Score 646; DB 17; Length 204;
Best Local Similarity 75.0%; Pred. No. 1.2e-60;
Matches 126; Conservative 13; Mismatches 23; Indels 6; Gaps

QY 1 MFQIPEFEPSEQEDSSAERGLGPGAGDGPSGGKHHRQAQGLLWDASHHQEQPTSSSH 60
Db | | | | | | | | | | : | | | | | | | | | | : | | | | | | | | | | : | | |
43 mfpqipefepseqedasatdrglgsitedqp---gpy--lagpllgslnhqggraatnsh 97

QY 61 HGAGAVEIRSRHSSYPAGTDEDEGHGEPPSPFRGRSAPPNLWAAQRYGRELRMADE 120
Db | | | | | | | | | | : | | | | | | | | | | : | | | | | | | | | | : | | |
98 hggagameptrrhssypagteedegmeeeelspfrgrsappnlwaaqrygrelrmsde 157

QY 121 FVDSFKKGLPRKSAGTATOMROSSSWTRVFQSWMDNLRGCSAPSAPSQ 168
Db | | | | | | | | | | : | | | | | | | | | | : | | | | | | | | | | : | | |
158 fegsf-kglprksagtatmrdsagwtvrlldswdrnlgkggstpsq 204

RESULT      8
AAW61315
ID AAW61315 standard; Protein; 204 AA.
XX AC AAW61315;
XX DT
XX DE Murine BCL-XL/BCL-2 associated cell death regulator.
KW Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein
KW serine substituted mutant; apoptosis; cancer; viral infection.
OS Mus sp.
XX PN WO9817682-A1.
XX PD
XX PF 30-APR-1998.
XX PF 17-OCT-1997;   97WO-US19175.
XX
```

KW cancer, viral infection; lymphoproliferative condition; arthritis;  
KW inflammation; autoimmune diseases.  
OS Mus sp.  
PN WO9809643-A1.  
PD 12-MAR-1998.  
XX 97WO-US15871.  
XX 09-SEP-1997;  
XX 09-SEP-1996;  
XX 96US-0707868.  
XX (UNIV ) UNIV WASHINGTON.  
PA Kormeyer SJ;  
PI WPI; 1998-207049/18.  
XX Serine-phosphorylated Bcl-X-L/Bcl-2 Associated cell Death regulator  
XX polypeptide - useful for modulation of apoptosis associated with,  
XX e.g. cancer and immunodeficiency diseases  
PS Claim 3; Fig 8: 61pp; English.  
XX This sequence represents a novel serine-phosphorylated protein, BAD  
CC (Bcl-XL/Bcl-2 associated cell death regulator). The serine residue is  
CC phosphorylated in a post-translational modification and allows binding  
CC to the 14-3-3 protein which is a signal transduction regulator.  
CC Modulators of phosphorylated BAD, which act through inhibition/activation  
CC of a phosphoserine phosphatase, are useful for preventing/treating  
CC increased/decreased apoptosis in a cell. The increased apoptosis may  
CC result from immunodeficiency diseases, senescence, neurodegenerative  
CC disease, ischaemic cell death, reperfusion cell death, infertility and  
CC wound-healing. Decreased apoptosis may result from cancer, viral  
CC infection, lymphoproliferative conditions, arthritis, infertility,  
CC inflammation and autoimmune diseases. Measuring the amount of  
CC phosphorylated compared to unphosphorylated BAD polypeptide and/or total  
CC BAD in a cell is useful for determining the apoptotic state of a cell.  
XX Sequence 204 AA;  
SQ  
Query Match 71.4%; Score 646; DB 19; Length 204;  
Best Local Similarity 75.0%; Pred. No. 1.2e-60;  
Matches 126; Conservative 13; Mismatches 23; Indels 6; Gaps 3;  
QY 1 MFOIPEFEPSEQEDSSAERGLGPGDPGSGKHRRQAPGLLWDASHQEQPTSSSH 60  
DB 43 mfiqpefepsegedasatdrglgsitedqp---gpy--lapglgslnhqggraatsnsh 97  
QY 61 HGAGAVEITRSRHSSYPAGTDEDEGMGEPSPPFRGRSRAPPNLAQRYGRELRRMADE 120  
DB 98 hggagamestrshssypagteedegmeelspfgrsrappnlwaqrygrellrmsde 157  
QY 121 FVDSFKKGLPRPKSAGTATQMRQSSWTRVFQSWDNRNLGRGSSAPQS 168  
DB 158 fegsf-kglprksagtatqmrqsagwtlrlqswdrnlrgkggstpsq 204  
RESULT 10  
ID AAB70369  
XX AAB70369 standard; protein; 204 AA.  
AC AAB70369;  
XX 02-MAY-2001 (first entry)  
DT Longer murine BAD mutant amino acid sequence SEQ ID NO:2.  
DE Bcl-XL/Bcl-2 associated cell death regulator; BAD; mutant; apoptosis;  
KW immunostimulant; neuroprotective; nootropic; antiischaemic; vulnerary;  
KW cyostatic; antiviral; antiarthritic; antiinflammatory; wound healing;

KW immunosuppressive; apoptosis inducer; apoptosis inhibitor; cancer;  
KW immunodeficiency disease; neurodegenerative disease; viral infection;  
KW ischaemic cell death; reperfusion cell death; arthritis; infertility;  
KW lymphoproliferative condition; inflammation; autoimmune disease.  
XX Mus musculus.  
OS Synthetic.  
XX WO200110888-A1.  
XX 15-FEB-2001.  
XX 30-MAY-2000; 2000WO-US11864.  
XX 28-MAY-1999; 99US-0136783.  
XX (APOP-) APOPTOSIS TECHNOLOGY INC.  
XX Zhou X;  
XX WPI; 2001-138734/14.  
XX New mutant Bcl-XL/Bcl-2 Associated Cell Death Regulator polypeptide,  
XX useful for screening for candidate compounds which induce or inhibit  
XX apoptosis, comprises amino acid substitutions at Ser118, Ser155 or  
XX Ser113 -  
XX Claim 4; Page 148; 157pp; English.  
XX The present invention describes an isolated or synthetic polypeptide  
XX (I) comprising a less than full length amino acid sequence of a mutant  
XX Bcl-XL/Bcl-2 associated cell death regulator polypeptide (BAD) or its  
XX fragment, which contains amino acid substitutions at Ser118 of a human  
XX BAD, Ser155 of a murine BAD (longer murine BAD) or Ser113 of a murine  
XX BAD (shorter murine BAD). (I) has immunostimulant, neuroprotective,  
XX nootropic, antiischaemic, vulnerary, cyostatic, antiviral,  
XX antiarthritic, antiinflammatory and immunosuppressive activities, and  
XX can be used as an apoptosis inducer or inhibitor. BAD polypeptides and  
XX polynucleotides can be used for screening candidate compounds and drugs  
XX for activity that promote cell survival or apoptosis. Other uses include  
XX inducing or inhibiting apoptosis in a cell. Candidate compounds  
XX identified and (mutant) BAD polypeptides are useful in treating  
XX immunodeficiency diseases, neurodegenerative diseases, ischaemic cell  
XX death, reperfusion cell death, wound healing, cancer, viral infections,  
XX lymphoproliferative conditions, arthritis, infertility, inflammation and  
XX autoimmune diseases. The present sequence represents a specifically  
XX claimed longer murine BAD mutant amino acid sequence from the present  
XX invention.  
XX Sequence 204 AA;  
SQ  
Query Match 71.4%; Score 646; DB 22; Length 204;  
Best Local Similarity 75.0%; Pred. No. 1.2e-60;  
Matches 126; Conservative 13; Mismatches 23; Indels 6; Gaps 3;  
QY 1 MFOIPEFEPSEQEDSSAERGLGPGDPGSGKHRRQAPGLLWDASHQEQPTSSSH 60  
DB 43 mfiqpefepsegedasatdrglgsitedqp---gpy--lapglgslnhqggraatsnsh 97  
QY 61 HGAGAVEITRSRHSSYPAGTDEDEGMGEPSPPFRGRSRAPPNLAQRYGRELRRMADE 120  
DB 98 hggagamestrshssypagteedegmeelspfgrsrappnlwaqrygrellrmsde 157  
QY 121 FVDSFKKGLPRPKSAGTATQMRQSSWTRVFQSWDNRNLGRGSSAPQS 168  
DB 158 fegsf-kglprksagtatqmrqsagwtlrlqswdrnlrgkggstpsq 204  
RESULT 11  
ID AAW61317  
XX AAW61317 standard; Protein; 204 AA.



AC AAW61317;  
XX 07-OCT-1998 (first entry)  
XX Mutant BCL-XL/BCL-2 associated cell death regulator #2.  
XX Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein;  
KW serine substituted mutant; apoptosis; cancer; viral infection.  
XX  
XX Mus sp.  
OS Synthetic.  
XX WO9817682-A1.  
PN 30-APR-1998.  
PD 17-OCT-1997; 97WO-US19175.  
PF 18-OCT-1996; 96US-0733505.  
XX (UNIW ) UNIV WASHINGTON.  
XX Korsmeyer SJ;  
XX  
XX WPI; 1998-261422/23.  
DR N-PSDB; AAV27835.  
XX New mutant BAD polypeptide with phosphorylatable serine replaced -  
PT useful for, e.g. treating reduced apoptosis such as in cancer or  
PT viral infection  
XX  
XX Claim 7; Page 60; 95pp; English.  
XX The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell  
CC death regulator) proteins, having an amino acid other than Ser at  
CC position 112 and/or 136, relative to the murine BAD 204 aa sequence. The  
CC present sequence represents a mutant BAD protein. Also described are: (1)  
CC fragments of mutant BAD protein able to decrease cell viability; (2)  
CC fusion proteins of mutant BAD with a heterologous polypeptide that  
CC increases intracellular delivery. Mutant BAD proteins are used to treat  
CC or prevent diseases associated with reduced apoptosis, e.g. cancer,  
CC viral infection, lymphoproliferation, arthritis, infertility,  
CC inflammation and autoimmune disease. Polynucleotide sequences encoding  
CC mutant BAD proteins can be used similarly by gene therapy or to produce  
CC transgenic animals for use as disease models or in drug screening. BAD  
CC proteins phosphorylated at specified Ser are used to screen for enhancers  
CC and inhibitors of serine-phosphatase. Inhibitors are potentially useful  
CC in treatment of excessive apoptosis such as AIDS, neurodegeneration,  
CC aging or ischaemic cell death. The apoptotic status of cells is  
CC determined by measuring relative amounts of phosphorylated and non-  
CC phosphorylated BAD, by usual immunoassays. Mutant BAD proteins have  
CC greater death-promoting activity than wild-type BAD which can become  
CC phosphorylated on the specified Ser, forming a product that does not  
CC heterodimerise with BCL-2 or BCL-XL but instead binds to 14-3-3 family  
CC proteins in the cytosol, thus promoting cell survival. The mutants with  
XX Ser substituted cannot bind 14-3-3.  
XX Sequence 204 AA;  
XX  
XX Query Match 71.0%; Score 643; DB 19; Length 204;  
XX Best Local Similarity 74.4%; Pred. No. 2.5e-60;  
XX Matches 125; Conservative 14; Mismatches 23; Indels 6; Gaps 3;  
QY 1 MFOIPEFPEQEDSSAERGLGSPAGDPSGSGKHHRQAPGLLWDASHHQEQPTSSSH 60  
DB 43 mfiqpefpeqedasatdrglgsitdqp---gpy--lapglglnhgdggraatnsh 97  
QY 61 HGGAGAVIRSHSSYPAGTDECGMEPSFPRGSRSAAPNLWAAORYGRELRRMADE 120  
DB 98 hggagameirshssypagtdeemeelspfgrsraapnlwaaqrgyrellrmsde 157  
QY 121 FVDSFKGLPRPKSAGTATQMRQSSSWTRVFQSWMDRNLGRGSSAPSQ 168

DB 158 fegsf-kglprpksagatqmrqsagwtrilqsdwdrnlkggstpsq 204  
RESULT 12  
AAW61316  
ID AAW61316 standard; Protein; 204 AA.  
XX AAW61316;  
XX 07-OCT-1998 (first entry)  
XX Mutant BCL-XL/BCL-2 associated cell death regulator #1.  
XX Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein;  
KW serine substituted mutant; apoptosis; cancer; viral infection.  
XX  
XX Mus sp.  
OS Synthetic.  
XX WO9817682-A1.  
PN 30-APR-1998.  
PD 17-OCT-1997; 97WO-US19175.  
PF 18-OCT-1996; 96US-0733505.  
XX (UNIW ) UNIV WASHINGTON.  
XX Korsmeyer SJ;  
XX WPI; 1998-261422/23.  
DR N-PSDB; AAV27834.  
XX New mutant BAD polypeptide with phosphorylatable serine replaced -  
PT useful for, e.g. treating reduced apoptosis such as in cancer or  
PT viral infection  
XX  
XX Claim 7; Page 59; 95pp; English.  
XX The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell  
CC death regulator) proteins, having an amino acid other than Ser at  
CC position 112 and/or 136, relative to the murine BAD 204 aa sequence. The  
CC present sequence represents a mutant BAD protein. Also described are: (1)  
CC fragments of mutant BAD protein able to decrease cell viability; (2)  
CC fusion proteins of mutant BAD with a heterologous polypeptide that  
CC increases intracellular delivery. Mutant BAD proteins are used to treat  
CC or prevent diseases associated with reduced apoptosis, e.g. cancer,  
CC viral infection, lymphoproliferation, arthritis, infertility,  
CC inflammation and autoimmune disease. Polynucleotide sequences encoding  
CC mutant BAD proteins can be used similarly by gene therapy or to produce  
CC transgenic animals for use as disease models or in drug screening. BAD  
CC proteins phosphorylated at specified Ser are used to screen for enhancers  
CC and inhibitors of serine-phosphatase. Inhibitors are potentially useful  
CC in treatment of excessive apoptosis such as AIDS, neurodegeneration,  
CC aging or ischaemic cell death. The apoptotic status of cells is  
CC determined by measuring relative amounts of phosphorylated and non-  
CC phosphorylated BAD, by usual immunoassays. Mutant BAD proteins have  
CC greater death-promoting activity than wild-type BAD which can become  
CC phosphorylated on the specified Ser, forming a product that does not  
CC heterodimerise with BCL-2 or BCL-XL but instead binds to 14-3-3 family  
CC proteins in the cytosol, thus promoting cell survival. The mutants with  
XX Ser substituted cannot bind 14-3-3.  
XX Sequence 204 AA;  
XX  
XX Query Match 70.7%; Score 640; DB 19; Length 204;  
XX Best Local Similarity 73.8%; Pred. No. 5.2e-60;  
XX Matches 124; Conservative 15; Mismatches 23; Indels 6; Gaps 3;  
QY 1 MFOIPEFPEQEDSSAERGLGSPAGDPSGSGKHHRQAPGLLWDASHHQEQPTSSSH 60

Db 43 mfiqifepesqedasatdrglpsltedqp---gpy--lapglgslnhqggraatsnsh 97  
QY 61 HGAGAVEIRSRHSSYPAGTDEDEGMEEPSRGRSAPPNLWAAQRYGRELRRMADE 120  
Db 98 hggagametrshsypagteedegmeelsprgrsraappnlwaaqrgygreilrmsde 157  
QY 121 FVDSFKKGLPRPKSAGTATQMRQSSWTRVFQSWDRNLGRGSSAPSQ 168  
Db 158 fegsf-kgiprksagatqmrqsagwtriigswdndnigkggstpsq 204  
RESULT 13  
AAW61318  
ID AAW61318 standard; Protein; 204 AA.  
XX  
AC AAW61318;  
XX  
DT 07-OCT-1998 (first entry)  
XX  
DE Mutant BCL-XL/BCL-2 associated cell death regulator #3.  
XX  
KW Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein;  
KW serine substituted mutant; apoptosis; cancer; viral infection.  
XX  
OS Mus sp.  
OS Synthetic.  
XX  
PN WO9817682-A1.  
XX  
PD 30-APR-1998.  
XX  
PF 17-OCT-1997; 97WO-US19175.  
XX  
PR 18-OCT-1996; 96US-0733505.  
XX  
PA (UNIW ) UNIV WASHINGTON.  
XX  
PI Korsmeyer SJ;  
XX  
DR WPI; 1998-261422/23.  
DR N-PSDB; AAV27836.  
XX  
PT New mutant BAD polypeptide with phosphorylatable serine replaced -  
PT useful for, e.g. treating reduced apoptosis such as in cancer or  
PT viral infection  
XX  
PS Claim 7; Page 60-61; 95pp; English.  
XX  
CC The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell  
CC death regulator) proteins, having an amino acid other than Ser at  
CC position 112 and/or 136, relative to the murine BAD 204 aa sequence. The  
CC present sequence represents a mutant BAD protein. Also described are: (1)  
CC fragments of mutant BAD protein able to decrease cell viability; (2)  
CC fusion proteins of mutant BAD with a heterologous polypeptide that  
CC increases intracellular delivery. Mutant BAD proteins are used to treat  
CC or prevent diseases associated with reduced apoptosis, e.g. cancer,  
CC viral infection, lymphoproliferation, arthritis, infertility,  
CC inflammation and autoimmune disease. Polynucleotide sequences encoding  
CC mutant BAD proteins can be used similarly by gene therapy or to produce  
CC transgenic animals for use as disease models or in drug screening. BAD  
CC proteins phosphorylated at specified Ser are used to screen for enhancers  
CC and inhibitors of serine-phosphatase. Inhibitors are potentially useful  
CC in treatment of excessive apoptosis such as AIDS, neurodegeneration,  
CC aging or ischaemic cell death. The apoptotic status of cells is  
CC determined by measuring relative amounts of phosphorylated and non-  
CC phosphorylated BAD, by usual immunoassays. Mutant BAD proteins have  
CC greater death-promoting activity than wild-type BAD which can become  
CC phosphorylated on the specified Ser, forming a product that does not  
CC heterodimerise with BCL-2 or BCL-XL but instead binds to 14-3-3 family  
CC proteins in the cytosol, thus promoting cell survival. The mutants with  
CC Ser substituted cannot bind 14-3-3.  
XX

SQ Sequence 204 AA;  
Query Match 70.7%; Score 640; DB 19; Length 204;  
Best Local Similarity 73.8%; Pred. No. 5.2e-60;  
Matches 124; Conservative 15; Mismatches 23; Indels 6; Gaps 3;  
QY 1 MFOIPFEPSEQEDSSAERGLSPAGDGPSSGKHROAPGLLWDASHOQBQPTSSSH 60  
Db 43 mfiqifepesqedasatdrglpsltedqp---gpy--lapglgslnhqggraatsnsh 97  
QY 61 HGAGAVEIRSRHSSYPAGTDEDEGMEEPSRGRSAPPNLWAAQRYGRELRRMADE 120  
Db 98 hggagametrshsypagteedegmeelsprgrsraappnlwaaqrgygreilrmsde 157  
QY 121 FVDSFKKGLPRPKSAGTATQMRQSSWTRVFQSWDRNLGRGSSAPSQ 168  
Db 158 fegsf-kgiprksagatqmrqsagwtriigswdndnigkggstpsq 204  
RESULT 14  
AAW61319  
ID AAW61319 standard; Protein; 59 AA.  
XX  
AC AAW61319;  
XX  
DT 07-OCT-1998 (first entry)  
XX  
DE Mutant BCL-XL/BCL-2 associated cell death regulator #4.  
XX  
KW Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein;  
KW serine substituted mutant; apoptosis; cancer; viral infection.  
XX  
OS Mus sp.  
OS Synthetic.  
XX  
PN WO9817682-A1.  
XX  
PD 30-APR-1998.  
XX  
PF 17-OCT-1997; 97WO-US19175.  
XX  
PR 18-OCT-1996; 96US-0733505.  
XX  
PA (UNIW ) UNIV WASHINGTON.  
XX  
PI Korsmeyer SJ;  
XX  
DR WPI; 1998-261422/23.  
DR N-PSDB; AAV27837.  
XX  
PT New mutant BAD polypeptide with phosphorylatable serine replaced -  
PT useful for, e.g. treating reduced apoptosis such as in cancer or  
PT viral infection  
XX  
PS Claim 8; Page 73; 95pp; English.  
XX  
CC The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell  
CC death regulator) proteins, having an amino acid other than Ser at  
CC position 112 and/or 136, relative to the murine BAD 204 aa sequence. The  
CC present sequence represents a mutant BAD protein. Also described are: (1)  
CC fragments of mutant BAD protein able to decrease cell viability; (2)  
CC fusion proteins of mutant BAD with a heterologous polypeptide that  
CC increases intracellular delivery. Mutant BAD proteins are used to treat  
CC or prevent diseases associated with reduced apoptosis, e.g. cancer,  
CC viral infection, lymphoproliferation, arthritis, infertility,  
CC inflammation and autoimmune disease. Polynucleotide sequences encoding  
CC mutant BAD proteins can be used similarly by gene therapy or to produce  
CC transgenic animals for use as disease models or in drug screening. BAD  
CC proteins phosphorylated at specified Ser are used to screen for enhancers  
CC and inhibitors of serine-phosphatase. Inhibitors are potentially useful  
CC in treatment of excessive apoptosis such as AIDS, neurodegeneration,  
CC aging or ischaemic cell death. The apoptotic status of cells is

CC determined by measuring relative amounts of phosphorylated and non-  
CC phosphorylated BAD, by usual immunoassays. Mutant BAD proteins have  
CC greater death-promoting activity than wild-type BAD which can become  
CC phosphorylated on the specified Ser, forming a product that does not  
CC heterodimerise with BCL-2 or BCL-XL but instead binds to 14-3-3 family  
CC proteins in the cytosol, thus promoting cell survival. The mutants with  
CC Ser substituted cannot bind 14-3-3.  
XX  
SQ Sequence 59 AA;

Query Match 34.4%; Score 311; DB 19; Length 59;  
Best Local Similarity 98.3%; Pred. No. 7.7e-26;  
Matches 58; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 63 GAGAVEIRSRHSSYPAGTDEDDGMEEPSPPFRGRSRSPPNLWAAORYGRELRMADEF 121  
|||||  
Db 1 gagaveirsrhssypagteddegmgpepsppfrgrsrspnlwaaqrgreirrmsdef 59

RESULT 15  
AAW61320  
ID AAW61320 standard; Protein; 59 AA.  
XX  
AC AAW61320;  
XX  
DT 07-OCT-1998 (first entry)  
XX  
DE Mutant BCL-XL/BCL-2 associated cell death regulator #5.  
XX  
KW Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein;  
KW serine substituted mutant; apoptosis; cancer; viral infection.  
XX  
OS Mus sp.  
OS Synthetic.  
XX  
FN W09817682-A1.  
XX  
PD 30-APR-1998.  
XX  
PF 17-OCT-1997; 97WO-US19175.  
XX  
PR 18-OCT-1996; 96US-0733505.  
XX  
PA (UNIW ) UNIV WASHINGTON.  
XX  
PI Korsmeyer SJ;  
XX  
DR WPI; 1998-261422/23.  
DR N-PSDB; AAV27838.  
XX  
PT New mutant BAD polypeptide with phosphorylatable serine replaced -  
PT useful for, e.g. treating reduced apoptosis such as in cancer or  
PT viral infection  
XX  
PS Claim 8; Page 73; 95pp; English.  
XX

The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell death regulator) proteins, having an amino acid other than Ser at position 112 and/or 136, relative to the murine BAD 204 aa sequence. The present sequence represents a mutant BAD protein. Also described are: (1) fragments of mutant BAD protein able to decrease cell viability; (2) fusion proteins of mutant BAD with a heterologous polypeptide that increases intracellular delivery. Mutant BAD proteins are used to treat or prevent diseases associated with reduced apoptosis, e.g. cancer, viral infection, lymphoproliferation, arthritis, infertility, inflammation and autoimmune disease. Polynucleotide sequences encoding mutant BAD proteins can be used similarly by gene therapy or to produce transgenic animals for use as disease models or in drug screening. BAD proteins phosphorylated at specified Ser are used to screen for enhancers and inhibitors of serine-phosphatase. Inhibitors are potentially useful in treatment of excessive apoptosis such as AIDS, neurodegeneration, aging or ischaemic cell death. The apoptotic status of cells is

CC determined by measuring relative amounts of phosphorylated and non-  
CC phosphorylated BAD, by usual immunoassays. Mutant BAD proteins have  
CC greater death-promoting activity than wild-type BAD which can become  
CC phosphorylated on the specified Ser, forming a product that does not  
CC heterodimerise with BCL-2 or BCL-XL but instead binds to 14-3-3 family  
CC proteins in the cytosol, thus promoting cell survival. The mutants with  
CC Ser substituted cannot bind 14-3-3.  
XX  
SQ Sequence 59 AA;

Query Match 34.4%; Score 311; DB 19; Length 59;  
Best Local Similarity 98.3%; Pred. No. 7.7e-26;  
Matches 58; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 63 GAGAVEIRSRHSSYPAGTDEDDGMEEPSPPFRGRSRSPPNLWAAORYGRELRMADEF 121  
|||||  
Db 1 gagaveirsrhssypagteddegmgpepsppfrgrsrspnlwaaqrgreirrmsdef 59

Search completed: October 9, 2001, 15:59:14  
Job time: 99 sec



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: October 9, 2001, 16:02:05 ; Search time 164.17 Seconds  
(without alignments)  
227.023 Million cell updates/sec

Title: 09-580523-LB

Perfect score: 905

Sequence: 1 MFQIPEFPEPSEQEDSSAER.....RVFQSWDRNLGRGSSAPSQ 168

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2803329 seqs, 221847457 residues

Total number of hits satisfying chosen parameters: 2803329

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending\_Patents\_AA\_Main:\*

- 1: /cgn2\_6/ptodata/2/paa/PTUS\_COMB.pep.\*
- 2: /cgn2\_6/ptodata/2/paa/US06\_COMB.pep.\*
- 3: /cgn2\_6/ptodata/2/paa/US07\_COMB.pep.\*
- 4: /cgn2\_6/ptodata/2/paa/US08\_COMB.pep.\*
- 5: /cgn2\_6/ptodata/2/paa/US081\_COMB.pep.\*
- 6: /cgn2\_6/ptodata/2/paa/US082\_COMB.pep.\*
- 7: /cgn2\_6/ptodata/2/paa/US083\_COMB.pep.\*
- 8: /cgn2\_6/ptodata/2/paa/US084\_COMB.pep.\*
- 9: /cgn2\_6/ptodata/2/paa/US085\_COMB.pep.\*
- 10: /cgn2\_6/ptodata/2/paa/US086\_COMB.pep.\*
- 11: /cgn2\_6/ptodata/2/paa/US087\_COMB.pep.\*
- 12: /cgn2\_6/ptodata/2/paa/US088\_COMB.pep.\*
- 13: /cgn2\_6/ptodata/2/paa/US089\_COMB.pep.\*
- 14: /cgn2\_6/ptodata/2/paa/US090\_COMB.pep.\*
- 15: /cgn2\_6/ptodata/2/paa/US091\_COMB.pep.\*
- 16: /cgn2\_6/ptodata/2/paa/US092\_COMB.pep.\*
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- 19: /cgn2\_6/ptodata/2/paa/US095\_COMB.pep.\*
- 20: /cgn2\_6/ptodata/2/paa/US096\_COMB.pep.\*
- 21: /cgn2\_6/ptodata/2/paa/US097\_COMB.pep.\*
- 22: /cgn2\_6/ptodata/2/paa/US098\_COMB.pep.\*
- 23: /cgn2\_6/ptodata/2/paa/US060\_COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	902	99.7	168	1	PCT-US00-11864-1
2	902	99.7	168	17	US-09-375-257-2
3	902	99.7	168	17	US-09-376-154-2
4	902	99.7	168	18	US-09-410-372-1
5	902	99.7	168	18	US-09-456-357-32
6	902	99.7	168	19	US-09-580-523-1
7	902	99.7	168	19	US-09-587-473-21
8	741	81.9	168	12	US-08-883-731-2
9	741	81.9	168	18	US-09-410-372-7
10	670	74.0	125	23	US-60-197-873-16338

11	646	71.4	162	1	PCT-US00-11864-3	Sequence 3, Appli
12	646	71.4	162	19	US-09-580-523-3	Sequence 3, Appli
13	646	71.4	204	1	PCT-US00-11864-2	Sequence 2, Appli
14	646	71.4	204	1	PCT-US97-15871-1	Sequence 1, Appli
15	646	71.4	204	1	PCT-US97-15871A-1	Sequence 1, Appli
16	646	71.4	204	1	PCT-US98-19765-41	Sequence 41, Appli
17	646	71.4	204	11	US-08-707-868-1	Sequence 1, Appli
18	646	71.4	204	11	US-08-733-505-1	Sequence 1, Appli
19	646	71.4	204	13	US-08-946-039-41	Sequence 41, Appli
20	646	71.4	204	19	US-09-580-523-2	Sequence 2, Appli
21	645	71.3	204	17	US-09-375-257-3	Sequence 3, Appli
22	645	71.3	204	17	US-09-376-154-3	Sequence 3, Appli
23	643	71.0	204	11	US-08-733-505-12	Sequence 12, Appli
24	643	71.0	204	11	US-08-733-505-13	Sequence 13, Appli
25	640	70.7	204	11	US-08-733-505-14	Sequence 14, Appli
26	640	70.7	567	20	US-09-639-245-4	Sequence 4, Appli
27	331	36.6	63	1	PCT-US97-15871A-12	Sequence 12, Appli
28	331	36.6	63	1	PCT-US98-19765-42	Sequence 42, Appli
29	331	36.6	63	13	US-08-946-039-42	Sequence 42, Appli
30	311	34.4	59	11	US-08-733-505-55	Sequence 55, Appli
31	308	34.0	59	11	US-08-733-505-56	Sequence 56, Appli
32	308	34.0	59	11	US-08-733-505-57	Sequence 57, Appli
33	305	33.7	59	11	US-08-733-505-58	Sequence 58, Appli
34	130	14.4	26	1	PCT-US00-11864-4	Sequence 4, Appli
35	130	14.4	26	1	PCT-US99-25285-5	Sequence 5, Appli
36	130	14.4	26	15	US-09-184-168A-5	Sequence 4, Appli
37	130	14.4	26	19	US-09-580-523-4	Sequence 4, Appli
38	129	14.3	25	20	US-09-656-399-10	Sequence 10, Appli
39	129	14.3	25	20	US-09-656-399A-10	Sequence 10, Appli
40	129	14.3	25	21	US-09-716-395-20	Sequence 20, Appli
41	126	13.9	25	20	US-09-656-399-17	Sequence 17, Appli
42	126	13.9	25	20	US-09-656-399A-17	Sequence 17, Appli
43	126	13.9	25	21	US-09-716-395-26	Sequence 26, Appli
44	125	13.8	25	20	US-09-656-399-15	Sequence 15, Appli
45	125	13.8	25	20	US-09-656-399-16	Sequence 16, Appli

ALIGNMENTS

RESULT 1  
PCT-US00-11864-1  
; Sequence 1, Application PC/TUS0011864  
; GENERAL INFORMATION:  
; APPLICANT: APOPTOSIS TECHNOLOGY, INC.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR REGULATING APOPTOSIS.  
; TITLE OF INVENTION: AND METHODS OF MAKING AND SCREENING FOR COMPOUNDS  
; TITLE OF INVENTION: THAT REGULATE APOPTOSIS  
; FILE REFERENCE: F137122  
; CURRENT APPLICATION NUMBER: PCT/US00/11864  
; CURRENT FILING DATE: 2000-05-30  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 168  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
PCT-US00-11864-1

Query Match	99.7%	Score	902;	DB	1;	Length	168;
Best Local Similarity	99.4%	Pred. No.	7.4e-71;				
Matches	167;	Conservative	1;	Mismatches	0;	Indels	0;
						Gaps	0;
QY	1	MFQIPEPESQEDSSAERGLGSPAGDGGSGKHKHRQAPGLLWDASHOQEPTSSSH	60				
Db	1	MFQIPEPESQEDSSAERGLGSPAGDGGSGKHKHRQAPGLLWDASHOQEPTSSSH	60				
QY	61	HGGAGAVEIRSHSSYPAGTDEDDGEMGEPSFPRGRSRSPPNLWAAOYRGELRRMADE	120				
Db	61	HGGAGAVEIRSHSSYPAGTDEDDGEMGEPSFPRGRSRSPPNLWAAOYRGELRRMSDE	120				
QY	121	FVDSFKKGLPRPKSAGTATQMRQSSWTRVFQSWDRNLGRGSSAPSQ	168				

Db 121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168  
|||||

## RESULT 2

US-09-375-257-2

; Sequence 2, Application US/09375257  
; GENERAL INFORMATION:  
; APPLICANT: Horne, William A.  
; TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC  
; TITLE OF INVENTION: ACIDS AND METHODS OF USE  
; FILE REFERENCE: 480140.428D1  
; CURRENT APPLICATION NUMBER: US/09/375,257  
; CURRENT FILING DATE: 1999-08-16  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 168  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-375-257-2

Query Match 99.7%; Score 902; DB 17; Length 168;  
Best Local Similarity 99.4%; Pred. No. 7.4e-71;  
Matches 167; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFQIPEFEPSEQEDSSAERGLGSPAGDPSGSGKHHRQAPGLLDASHQOEPTSSSH 60  
|||||  
Db 1 MFQIPEFEPSEQEDSSAERGLGSPAGDPSGSGKHHRQAPGLLDASHQOEPTSSSH 60  
|||||  
QY 61 HGGAGAVEIRSRHSSYPACTDEDEGMGEPPSPFGRSRSAPPNLWAAQRYGRELRRMADE 120  
|||||  
Db 61 HGGAGAVEIRSRHSSYPACTDEDEGMGEPPSPFGRSRSAPPNLWAAQRYGRELRRMSDE 120  
|||||  
QY 121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168  
|||||  
Db 121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168  
|||||

## RESULT 3

US-09-376-154-2

; Sequence 2, Application US/09376154  
; GENERAL INFORMATION:  
; APPLICANT: Horne, William A.  
; APPLICANT: Oltersdorf, Tilman  
; TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC  
; TITLE OF INVENTION: ACIDS AND METHODS OF USE  
; FILE REFERENCE: 480140.428D2  
; CURRENT APPLICATION NUMBER: US/09/376,154  
; CURRENT FILING DATE: 1999-08-17  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 168  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-376-154-2

Query Match 99.7%; Score 902; DB 17; Length 168;  
Best Local Similarity 99.4%; Pred. No. 7.4e-71;  
Matches 167; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFQIPEFEPSEQEDSSAERGLGSPAGDPSGSGKHHRQAPGLLDASHQOEPTSSSH 60  
|||||  
Db 1 MFQIPEFEPSEQEDSSAERGLGSPAGDPSGSGKHHRQAPGLLDASHQOEPTSSSH 60  
|||||  
QY 61 HGGAGAVEIRSRHSSYPACTDEDEGMGEPPSPFGRSRSAPPNLWAAQRYGRELRRMADE 120  
|||||  
Db 61 HGGAGAVEIRSRHSSYPACTDEDEGMGEPPSPFGRSRSAPPNLWAAQRYGRELRRMSDE 120  
|||||

QY 121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168  
|||||  
Db 121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168  
|||||

## RESULT 4

US-09-410-372-1  
; Sequence 1, Application US/09410372  
; GENERAL INFORMATION:  
; APPLICANT: Hillman, Jennifer L.  
; APPLICANT: Yue, Henry  
; APPLICANT: Lal, Preeti  
; APPLICANT: Shah, Purvi  
; APPLICANT: Corley, Neil C.  
; TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL  
; TITLE OF INVENTION: PROLIFERATION  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Dr.  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/410,372  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/985,335  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Billings, Lucy J.  
; REGISTRATION NUMBER: 36,749  
; REFERENCE/DOCKET NUMBER: PF-0421 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-855-0555  
; TELEFAX: 650-845-4166  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 168 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: SYNORAB01  
; CLONE: 358673  
US-09-410-372-1

Query Match 99.7%; Score 902; DB 18; Length 168;  
Best Local Similarity 99.4%; Pred. No. 7.4e-71;  
Matches 167; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFQIPEFEPSEQEDSSAERGLGSPAGDPSGSGKHHRQAPGLLDASHQOEPTSSSH 60  
|||||  
Db 1 MFQIPEFEPSEQEDSSAERGLGSPAGDPSGSGKHHRQAPGLLDASHQOEPTSSSH 60  
|||||  
QY 61 HGGAGAVEIRSRHSSYPACTDEDEGMGEPPSPFGRSRSAPPNLWAAQRYGRELRRMADE 120  
|||||  
Db 61 HGGAGAVEIRSRHSSYPACTDEDEGMGEPPSPFGRSRSAPPNLWAAQRYGRELRRMSDE 120  
|||||  
QY 121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168  
|||||  
Db 121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168  
|||||

## RESULT 5

US-09-456-357-32

```
; Sequence 32, Application US/09456357
; GENERAL INFORMATION:
; APPLICANT: 3921-1-1-1
; TITLE OF INVENTION: VIRAL VECTORS ENCODING APOPTOSIS-INDUCING PROTEINS AND
; TITLE OF INVENTION: METHODS FOR MAKING AND USING THE SAME
; FILE REFERENCE: 3921-1-1-1
; CURRENT APPLICATION NUMBER: US/09/456,357
; CURRENT FILING DATE: 1999-12-08
; EARLIER APPLICATION NUMBER: 60/134,416
; EARLIER FILING DATE: 1999-05-17
; EARLIER APPLICATION NUMBER: 09/087,195
; EARLIER FILING DATE: 1998-05-29
; EARLIER APPLICATION NUMBER: 08/378,507
; EARLIER FILING DATE: 1995-01-26
; EARLIER APPLICATION NUMBER: 08/250,478
; EARLIER FILING DATE: 1994-05-27
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 32
; LENGTH: 168
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-456-357-32

Query Match          99.7%; Score 902; DB 18; Length 168;
Best Local Similarity 99.4%; Pred. No. 7.4e-71;
Matches 167; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFQIPEFSPQEDSSAERGLGSPAGDGPSSGKHHRRQAPGLLDASHHQEQPTSSSH 60
Db 1 MFQIPEFSPQEDSSAERGLGSPAGDGPSSGKHHRRQAPGLLDASHHQEQPTSSSH 60

Qy 61 HGGAGAVEIRSRHSSYPAGTDEDDGMEGEEPFRGRSRAPPNLWAAQRYGRELRRMADE 120
Db 61 HGGAGAVEIRSRHSSYPAGTDEDDGMEGEEPFRGRSRAPPNLWAAQRYGRELRRMSDE 120

Qy 121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWMDRNLGRGSSAPSQ 168
Db 121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWMDRNLGRGSSAPSQ 168

RESULT 6
US-09-580-523-1
; Sequence 1, Application US/09580523
; GENERAL INFORMATION:
; APPLICANT: Zhou, Xiao-Mai
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR REGULATING APOPTOSIS.
; TITLE OF INVENTION: AND METHODS OF MAKING AND SCREENING FOR COMPOUNDS
; TITLE OF INVENTION: THAT REGULATE APOPTOSIS
; FILE REFERENCE: A7483
; CURRENT APPLICATION NUMBER: US/09/580,523
; CURRENT FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 168
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-580-523-1

Query Match          99.7%; Score 902; DB 19; Length 168;
Best Local Similarity 99.4%; Pred. No. 7.4e-71;
Matches 167; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFQIPEFSPQEDSSAERGLGSPAGDGPSSGKHHRRQAPGLLDASHHQEQPTSSSH 60
Db 1 MFQIPEFSPQEDSSAERGLGSPAGDGPSSGKHHRRQAPGLLDASHHQEQPTSSSH 60

Qy 61 HGGAGAVEIRSRHSSYPAGTDEDDGMEGEEPFRGRSRAPPNLWAAQRYGRELRRMADE 120
Db 61 HGGAGAVEIRSRHSSYPAGTDEDDGMEGEEPFRGRSRAPPNLWAAQRYGRELRRMSDE 120
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Qy 121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWMDRNLGRGSSAPSQ 168
Db 121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWMDRNLGRGSSAPSQ 168

RESULT 7
US-09-587-473-21
; Sequence 21, Application US/09587473
; GENERAL INFORMATION:
; APPLICANT: Zhang, Hui
; APPLICANT: Tsvetkov, Lyuben
; TITLE OF INVENTION: Protein Knockout Technology
; FILE REFERENCE: 44574-5047-WO
; CURRENT APPLICATION NUMBER: US/09/587,473
; CURRENT FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: US 60/137,494
; PRIOR FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 168
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-587-473-21

Query Match          99.7%; Score 902; DB 19; Length 168;
Best Local Similarity 99.4%; Pred. No. 7.4e-71;
Matches 167; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFQIPEFSPQEDSSAERGLGSPAGDGPSSGKHHRRQAPGLLDASHHQEQPTSSSH 60
Db 1 MFQIPEFSPQEDSSAERGLGSPAGDGPSSGKHHRRQAPGLLDASHHQEQPTSSSH 60

Qy 61 HGGAGAVEIRSRHSSYPAGTDEDDGMEGEEPFRGRSRAPPNLWAAQRYGRELRRMADE 120
Db 61 HGGAGAVEIRSRHSSYPAGTDEDDGMEGEEPFRGRSRAPPNLWAAQRYGRELRRMSDE 120

Qy 121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWMDRNLGRGSSAPSQ 168
Db 121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWMDRNLGRGSSAPSQ 168

RESULT 8
US-08-883-731-2
; Sequence 2, Application US/08883731
; GENERAL INFORMATION:
; APPLICANT: Zhu, Li
; APPLICANT: Xudong, Yin
; TITLE OF INVENTION: Gene and Protein for Regulation Cell Death
; FILE REFERENCE: D6120
; CURRENT APPLICATION NUMBER: US/08/883,731
; CURRENT FILING DATE: 1997-06-27
; EARLIER APPLICATION NUMBER: US 08/665,617
; EARLIER FILING DATE: 1996-06-18
; NUMBER OF SEQ ID NOS: 3
; SEQ ID NO 2
; LENGTH: 168
; TYPE: PRT
; ORGANISM: unknown
; FEATURE:
; LOCATION:
; OTHER INFORMATION: Protein encoded by the BBC6 gene.
US-08-883-731-2

Query Match          81.9%; Score 741; DB 12; Length 168;
Best Local Similarity 84.5%; Pred. No. 9.3e-57;
Matches 142; Conservative 1; Mismatches 25; Indels 0; Gaps 0;

Qy 1 MFQIPEFSPQEDSSAERGLGSPAGDGPSSGKHHRRQAPGLLDASHHQEQPTSSSH 60
Db 1 MFQIPEFSPQEDSSAERGLGSPAGDGPSSGKHHRRQAPGLLDASHHQEQPTSSSH 60
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Db 1 MFQIPEFEPSEQEDSSAERGLGSPAGDPSGSGKHHRQAPGLLDASHQOQPTSSSH 60  
QY 61 HGCAGAVEIRSRHSSYPAGTDEDEGMEPSPFRGRSRSAPPNLWAAQRYGRELRRMADE 120  
Db 61 HGRWCGDPSPQLPRDGGRRDGGGAQPFGRSRSAPPNLWAAQRYGRELRRMSDE 120  
QY 121 FVDSFKKGLPRKSGAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168  
Db 121 FVDSFKKGLPRKSGAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168

RESULT 9  
US-09-410-372-7  
; Sequence 7, Application US/09410372  
; GENERAL INFORMATION:  
; APPLICANT: Hillman, Jennifer L.  
; APPLICANT: Yue, Henry  
; APPLICANT: Lal, Preeti  
; APPLICANT: Shah, Purvi  
; APPLICANT: Corley, Neil C.  
; TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL  
; TITLE OF INVENTION: PROLIFERATION  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Dr.  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/410,372  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/985,335  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Billings, Lucy J.  
; REGISTRATION NUMBER: 36,749  
; REFERENCE/DOCKET NUMBER: PF-0421 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-855-0555  
; TELEFAX: 650-845-4166  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 168 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: GenBank  
; CLONE: 1683637  
US-09-410-372-7

Query Match 81.9%; Score 741; DB 18; Length 168;  
Best Local Similarity 84.5%; Pred. No. 9.3e-57;  
Matches 142; Conservative 1; Mismatches 25; Indels 0; Gaps 0;

QY 1 MFQIPEFEPSEQEDSSAERGLGSPAGDPSGSGKHHRQAPGLLDASHQOQPTSSSH 60  
Db 1 MFQIPEFEPSEQEDSSAERGLGSPAGDPSGSGKHHRQAPGLLDASHQOQPTSSSH 60  
QY 61 HGCAGAVEIRSRHSSYPAGTDEDEGMEPSPFRGRSRSAPPNLWAAQRYGRELRRMADE 120  
Db 61 HGRWCGDPSPQLPRDGGRRDGGGAQPFGRSRSAPPNLWAAQRYGRELRRMSDE 120  
QY 121 FVDSFKKGLPRKSGAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168

Db 121 FVDSFKKGLPRKSGAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168

RESULT 10  
US-60-197-873-16338  
; Sequence 16338, Application US/60197873  
; GENERAL INFORMATION:  
; APPLICANT: Bejanin, Stephane  
; APPLICANT: Tanaka, Hiroaki  
; APPLICANT: Dumas Milne Edwards, Jean Baptiste  
; APPLICANT: Jobert, Severin  
; APPLICANT: Giordano, Jean-Yves  
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.  
; FILE REFERENCE: 81 US1 PRO  
; CURRENT APPLICATION NUMBER: US/60/197,873  
; CURRENT FILING DATE: 2000-04-18  
; NUMBER OF SEQ ID NOS: 52153  
; SOFTWARE: Patent.pm  
; SEQ ID NO 16338  
; LENGTH: 125  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-60-197-873-16338

Query Match 74.0%; Score 670; DB 23; Length 125;  
Best Local Similarity 99.2%; Pred. No. 1.1e-50;  
Matches 124; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFQIPEFEPSEQEDSSAERGLGSPAGDPSGSGKHHRQAPGLLDASHQOQPTSSSH 60  
Db 1 MFQIPEFEPSEQEDSSAERGLGSPAGDPSGSGKHHRQAPGLLDASHQOQPTSSSH 60  
QY 61 HGCAGAVEIRSRHSSYPAGTDEDEGMEPSPFRGRSRSAPPNLWAAQRYGRELRRMADE 120  
Db 61 HGCAGAVEIRSRHSSYPAGTDEDEGMEPSPFRGRSRSAPPNLWAAQRYGRELRRMSDE 120  
QY 121 FVDSF 125  
Db 121 FVDSF 125

RESULT 11  
PCT-US00-11864-3  
; Sequence 3, Application PC/TUS0011864  
; GENERAL INFORMATION:  
; APPLICANT: APOPTOSIS TECHNOLOGY, INC.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR REGULATING APOPTOSIS.  
; TITLE OF INVENTION: AND METHODS OF MAKING AND SCREENING FOR COMPOUNDS  
; TITLE OF INVENTION: THAT REGULATE APOPTOSIS  
; FILE REFERENCE: F137122  
; CURRENT APPLICATION NUMBER: PCT/US00/11864  
; CURRENT FILING DATE: 2000-05-30  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 162  
; TYPE: PRT  
; ORGANISM: Mus musculus  
PCT-US00-11864-3

Query Match 71.4%; Score 646; DB 1; Length 162;  
Best Local Similarity 75.0%; Pred. No. 1.9e-48;  
Matches 126; Conservative 13; Mismatches 23; Indels 6; Gaps 3;

QY 1 MFQIPEFEPSEQEDSSAERGLGSPAGDPSGSGKHHRQAPGLLDASHQOQPTSSSH 60  
Db 1 MFQIPEFEPSEQEDASATDGLGSLTDEQP---GPY--LAPGLGSLNTHOOGRAATNSH 55  
QY 61 HGCAGAVEIRSRHSSYPAGTDEDEGMEPSPFRGRSRSAPPNLWAAQRYGRELRRMADE 120



Db            56 HGGAGAMETRSHSSYPACTEEDEGMEELSPFGRGRSAPPNLAAQRYGRELRMSDE 115

QY          121 FVDSFKGLPRPKASATATQMROSSWTRVFOSWDNRLGRSSAPSQ 168  
       | ||| ||||| ||||| : ||| : ||||| : |||  
Db          116 FEGSF-KGLPRPKASATATMQRSAGWTRIIOSWDNRLKGSGTSPQ 162

```

RESULT 12
US-09-580-523-3
; Sequence 3, Application US/09580523
; GENERAL INFORMATION:
; APPLICANT: Zhou, Xiao-Mai
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR REGULATING APOPTOSIS,
; TITLE OF INVENTION: AND METHODS OF MAKING AND SCREENING FOR COMPOUNDS
; TITLE OF INVENTION: THAT REGULATE APOPTOSIS
; FILE REFERENCE: A7483
; CURRENT APPLICATION NUMBER: US/09/580,523
; CURRENT FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 3
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-580-523-3

```

```

RESULT 13
PCT-US00-11864-2
; Sequence 2, Application PC/TUS0011864
; GENERAL INFORMATION:
; APPLICANT: APOPTOSIS TECHNOLOGY, INC.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR REGULATING APOPTOSIS,
; TITLE OF INVENTION: AND METHODS OF MAKING AND SCREENING FOR COMPOUNDS
; TITLE OF INVENTION: THAT REGULATE APOPTOSIS
; FILE REFERENCE: F137122
; CURRENT APPLICATION NUMBER: PCT/US00/11864
; CURRENT FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 204
; TYPE: PRT
; ORGANISM: Mus musculus
PCT-US00-11864-2

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Db	98	HGAGAGMETRSRHSSYPAGTEDEGMBEELSPPRGRSRSPAPNLWAAQRYGRELRRMSDE	157
Qy	121	FVDSFKKGLPRPSAGTATOMROSSWTRVFQSWDNLORGSSAPSQ	168
Db	158	FEGSFF-KGLPRPSAGTATOMROSAGWTRIOSWDNLKGKSTPSS	204

```

RESULT 14
PCT-US97-15871-1
: Sequence 1, Application PC/TUS9715871
: GENERAL INFORMATION:
: APPLICANT: KORSMEYER, STANLEY J.
: TITLE OF INVENTION: MODULATION OF APOPTOSIS BY SERINE
: TITLE OF INVENTION: PHOSPHORYLATION OF BCL-X1/BCL-2 ASSOCIATED CELL DEATH
: TITLE OF INVENTION: REGULATOR
: NUMBER OF SEQUENCES: 11
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: HOWELL & HAFERKAMP, L.C.
: STREET: 7733 FORSYTH BLVD., SUITE 1400
: CITY: ST. LOUIS
: STATE: MISSOURI
: COUNTRY: USA
: ZIP: 63146
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US97/15871
: FILING DATE:
: CLASSIFICATION:
: ATTORNEY/AGENT INFORMATION:
: NAME: HOLLAND, DONALD R.
: REGISTRATION NUMBER: 35,197
: REFERENCE/DOCKET NUMBER: 965018
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (314) 727-5188
: TELEFAX: (314) 727-6092
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 204 amino acids
: TYPE: amino acid
: STRANDEDNESS:
: TOPOLOGY: linear
: MOLECULE TYPE: protein
PCT-US97-15871-1

```

```

RESULT 15
PCT-US97-15871A-1
; Sequence 1, Application PC/TUS9715871A
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, STANLEY J
; TITLE OF INVENTION: MODULATION OF APOPTOSIS BY SERINE

```

Search completed: October 9, 2001, 16:02:05  
Job time: 270 sec.

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 9, 2001, 15:54:04 ; Search time 28.81 seconds  
(without alignments)  
68.745 Million cell updates/sec

Title: US-09-580-523-1-copy\_143\_168

Perfect score: 145

Sequence: 1 QSSSWTRVFQSWDRNLGRGSSAPSQ 26

Scoring table:

BLOSUM62  
Gapop 10.0 , -Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR\_68.\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	120	82.8	204	2 A55671	bad protein - mous
2	57	39.3	3068	1 A44062	genome polyprotein
3	54	37.2	1632	2 C70752	probable ctpi prot
4	53	36.6	245	2 S68691	neutrophil granule
5	53	36.6	476	2 B83006	two-component resp
6	53	36.6	807	2 T39479	histone transcript
7	53	36.6	3163	1 JQ1895	genome polyprotein
8	51	35.2	855	2 F45557	external glycoprot
9	50.5	34.8	328	2 F75357	hypothetical prote
10	50	34.5	144	2 S29946	surface glycoprote
11	50	34.5	157	2 P00619	envelope protein -
12	50	34.5	243	2 B33329	cysteine-rich secr
13	50	34.5	264	2 T31521	hypothetical prote
14	50	34.5	299	2 B83081	hypothetical prote
15	50	34.5	634	2 A48335	cytoplasmic inclus
16	50	34.5	1170	1 TSHUPL	thrombospondin 1 p
17	50	34.5	1170	2 A40558	thrombospondin 1 p
18	50	34.5	3061	1 JN0545	genome polyprotein
19	50	34.5	3063	2 J50166	genome polyprotein
20	49.5	34.1	335	2 T10074	cytochrome-c perox
21	49.5	34.1	358	1 QJ1870	ALI protein - toma
22	49	33.8	226	2 S29952	surface glycoprote
23	49	33.8	242	2 P00626	envelope protein -
24	49	33.8	246	2 A24609	acidic epididymal
25	49	33.8	460	2 F84764	hypothetical prote
26	49	33.8	643	2 B83635	conserved hypothet
27	49	33.8	726	2 G83310	conserved hypothet
28	49	33.8	741	2 D83633	conserved hypothet
29	49	33.8	1148	2 T09073	splicing factor S1

ALIGNMENTS

RESULT 1

A55671

bad protein - mouse

C:Species: Mus musculus (house mouse)

C:Date: 03-Mar-1995 #sequence\_revision 03-Mar-1995 #text\_change 05-Nov-1999

C:Accession: A55671

R:Yang, E.; Zha, J.; Jockel, J.; Boise, L.H.; Thompson, C.B.; Korsmeyer, S.J.

Cell 80, 285-291, 1995

A:Title: Bad, a heterodimeric partner for Bcl-x-L and Bcl-2, displaces Bax and promot

A:Reference number: A55671; MUID:95136361

A:Accession: A55671

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-204 <YAN>

A:Cross-references: GB:L37296; NID:g639778; PIDN:AAA64465.1; PID:g639779

C:Keywords: heterodimer

Query Match 82.8%; Score 120; DB 2; Length 204;

Best Local Similarity 73.1%; Pred. No. 9.9e-10;

Matches 19; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Oy 1 QSSSWTRVFQSWDRNLGRGSSAPSQ 26

||: |||: ||||| |||||: |||

Db 179 QSAGWTRIIQSWDRNLGRGSGTPSQ 204

RESULT 2

A44062

genome polyprotein - pepper mottle virus (strain California)

N:Contains: 29K protein; 34K protein; coat protein; cylindrical inclusion protein; he

C:Species: pepper mottle virus

C:Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 19-Jan-2001

C:Accession: A44062

R:Vance, V.B.; Moore, D.; Turpen, T.H.; Bracker, A.; Hollowell, V.C.

Virolgy 191, 19-30, 1992

A:Title: The complete nucleotide sequence of pepper mottle virus genomic RNA: compari

A:Reference number: A44062; MUID:93033110

A:Accession: A44062

A:Molecule type: genomic RNA

A:Residues: 1-3068 <VAN>

A:Cross-references: GB:M96425; NID:g332869; PIDN:AAA46903.1; PID:g332870

C:Superfamily: tobacco etch virus genome polyprotein

C:Keywords: ATP; coat protein; cylindrical inclusion protein; genome-linked protein;

F:1-287/Product: 34K protein #status predicted <KPT>

F:288-743/Product: helper component protein #status predicted <HCP>

F:744-1156/Product: 29K protein #status predicted <KPR>

F:1157-1790/Product: cylindrical inclusion protein #status predicted <CIP>

F:1241-1248/Region: nucleotide-binding motif A (P-loop)

F:1326-1331/Region: nucleotide-binding motif B

F:1330-1333/Region: DEXH motif

F:1791-2276/Product: nuclear inclusion protein a #status predicted <NIA>

F;2277-2799/Product: nuclear inclusion protein b #status predicted <NTB>  
F;2800-3068/Product: coat protein #status predicted <Cp>  
F;1906/Binding site: phosphoryl-RNA (Tyr) (covalent) #status predicted

Query Match 39.3%; Score 57; DB 1; Length 3068;  
Best Local Similarity 50.0%; Pred. No. 12;  
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 9 FQSWDRNLGRSSAP 24  
I:|||||:|||||  
Db 1191 FESWDEQVARGFTIP 1206

RESULT 3  
C70752  
Probable ctpI protein - Mycobacterium tuberculosis (strain H37RV)  
C:Species: Mycobacterium tuberculosis  
C:Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 22-Oct-1999  
C:Accession: C70752  
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.  
Nature 393, 537-544, 1998  
A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.  
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome  
A:Reference number: A70500; MUID:98295987  
A:Accession: C70752  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-1632 <COL>  
A:Cross-references: GB:Z74410; GB:AL123456; PIDN:CAA98940.1; PID:el299890;  
A:Experimental source: strain H37RV  
C:Genetics:  
A:Gene: ctpI  
C:Superfamily: ATPase nucleotide-binding domain homology  
F;1237-1406/Domain: ATPase nucleotide-binding domain homology <ATN>

Query Match 37.2%; Score 54; DB 2; Length 1632;  
Best Local Similarity 71.4%; Pred. No. 16;  
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 13 WDRNLGRSSAPSQ 26  
I:|||||  
Db 1576 WDRSPGRASSAPRQ 1589

RESULT 4  
S68691  
neutrophil granules matrix glycoprotein SGP28 precursor - human  
C:Species: Homo sapiens (man)  
C:Date: 15-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 17-Nov-2000  
C:Accession: S68691; S74313; S68683  
R;Kjeldsen, L.; Cowland, J.B.; Johnsen, A.H.; Borregaard, N.  
FEBS Lett. 380, 246-250, 1996  
A:Title: SGP28, a novel matrix glycoprotein in specific granules of human neutrophils with a novel domain  
A:Reference number: S68691; MUID:96186934  
A:Accession: S68691  
A:Molecule type: mRNA  
A:Residues: 1-245 <KJE>  
A:Cross-references: EMBL:X94323; NID:g1213612; PIDN:CAA63984.1; PID:g1213613  
A:Accession: S74313  
A:Molecule type: protein  
A:Residues: 33-83;96-143;165-217;221-226 <KIL>  
R;Kraetzschmar, J.; Haendler, B.; Eberspaecher, U.; Roosterman, D.; Donner, P.; Schleuning, J.  
Eur. J. Biochem. 236, 827-836, 1996  
A:Title: The human cysteine-rich secretory protein (CRISP) family. Primary structure and function  
A:Reference number: S68681; MUID:96270732  
A:Accession: S68683  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-105,'S',107-245 <KRA>

A:Cross-references: EMBL:X95240; NID:g1262818; PIDN:CAA64527.1; PID:g1262819  
C:Genetics:  
A:Gene: SGP28  
C:Superfamily: cysteine-rich secretory protein 1  
F;1-19/Domain: signal sequence #status predicted <SIG>  
F;20-245/Product: neutrophil granules matrix glycoprotein SGP28 #status predicted <MA

Query Match 36.6%; Score 53; DB 2; Length 245;  
Best Local Similarity 37.0%; Pred. No. 3.3;  
Matches 10; Conservative 5; Mismatches 8; Indels 4; Gaps 1;

QY 3 SSWTRVFQSWDR----NLGRSSAPS 25  
I:|||||:|||||  
Db 107 SWSQAIQSWFDEYNDFGCGPKTPN 133

RESULT 5  
E83006  
two-component response regulator NtrC PA5125 [imported] - Pseudomonas aeruginosa (str C:Species: Pseudomonas aeruginosa  
C:Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000  
C:Accession: E83006  
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L.; Lory, S.; Olson, M.V.  
Nature 406, 959-964, 2000  
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen  
A:Reference number: A82950; MUID:20437337  
A:Accession: E83006  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-476 <STO>  
A:Cross-references: GB:AE004925; GB:AE004091; NID:g9951415; PIDN:AA08510.1; GSPDB:GN  
A:Experimental source: strain PA01  
C:Genetics:  
A:Gene: ntrC; PA5125  
C:Superfamily: nitrogen assimilation regulatory protein ntrC; response regulator homo

Query Match 36.6%; Score 53; DB 2; Length 476;  
Best Local Similarity 38.1%; Pred. No. 6.4;  
Matches 8; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 2 SSSWTRVFQSWDRNLGRSS 22  
I:|||||  
Db 396 AANNEQALRWADQALGRQS 416

RESULT 6  
T39479  
histone transcription regulator beta-transducin homolog - fission yeast (Schizosaccharomyces pombe)  
C:Species: Schizosaccharomyces pombe  
C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 26-May-2000  
C:Accession: T39479  
R;Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Lucas, M.; Gaillardin, C.  
submitted to the EMBL Data Library, August 1997  
A:Reference number: Z21858  
A:Accession: T39479  
A:Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-807 <LYN>  
A:Cross-references: EMBL:AL031349; PIDN:CAA20478.1; GSPDB:GN00067; SPDB:SPBC15D4.03  
A:Experimental source: strain 972h-; cosmid cl5D4  
C:Genetics:  
A:Gene: SPDB:SPBC15D4.03  
A:Map position: 2  
C:Superfamily: unassigned WD repeat proteins; WD repeat homology

Query Match 36.6%; Score 53; DB 2; Length 807;  
Best Local Similarity 66.7%; Pred. No. 11;  
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 SSSWTRVFQSWW 13  
||||| : :  
Db 624 SSSWLRVSGW 635

RESULT 7  
JQ1895  
genome polyprotein - turnip mosaic virus  
N:Contains: coat protein; cytoplasmic inclusion protein; helper component protein; nucleocapsid protein  
C:Species: turnip mosaic virus, TuMV  
C:Date: 17-Feb-1994 #sequence\_revision 17-Feb-1994 #text\_change 19-Jan-2001  
C:Accession: JQ1895; JQ1168; PQ0217  
R:Nicolas, O.; Laliberte, J.F.  
J. Gen. Virol. 73, 2785-2793, 1992  
A:Title: The complete nucleotide sequence of turnip mosaic polyvirus RNA.  
A:Reference number: JQ1895; MUID:93057350  
A:Accession: JQ1895  
A:Molecule type: mRNA  
A:Residues: 1-3163 <NIC>  
A:Cross-references: DBJ:D10927; NID:g2222660; PIDN:BAA01725.1; PID:g2222661  
A:Experimental source: strain Quebec  
R:Tremblay, M.F.; Nicolas, O.; Sinha, R.C.; Lazure, C.; Laliberte, J.F.  
J. Gen. Virol. 71, 2769-2772, 1990  
A:Title: Sequence of the 3'-terminal region of turnip mosaic virus RNA and the capsid protein.  
A:Reference number: JQ1168; MUID:91073142  
A:Accession: JQ1168  
A:Molecule type: genomic RNA  
A:Residues: 1534-2861, G', 2863-3163 <TRE>  
A:Cross-references: GB:D10601; GB:D01090; NID:g2222658; PIDN:BAA01452.1; PID:g2222659  
A:Accession: PQ0217  
A:Molecule type: protein  
A:Residues: 2876-2892; 2929-2941; 3118-3141 <TR2>  
C:Superfamily: tobacco etch virus genome polyprotein  
C:Keywords: ATP; coat protein; genome-linked protein; inclusion protein; nucleotide binding site  
F:1-362/Product: P1 protein #status predicted <P1>  
F:363-820/Product: helper component protein #status predicted <HCP>  
F:821-1175/Product: P3 protein #status predicted <P3p>  
F:1176-1227/Product: p6K1 protein #status predicted <P6p>  
F:1228-1870/Product: cytoplasmic inclusion protein #status predicted <CIP>  
F:1313-1320/Region: nucleotide-binding motif A (P-loop)  
F:1398-1403/Region: nucleotide-binding motif B  
F:1402-1405/Region: DEXH motif  
F:1871-1923/Product: p6K2 protein #status predicted <PKP>  
F:1924-2115/Product: VPg protein #status predicted <VPG>  
F:2116-2358/Product: nuclear inclusion a protein #status predicted <NIA>  
F:2359-2875/Product: nuclear inclusion b protein #status predicted <NIB>  
F:2876-3163/Product: coat (capsid) protein #status experimental <CAP>  
F:1986/Binding site: phosphoryl-RNA (Tyr) (covalent) #status predicted

Query Match 36.6%; Score 53; DB 1; Length 3163;  
Best Local Similarity 44.4%; Pred. No. 45;  
Matches 8; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 7 RVFQSWDRNLGRGSSAP 24  
: ||| : :  
Db 1261 KTFASWWSHQLSRGTIP 1278

RESULT 8  
F45557  
external glycoprotein: transmembrane protein (external glycoprotein, EGP, transmembrane protein)  
C:Species: feline immunodeficiency virus  
C:Date: 22-Apr-1993 #sequence\_revision 18-Nov-1994 #text\_change 16-Feb-1997  
C:Accession: F45557  
R:Maki, N.; Miyazawa, T.; Fukasawa, M.; Hasegawa, A.; Hayami, M.; Miki, K.; Mikami, T.  
Arch. Virol. 123, 29-45, 1992  
A:Title: Molecular characterization and heterogeneity of feline immunodeficiency virus isolates.  
A:Reference number: A45557; MUID:92198230  
A:Accession: F45557  
A:Status: preliminary

A:Molecule type: DNA  
A:Residues: 1-855 <MAK>  
A:Experimental source: strain TM2  
A:Note: sequence extracted from NCBI backbone (NCBIN:89826, NCBIIP:89854)  
C:Superfamily: feline immunodeficiency virus env polyprotein  
C:Keywords: glycoprotein; transmembrane protein

Query Match 35.2%; Score 51; DB 2; Length 855;  
Best Local Similarity 56.2%; Pred. No. 22;  
Matches 9; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 QSSWTRVFQSWMDRN 16  
||| : :  
Db 383 QSGSWIRTISSWKQRN 398

RESULT 9  
F75357  
hypothetical protein - Deinococcus radiodurans (strain R1)  
C:Species: Deinococcus radiodurans  
C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 31-Mar-2000  
C:Accession: F75357  
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Smith, H.O.; Venter, J.C.; Fraser, C.M.  
Science 286, 1571-1577, 1999  
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.  
A:Reference number: A75250; MUID:20036896  
A:Accession: F75357  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-328 <WHI>  
A:Cross-references: GB:AE002017; GB:AE000513; NID:g6459527; PIDN:AAF11318.1; PID:g6459527  
A:Experimental source: strain R1  
C:Genetics:  
A:Gene: DR1757  
A:Map position: 1

Query Match 34.8%; Score 50.5; DB 2; Length 328;  
Best Local Similarity 41.7%; Pred. No. 9.9;  
Matches 10; Conservative 3; Mismatches 6; Indels 5; Gaps 2;

QY 1 QSSWTRVFQSWMDNLGRGSSAP 24  
: ||| : :  
Db 83 EHGWTTR----WWNRQ-GRGMPSP 101

RESULT 10  
S29946  
surface glycoprotein - feline immunodeficiency virus (fragment)  
C:Species: feline immunodeficiency virus  
C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 26-Aug-1999  
C:Accession: S29946  
R:Rigby, M.A.  
submitted to the EMBL Data Library, November 1992  
A:Reference number: S29946  
A:Accession: S29946  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-144 <RIG>  
A:Cross-references: EMBL:X69495; NID:g59269; PIDN:CAA49249.1; PID:g938167  
C:Superfamily: feline immunodeficiency virus env polyprotein  
C:Keywords: glycoprotein

Query Match 34.5%; Score 50; DB 2; Length 144;  
Best Local Similarity 56.2%; Pred. No. 5;  
Matches 9; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 QSSWTRVFQSWMDRN 16  
: ||| : :  
Db 383 QSGSWIRTISSWKQRN 398

Db 41 QPGSWLRVSISSWKORN 56

RESULT 11

PQ0619  
envelope protein - feline immunodeficiency virus (isolate UK 5) (fragment)  
C:Species: feline immunodeficiency virus  
C>Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 07-May-1999  
C:Accession: PQ0619  
R:Rigby, M.A.; Holmes, E.C.; Pistello, M.; Mackay, A.; Brown, A.J.L.; Neil, J.C.  
J. Gen. Virol. 74, 425-436, 1993

A:Title: Evolution of structural proteins of feline immunodeficiency virus: Molecular evolution  
A:Reference number: JQ2003; MUID:93187604  
A:Accession: PQ0619  
A:Status: nucleic acid sequence not shown  
A:Molecule type: DNA  
A:Residues: 1-157 <RIG>  
A:Cross-references: GB:X69495  
C:Genetics:  
A:Gene: env  
C:Superfamily: feline immunodeficiency virus env polyprotein  
C:Keywords: envelope protein; glycoprotein  
F:92/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 34.5%; Score 50; DB 2; Length 157;  
Best Local Similarity 56.2%; Pred. No. 5.5;  
Matches 9; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 QSSWTRVFQSWDRN 16

Db 57 QPGSWLRVSISSWKORN 72

RESULT 12

B33329  
cysteine-rich secretory protein 2 type I precursor - human  
N:Alternate names: testis-specific protein  
C:Species: Homo sapiens (man)  
C>Date: 09-Mar-1990 #sequence\_revision 09-Mar-1990 #text\_change 20-Jun-2000  
C:Accession: B33329; S68682  
R:Kasahara, M.; Gutknecht, J.; Brew, K.; Spurr, N.; Goodfellow, P.N.  
Genomics 5, 527-534, 1989  
A:Title: Cloning and mapping of a testis-specific gene with sequence similarity to a sperm  
A:Reference number: A33329; MUID:90129048  
A:Accession: B33329  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-243 <RAS>  
A:Cross-references: GB:M25532; NID:g339882; PIDN:AAA61220.1; PID:g339883  
R:Kraetzschmar, J.; Haendler, B.; Eberspaecher, U.; Roosterman, D.; Donner, P.; Schleuniger, J. J. Biochem. 236, 827-836, 1996

A:Title: The human cysteine-rich secretory protein (CRISP) family. Primary structure and  
A:Reference number: S68681; MUID:96270732

A:Accession: S68682

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-243 <KRA>

A:Cross-references: EMBL:X95239; NID:g1262816; PIDN:CAA64526.1; PID:g1262817

C:Genetics:

A:Gene: GDB:TPX1

A:Cross-references: GDB:I20760; OMIM:187430

A:Map position: 6p21-qter

C:Superfamily: cysteine-rich secretory protein 1

F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-243/Product: cysteine-rich secretory protein 2 type I #status predicted <MAT>

Query Match 34.5%; Score 50; DB 2; Length 243;  
Best Local Similarity 37.0%; Pred. No. 8.6;  
Matches 10; Conservative 5; Mismatches 8; Indels 4; Gaps 1;

QY 3 SSWTRVFQSWDRNL-----GRGSAPS 25

Db 105 TSWSSAIQSWYDEILDVYGVGPKSPN 131

RESULT 13

T31521  
hypothetical protein Y116A8C.23 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C>Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 04-Mar-2000  
C:Accession: T31521  
R:McMurray, A.

submitted to the EMBL Data Library, October 1999

A:Reference number: Z21041

A:Accession: T31521

A:Status: preliminary; translated from GB/EMBL/DDBU

A:Molecule type: DNA

A:Residues: 1-264 <WIL>

A:Cross-references: EMBL:AL117204; PIDN:CAB55155.1; CESP:Y116A8C.23

A:Experimental source: clone Y116A8C

C:Genetics:

A:Gene: CESP:Y116A8C.23

A:Introns: 42/3; 102/3; 178/3; 213/3

C:Superfamily: Caenorhabditis elegans hypothetical protein Y116A8C.23

Query Match 34.5%; Score 50; DB 2; Length 264;  
Best Local Similarity 56.2%; Pred. No. 9.3;  
Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 11 SWWDRNLGRGSSAPSQ 26

Db 235 SYWERTFGRARSASQ 250

RESULT 14

B83081  
hypothetical protein PA4512 [imported] - Pseudomonas aeruginosa (strain PAO1)  
C:Species: Pseudomonas aeruginosa  
C>Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000  
C:Accession: B83081  
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Adaman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lory, S.; Olson, M.V.  
Nature 406, 959-964, 2000  
A:Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathogen  
A:Reference number: A82950; MUID:20437337  
A:Accession: B83081  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-299 <STO>

A:Cross-references: GB:AE004865; GB:AE004091; NID:g9950752; PIDN:AAG07900.1; GSPDB:GN

A:Experimental source: strain PAO1

C:Genetics:

A:Gene: PA4512

Query Match 34.5%; Score 50; DB 2; Length 299;  
Best Local Similarity 29.2%; Pred. No. 11;  
Matches 7; Conservative 6; Mismatches 11; Indels 0; Gaps 0;

QY 2 SSSWTRVFQSWDRNLGRGSSAPS 25

Db 224 TQGWATAFNRWFSRNVMAAAPN 247

RESULT 15

A48335  
cytoplasmic inclusion protein - potato virus Y (strain O)  
C:Species: potato virus Y, PVY  
C>Date: 17-Feb-1994 #sequence\_revision 17-Feb-1994 #text\_change 02-Feb-2001  
C:Accession: A48335  
R:Ohshima, K.; Inoue, A.K.; Shikata, E.  
Arch. Virol. 128, 15-27, 1993

A:Title: Molecular cloning, sequencing, and expression in Escherichia coli of the potato  
A:Reference number: A48335; MUID:93119268  
A:Accession: A48335  
A>Status: preliminary  
A:Molecule type: genomic RNA  
A:Residues: 1-634 <OHS>  
A:Cross-references: GB:S51663; NID:g262852; PIDN:AAB24777.1; PID:g262853  
A>Note: sequence extracted from NCBI backbone (NCBIN:121707, NCBIP:121709)  
C:Superfamily: tobacco etch virus genome polyprotein  
C:Keywords: nucleotide binding; P-loop  
F:85-92/Region: nucleotide-binding motif A (P-loop)

Query Match 34.5%; Score 50; DB 2; Length 634;  
Best Local Similarity 43.8%; Pred. No. 23;  
Matches 7; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 9 FQSWMDRNLGRGSSAP 24  
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Db 35 FSDWMDRQIQMGHTLP 50

Search completed: October 9, 2001, 15:54:05  
Job time: 235 sec

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MRQSSSWTRVTFQSWWDRNLGRGSSAPSQ1

Part 2

; Entered [jdelaval 9-Oct-01 15:46]  
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SRHSSYPAGTDEDEGMGEEPSFPRGRSRSAFNNLWAAQRYGRELRRMXDEFVDSFKKGLPRPKSAGTATQ  
MRQSSSWTRVTFQSWWDRNLGRGSSAPSQ1

Part 3

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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 9, 2001, 15:52:36 ; Search time 25.99 Seconds  
(without alignments)  
16.637 Million cell updates/sec

Title: US-09-580-523-l\_copy\_103\_123  
Perfect score: 112  
Sequence: 1 NLWAAQRYGRELRLMSDEFVD 21

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 197339 seqs, 20590346 residues

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
1: /cgn2\_6/ptodata/2/1aa/5A\_COMB.pep:\*  
2: /cgn2\_6/ptodata/2/1aa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/2/1aa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/2/1aa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/2/1aa/PTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/2/1aa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	112	100.0	166	1	US-08-665-617-2
2	112	100.0	168	2	US-08-717-123-2
3	112	100.0	168	3	US-08-985-335-1
4	112	100.0	168	3	US-08-985-335-7
5	102	91.1	23	1	US-08-333-565-10
6	102	91.1	23	2	US-08-661-479-10
7	102	91.1	59	2	US-08-733-505A-55
8	102	91.1	59	2	US-08-733-505A-56
9	102	91.1	59	2	US-08-733-505A-57
10	102	91.1	59	2	US-08-733-505A-58
11	102	91.1	204	1	US-08-333-565-2
12	102	91.1	204	2	US-08-661-479-2
13	102	91.1	204	2	US-08-733-505A-1
14	102	91.1	204	2	US-08-733-505A-12
15	102	91.1	204	2	US-08-733-505A-13
16	102	91.1	204	2	US-08-733-505A-14
17	99	88.4	204	2	US-08-717-123-3
18	86	76.8	16	1	US-08-333-565-26
19	86	76.8	16	2	US-08-661-479-26
20	61	54.5	11	2	US-08-733-505A-34
21	61	54.5	11	2	US-08-706-741B-69
22	61	54.5	11	2	US-08-924-695A-69
23	45	40.2	380	1	US-08-153-848-40
24	45	40.2	380	3	US-09-299-843A-40
25	45	40.2	380	5	PCT-US93-11153-40
26	44	39.3	587	4	US-09-147-923-2
27	44	39.3	1008	2	US-08-680-336-30

28	42	37.5	432	3	US-09-075-087-2	Sequence 2, Appli
29	42	37.5	432	4	US-09-472-971-1	Sequence 1, Appli
30	42	37.5	876	1	US-08-785-429-2	Sequence 2, Appli
31	42	37.5	876	3	US-08-996-621-2	Sequence 2, Appli
32	41	36.6	883	2	US-08-596-366-2	Sequence 2, Appli
33	41	36.6	883	2	US-08-967-104-2	Sequence 2, Appli
34	41	36.6	1410	3	US-09-335-409-3	Sequence 3, Appli
35	39	34.8	185	1	US-08-233-389C-1	Sequence 1, Appli
36	39	34.8	185	2	US-08-801-863-1	Sequence 1, Appli
37	39	34.8	185	2	US-08-486-596A-1	Sequence 1, Appli
38	39	34.8	185	2	US-09-004-713-1	Sequence 1, Appli
39	38	33.9	186	1	US-08-698-551-6	Sequence 6, Appli
40	38	33.9	186	2	US-08-602-228-6	Sequence 6, Appli
41	38	33.9	186	2	US-08-649-341A-6	Sequence 6, Appli
42	38	33.9	186	2	US-08-494-440B-6	Sequence 6, Appli
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45	38	33.9	186	2	US-08-839-031A-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1  
US-08-665-617-2  
; Sequence 2, Application US/08665617  
; Patent No. 5663316  
; GENERAL INFORMATION:  
; APPLICANT: Xudong, Yin  
; TITLE OF INVENTION: Gene and Protein for Regulation of Cell Death  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Saliwanchik & Saliwanchik  
; STREET: 2421 N.W. 41st Street, Suite A-1  
; CITY: Gainesville  
; STATE: Florida  
; COUNTRY: USA  
; ZIP: 32606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/665.617  
; FILING DATE:  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Saliwanchik, David R.  
; REGISTRATION NUMBER: 31,794  
; REFERENCE/DOCKET NUMBER: CL-8  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (352) 375-8100  
; TELEFAX: (352) 372-5800  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 166 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-665-617-2

Query Match 100.0%; Score 112; DB 1; Length 166;  
Best Local Similarity 100.0%; Pred. No. 5.9e-11;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 NLWAAQRYGRELRLMSDEFVD 21  
Db 101 NLWAAQRYGRELRLMSDEFVD 121

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RESULT      3
US-08-985-335-1
; Sequence 1, Application US/08985335
; Patent No. 6080847
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Yue, Henry
; APPLICANT: Lal, Preeti
; APPLICANT: Shah, Purvi
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
; TITLE OF INVENTION: PROLIFERATION
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER-READABLE FORM:
; MEDIUM TYPE: Diskette

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3  US-08-985-335-7
4  ; Sequence 7, Application US/08985335
5  ; Patent No. 6080847
6  ;
7  ; GENERAL INFORMATION:
8  ;
9  ; APPLICANT: Hillman, Jennifer L.
10 ; APPLICANT: Yue, Henry
11 ; APPLICANT: Lai, Preeti
12 ; APPLICANT: Shah, Purvi
13 ; APPLICANT: Corley, Neil C.
14 ;
15 ; TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
16 ;
17 ; TITLE OF INVENTION: PROLIFERATION
18 ;
19 ; NUMBER OF SEQUENCES: 9
20 ;
21 ; CORRESPONDENCE ADDRESS:
22 ;
23 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.
24 ;
25 ; STREET: 3174 Porter Dr.
26 ;
27 ; CITY: Palo Alto
28 ;
29 ; STATE: CA
30 ;
31 ; COUNTRY: USA
32 ;
33 ; ZIP: 94304
34 ;
35 ; COMPUTER READABLE FORM:
36 ;
37 ; MEDIUM TYPE: Diskette
38 ;
39 ; COMPUTER: IBM Compatible
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41 ; OPERATING SYSTEM: DOS
42 ;
43 ; SOFTWARE: FastSEQ for Windows Version 2.0
44 ;
45 ; CURRENT APPLICATION DATA:
46 ;
47 ; APPLICATION NUMBER: US/08/985,335
48 ;
49 ; FILING DATE: Filed herewith
50 ;
51 ; PRIORITY APPLICATION DATA:
52 ;
53 ; APPLICATION NUMBER:
54 ;
55 ; FILING DATE:
56 ;
57 ; ATTORNEY/AGENT INFORMATION:
58 ;
59 ; NAME: Billings, Lucy J.
60 ;
61 ; REGISTRATION NUMBER: 36,749
62 ;
63 ; REFERENCE/DOCKET NUMBER: PF-0421 US
64 ;
65 ; TELECOMMUNICATION INFORMATION:

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; TELEPHONE: 650-855-0555  
; TELEFAX: 650-845-4166  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 168 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: GenBank  
; CLONE: 1683637  
US-08-985-335-7

Query Match 100.0%; Score 112; DB 3; Length 168;  
Best Local Similarity 100.0%; Pred. No. 6e-11;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLWAAQRYGRELRRMSDEFVD 21  
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DB 103 NLWAAQRYGRELRRMSDEFVD 123

RESULT 5  
US-08-333-565-10  
; Sequence 10, Application US/08333565  
; Patent No. 5622852  
; GENERAL INFORMATION:  
; APPLICANT: KORSMEYER, Stanley J.  
; TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH  
; TITLE OF INVENTION: REGULATOR  
; NUMBER OF SEQUENCES: 59  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend Khourie and Crew  
; STREET: 379 Lytton Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: US  
; ZIP: 94301  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/333,565  
; FILING DATE: 31-OCT-1994  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 15726A-000700  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 326-2400  
; TELEFAX: (415) 326-2422  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 23 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-333-565-10

Query Match 91.1%; Score 102; DB 1; Length 23;  
Best Local Similarity 100.0%; Pred. No. 3e-10;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLWAAQRYGRELRRMSDEF 19  
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DB 3 NLWAAQRYGRELRRMSDEF 21

RESULT 6  
US-08-661-479-10  
; Sequence 10, Application US/08661479  
; Patent No. 584209  
; GENERAL INFORMATION:  
; APPLICANT: KORSMEYER, Stanley J.  
; TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH  
; TITLE OF INVENTION: REGULATOR  
; NUMBER OF SEQUENCES: 59  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend Khourie and Crew  
; STREET: 379 Lytton Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: US  
; ZIP: 94301  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/661,479  
; FILING DATE: 11-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/333,565  
; FILING DATE: 31-OCT-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 15726A-000700  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 326-2400  
; TELEFAX: (415) 326-2422  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 23 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-661-479-10

Query Match 91.1%; Score 102; DB 2; Length 23;  
Best Local Similarity 100.0%; Pred. No. 3e-10;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLWAAQRYGRELRRMSDEF 19  
|||||  
DB 3 NLWAAQRYGRELRRMSDEF 21

RESULT 7  
US-08-733-505A-55  
; Sequence 55, Application US/08733505A  
; Patent No. 5856445  
; GENERAL INFORMATION:  
; APPLICANT: KORSMEYER, STANLEY J.  
; TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF  
; TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR  
; NUMBER OF SEQUENCES: 60  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: HOWELL & HAFFERKAMP, L.C.  
; STREET: 7733 FORSYTH BLVD., SUITE 1400  
; CITY: ST. LOUIS  
; STATE: MISSOURI  
; COUNTRY: USA  
; ZIP: 63105  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/733,505A  
FILING DATE:  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: HOLLAND, DONALD R.  
REGISTRATION NUMBER: 35,197  
REFERENCE/DOCKET NUMBER: 965458  
TELEPHONE: (314) 727-5188  
TELEFAX: (314) 727-6092  
INFORMATION FOR SEQ ID NO: 55:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 59 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-733-505A-55

Query Match 91.1%; Score 102; DB 2; Length 59;  
Best Local Similarity 100.0%; Pred. No. 8.2e-10;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLWAAQRYGRELRRMSDEF 19  
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Db 41 NLWAAQRYGRELRRMSDEF 59

RESULT 8  
US-08-733-505A-56  
Sequence 56, Application US/087333505A  
Patent No. 5856445  
GENERAL INFORMATION:  
APPLICANT: KORSMEYER, STANLEY J.  
TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF  
BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR  
NUMBER OF SEQUENCES: 60  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: HOWELL & HAFERKAMP, L.C.  
STREET: 7733 FORSYTH BLVD., SUITE 1400  
CITY: ST. LOUIS  
STATE: MISSOURI  
COUNTRY: USA  
ZIP: 63105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/733,505A  
FILING DATE:  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: HOLLAND, DONALD R.  
REGISTRATION NUMBER: 35,197  
REFERENCE/DOCKET NUMBER: 965458  
TELEPHONE: (314) 727-5188  
TELEFAX: (314) 727-6092  
INFORMATION FOR SEQ ID NO: 56:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 59 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-733-505A-56

Query Match 91.1%; Score 102; DB 2; Length 59;  
Best Local Similarity 100.0%; Pred. No. 8.2e-10;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLWAAQRYGRELRRMSDEF 19  
|||||  
Db 41 NLWAAQRYGRELRRMSDEF 59

RESULT 9  
US-08-733-505A-57  
Sequence 57, Application US/087333505A  
Patent No. 5856445  
GENERAL INFORMATION:  
APPLICANT: KORSMEYER, STANLEY J.  
TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF  
BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR  
NUMBER OF SEQUENCES: 60  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: HOWELL & HAFERKAMP, L.C.  
STREET: 7733 FORSYTH BLVD., SUITE 1400  
CITY: ST. LOUIS  
STATE: MISSOURI  
COUNTRY: USA  
ZIP: 63105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/733,505A  
FILING DATE:  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: HOLLAND, DONALD R.  
REGISTRATION NUMBER: 35,197  
REFERENCE/DOCKET NUMBER: 965458  
TELEPHONE: (314) 727-5188  
TELEFAX: (314) 727-6092  
INFORMATION FOR SEQ ID NO: 57:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 59 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-733-505A-57

Query Match 91.1%; Score 102; DB 2; Length 59;  
Best Local Similarity 100.0%; Pred. No. 8.2e-10;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLWAAQRYGRELRRMSDEF 19  
|||||  
Db 41 NLWAAQRYGRELRRMSDEF 59

RESULT 10  
US-08-733-505A-58  
Sequence 58, Application US/087333505A  
Patent No. 5856445  
GENERAL INFORMATION:  
APPLICANT: KORSMEYER, STANLEY J.  
TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF  
BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR  
NUMBER OF SEQUENCES: 60  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: HOWELL & HAFERKAMP, L.C.



RESULT 14  
US-08-733-505A-12  
; Sequence 12, Application US/08733505A  
; Patent No. 5856445  
; GENERAL INFORMATION:  
; APPLICANT: KORSMEYER, STANLEY J.  
; TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF  
; BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR  
; NUMBER OF SEQUENCES: 60  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: HOWELL & HAFERKAMP, L.C.  
; STREET: 7733 FORSYTH BLVD., SUITE 1400  
; CITY: ST. LOUIS

CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: HOLLAND, DONALD R.  
REGISTRATION NUMBER: 35,197  
REFERENCE/DOCKET NUMBER: 965458  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (314) 727-5188  
TELEFAX: (314) 727-6092  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 204 amino acids





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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 9, 2001, 16:08:31 ; Search time 36.31 Seconds  
(without alignments)  
27.430 Million cell updates/sec

Title: US-09-580-523-1\_COPY\_103\_123  
Perfect score: 112  
Sequence: 1 NLWAAQRYGRELRLMSDEFVD 21

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 311045 seqs, 47428042 residues

Total number of hits satisfying chosen parameters: 311045

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending\_Patents\_AA\_New:\*  
1: /cgn2\_6/ptodata/2/paa/PCT\_NEW\_COMB.pep.\*  
2: /cgn2\_6/ptodata/2/paa/US06\_NEW\_COMB.pep.\*  
3: /cgn2\_6/ptodata/2/paa/US07\_NEW\_COMB.pep.\*  
4: /cgn2\_6/ptodata/2/paa/US08\_NEW\_COMB.pep.\*  
5: /cgn2\_6/ptodata/2/paa/US09\_NEW\_COMB.pep.\*  
6: /cgn2\_6/ptodata/2/paa/US60\_NEW\_COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	112	100.0	125	5	US-09-834-366-16338
2	112	100.0	168	5	US-09-922-378-2
3	112	100.0	201	1	PCT-US01-18569-2762
4	99	88.4	204	5	US-09-922-378-3
5	50	44.6	232	5	US-09-902-540-9711
6	46	41.1	483	1	PCT-US01-08631-38983
7	46	41.1	484	5	US-09-902-540-13700
8	45	40.2	380	5	US-09-088-337B-40
9	43.5	38.8	168	1	PCT-US01-08631-43907
10	43.5	38.8	681	1	PCT-US01-08631-52397
11	43	38.4	200	5	US-09-758-475-257
12	43	38.4	270	1	PCT-US01-26189-162
13	43	38.4	270	5	US-09-934-455-162
14	42.5	37.9	572	5	US-09-902-540-13770
15	42	37.5	262	5	US-09-803-110-9772
16	42	37.5	526	5	US-09-573-655A-1977
17	41.5	37.1	189	5	US-09-803-110-11897
18	41.5	37.1	465	1	PCT-US01-08631-35041
19	41	36.6	83	5	US-09-834-366-26246
20	41	36.6	208	1	PCT-US01-08631-37956
21	41	36.6	208	1	PCT-US01-08631-41486
22	41	36.6	209	1	PCT-US01-08631-44176
23	41	36.6	292	5	US-09-738-626-4426
24	41	36.6	319	5	US-09-927-796-64
25	41	36.6	362	5	US-09-925-298-617
26	41	36.6	848	5	US-09-902-540-10014
27	40.5	36.2	380	1	PCT-US01-08631-37140

28	40.5	36.2	877	1	PCT-US01-14827-15394	Sequence 15394, A
29	40.5	36.2	1309	1	PCT-US01-14827-15396	Sequence 15396, A
30	40.5	36.2	1350	1	PCT-US01-14827-15390	Sequence 15390, A
31	40	35.7	69	5	US-09-649-866A-2290	Sequence 2290, Ap
32	40	35.7	126	5	US-09-758-453-337	Sequence 337, App
33	40	35.7	126	5	US-09-758-453-337	Sequence 337, App
34	40	35.7	141	1	PCT-US01-08631-51026	Sequence 51026, A
35	40	35.7	172	5	US-09-758-466-567	Sequence 567, App
36	40	35.7	243	5	US-09-803-110-10646	Sequence 10646, A
37	40	35.7	294	5	US-09-803-110-11563	Sequence 11563, A
38	40	35.7	398	1	PCT-US01-08631-38702	Sequence 38702, A
39	40	35.7	447	1	PCT-US01-08631-48287	Sequence 48287, A
40	40	35.7	463	1	PCT-US01-08631-53631	Sequence 53631, A
41	40	35.7	568	5	US-09-902-540-14309	Sequence 14309, A
42	40	35.7	663	5	US-60-312-544-10009	Sequence 10009, A
43	40	35.7	1241	1	PCT-US01-08631-36270	Sequence 36270, A
44	39.5	35.3	112	5	US-09-595-332A-1432	Sequence 1432, Ap
45	39	34.8	83	5	US-09-834-366-18666	Sequence 18666, A

ALIGNMENTS

RESULT 1  
US-09-834-366-16338  
; Sequence 16338, Application US/09834366  
; GENERAL INFORMATION:  
; APPLICANT: Bejanin, Stephanie  
; APPLICANT: Tanaka, Hiroaki  
; APPLICANT: Dumas Milne Edwards, Jean Baptiste  
; APPLICANT: Jobert, Severin  
; APPLICANT: Giordano, Jean-Yves  
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.  
; FILE REFERENCE: 81.US2.REG  
; CURRENT APPLICATION NUMBER: US/09/834,366  
; PRIOR FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: US 60/197,873  
; NUMBER OF SEQ ID NOS: 52153  
; SOFTWARE: Patent.pm  
; SEQ ID NO 16338  
; LENGTH: 125  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-834-366-16338

Query Match 100.0%; Score 112; DB 5; Length 125;  
Best Local Similarity 100.0%; Pred. No. 2.1e-10;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 NLWAAQRYGRELRLMSDEFVD 21  
Db 103 NLWAAQRYGRELRLMSDEFVD 123

RESULT 2  
US-09-922-378-2  
; Sequence 2, Application US/09922378  
; GENERAL INFORMATION:  
; APPLICANT: Horne, William A.  
; APPLICANT: Oltersdorf, Tilman  
; TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC  
; FILE REFERENCE: 480140.428D3  
; CURRENT APPLICATION NUMBER: US/09/922,378  
; CURRENT FILING DATE: 2001-08-03  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 168  
; TYPE: PRT  
; ORGANISM: Homo sapiens

US-09-922-378-2

Query Match 100.0%; Score 112; DB 5; Length 168;  
Best Local Similarity 100.0%; Pred. No. 2.9e-10;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLWAAQRYGRELRRMSDEFVD 21  
|||||  
Db 103 NLWAAQRYGRELRRMSDEFVD 123

RESULT 3

PCT-US01-18569-2762  
; Sequence 2762, Application PC/TUS0118569  
; GENERAL INFORMATION:  
; APPLICANT: Human Genome Sciences, Inc.  
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
; FILE REFERENCE: PA133PCT  
; CURRENT APPLICATION NUMBER: PCT/US01/18569  
; CURRENT FILING DATE: 2001-06-07  
; PRIOR APPLICATION NUMBER: 60/209,467  
; PRIOR FILING DATE: 2000-06-07  
; NUMBER OF SEQ ID NOS: 4360  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2762  
; LENGTH: 201  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (37)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
; NAME/KEY: SITE  
; LOCATION: (146)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
; NAME/KEY: SITE  
; LOCATION: (169)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
; NAME/KEY: SITE  
; LOCATION: (174)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
PCT-US01-18569-2762

Query Match 100.0%; Score 112; DB 1; Length 201;  
Best Local Similarity 100.0%; Pred. No. 3.6e-10;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLWAAQRYGRELRRMSDEFVD 21  
|||||  
Db 111 NLWAAQRYGRELRRMSDEFVD 131

RESULT 4

US-09-922-378-3  
; Sequence 3, Application US/09922378  
; GENERAL INFORMATION:  
; APPLICANT: Horne, William A.  
; APPLICANT: Oltersdorf, Tilman  
; TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC  
; TITLE OF INVENTION: ACIDS AND METHODS OF USE  
; FILE REFERENCE: 480140.428D3  
; CURRENT APPLICATION NUMBER: US/09/922,378  
; CURRENT FILING DATE: 2001-08-03  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 204  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-922-378-3

Query Match 88.4%; Score 99; DB 5; Length 204;  
Best Local Similarity 94.7%; Pred. No. 4e-08;  
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLWAAQRYGRELRRMSDEF 19  
|||||  
Db 140 NLWAAQRYGRELRRMTDEF 158

RESULT 5

US-09-902-540-9711  
; Sequence 9711, Application US/09902540  
; GENERAL INFORMATION:  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Wiegand, Roger C.  
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof  
; FILE REFERENCE: 38-10(15849)B  
; CURRENT APPLICATION NUMBER: US/09/902,540  
; CURRENT FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: 60/217,883  
; PRIOR FILING DATE: 2000-07-10  
; NUMBER OF SEQ ID NOS: 16825  
; SEQ ID NO 9711  
; LENGTH: 232  
; TYPE: PRT  
; ORGANISM: Myxococcus xanthus  
US-09-902-540-9711

Query Match 44.6%; Score 50; DB 5; Length 232;  
Best Local Similarity 50.0%; Pred. No. 2.2;  
Matches 9; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 NLWAAQRYGRELRRMSDE 18  
|||  
Db 157 SLWIGHRWGKGLRRMHCE 174

RESULT 6

PCT-US01-08631-38983  
; Sequence 38983, Application PC/TUS0108631  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc  
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES  
; FILE REFERENCE: 21272-049  
; CURRENT APPLICATION NUMBER: PCT/US01/08631  
; CURRENT FILING DATE: 2001-03-30  
; PRIOR APPLICATION NUMBER: 09/540,217  
; PRIOR FILING DATE: 2000-03-31  
; PRIOR APPLICATION NUMBER: 09/649,167  
; PRIOR FILING DATE: 2000-08-23  
; NUMBER OF SEQ ID NOS: 60736  
; SOFTWARE: Custom  
; SEQ ID NO 38983  
; LENGTH: 483  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: DOMAIN  
; LOCATION: (41)..(93)  
; OTHER INFORMATION: Heat shock hsp70 proteins family proteins domain identified  
; OTHER INFORMATION: by eMATRIX, accession number BL00297C, p-value=1.000e-40, raw  
; OTHER INFORMATION: of 9.51  
; NAME/KEY: DOMAIN  
; LOCATION: (1)..(450)  
; OTHER INFORMATION: Hsp70 protein domain identified by Pfam, accession name  
; OTHER INFORMATION: HSP70, E-value=3.2e-153, Pfam score of 522.4  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(483)  
; OTHER INFORMATION: Xaa = X or \* as defined in Table 2



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; SOFTWARE: Custom
; SEQ ID NO 52397
; LENGTH: 681
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (13)..(33)
; OTHER INFORMATION: ALPHA-2A ADRENERGIC RECEPTOR SIGNATURE domain identified by
; OTHER INFORMATION: eMATRIX, accession number PR00558C, p-value=7.330e-09, raw score
; OTHER INFORMATION: 6.54
; NAME/KEY: DOMAIN
; LOCATION: (421)..(509)
; OTHER INFORMATION: PCI domain identified by Pfam, accession name PCI, E-value=
; OTHER INFORMATION: 2.1e-13, Pfam score of 58.0
; NAME/KEY: misc_feature
; LOCATION: (1)..(681)
; OTHER INFORMATION: Xaa = X or * as defined in Table 2
PCT-US01-08631-52397
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Query Match 38.8%; Score 43.5; DB 1; Length 681;
Best Local Similarity 55.6%; Pred. No. 76;
Matches 10; Conservative 1; Mismatches 6; Indels 1; Gaps 1;

QY 3 WAAQRYGRELRRMSD-EF 19
   : || || | | | |
Db 525 WSLQNRGRERRKQDLEF 542
```

```
RESULT 11
US-09-758-475-257
; Sequence 257, Application US/09758475
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PM035
; CURRENT APPLICATION NUMBER: US/09/758,475
; CURRENT FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 466
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 257
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (7)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-758-475-257
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Query Match 38.4%; Score 43; DB 5; Length 100;
Best Local Similarity 45.0%; Pred. No. 11;
Matches 9; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

QY 1 NLWAAQRYGRELRRMSDEFV 20
   : || | | | |
Db 20 NMWAAQLTGKARRWQVEFV 39
```

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RESULT 12
PCT-US01-26189-162
; Sequence 162, Application PC/TUS0126189
; GENERAL INFORMATION:
; APPLICANT: Pilgrim, Marsha
; APPLICANT: Creelman, Robert
; APPLICANT: Dubell, Arnold
; APPLICANT: Heard, Jacqueline
```

```
; APPLICANT: Jiang, Cai-Zhong
; APPLICANT: Keddle, James
; APPLICANT: Adam, Luc
; APPLICANT: Ratcliffe, Oliver
; APPLICANT: Reuber, Lynne
; APPLICANT: Riechmann, Jose Luis
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Pineda, Omaira
; TITLE OF INVENTION: Genes for Modifying Plant Traits IV
; FILE REFERENCE: MBI-0024
; CURRENT APPLICATION NUMBER: PCT/US01/26189
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227439
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: MBI-0022
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: MBI-0023
; PRIOR FILING DATE: 2001-04-17
; NUMBER OF SEQ ID NOS: 464
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 162
; LENGTH: 270
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
PCT-US01-26189-162
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Query Match 38.4%; Score 43; DB 1; Length 270;
Best Local Similarity 40.0%; Pred. No. 33;
Matches 8; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 NLWAAQRYGRELRRMSDEFV 20
   : || | | | |
Db 78 NMEQPIYGRDFKRSSSMV 97
```

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RESULT 13
US-09-934-455-162
; Sequence 162, Application US/09934455
; GENERAL INFORMATION:
; APPLICANT: Adam, Luc
; APPLICANT: Creelman, Robert
; APPLICANT: Dubell, Arnold
; APPLICANT: Heard, Jacqueline
; APPLICANT: Jiang, Cai-Zhong
; APPLICANT: Keddle, James
; APPLICANT: Pilgrim, Marsha
; APPLICANT: Ratcliffe, Oliver
; APPLICANT: Reuber, Lynne
; APPLICANT: Riechmann, Jose Luis
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Pineda, Omaira
; TITLE OF INVENTION: Genes for Modifying Plant Traits IV
; FILE REFERENCE: MBI-0025
; CURRENT APPLICATION NUMBER: US/09/934,455
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227439
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: MBI-0022
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: MBI-0023
; PRIOR FILING DATE: 2001-04-17
; NUMBER OF SEQ ID NOS: 516
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 162
; LENGTH: 270
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-934-455-162
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Query Match 38.4%; Score 43; DB 5; Length 270;
Best Local Similarity 40.0%; Pred. No. 33;
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Job time: 381 sec

Matches	8;	Conservative	4;	Mismatches	8;	Indels	0;	Gaps	0;
---------	----	--------------	----	------------	----	--------	----	------	----

Qy 1 NLWAAQRYGRELRRMSDEFV 20  
|::| |||:::| | |  
Db 78 NMFQPQIYGRDFKRSSSMV 97

**RESULT 14**

```

US-09-902-540-13770
; Sequence 13770, Application US/09902540
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 13770
; LENGTH: 572
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-13770

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Query Match 37.9%; Score 42.5; DB 5; Length 572;

Query Match	37.9%	Score 42.5;	DB 5;	Length 572;
Best Local Similarity	50.0%;	Pred. No. 90;		
Matches 10;	Conservative	1;	Mismatches	2;
			Indels	7;
			Gaps	1;

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QY 1 NLWAAQRY-----GRELR 13
    ||||:||| ||||
Db 553 NLWAGRRYQPPALNPGRVLR 57
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**RESULT** 15

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US-09-803-110-9772
; Sequence 9772, Application US/09803110
; GENERAL INFORMATION:
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15490)D
; CURRENT APPLICATION NUMBER: US/09/803,110
; CURRENT FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 09/739,449
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: US 09/514,000
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: US 60/168,139
; PRIOR FILING DATE: 1999-12-01
; NUMBER OF SEQ ID NOS: 13351
; SEQ ID NO 9772
; LENGTH: 262
; TYPE: PRT
; ORGANISM: Agrobacterium tumefaciens
US-09-803-110-9772

```

### Query Match

Query Match	37.58;	Score 42;	DB 5;	Length 262;
Best Local Similarity	58.3%;	Pred. No. 46;		
Matches	7;	Conservative	2;	Mismatches
			3;	Indels
			0;	Gaps

Qy	1	NLWAAQRYGREL	12
		: : : : : :	
Db	38	NIWAAAYREGHEI	49

Search completed: October 9, 2001, 16:08:31





GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: October 9, 2001, 15:53:27 ; Search time 44.37 Seconds  
(without alignments)  
28.693 Million cell updates/sec

Title: US-09-580-523-1\_copy\_103\_123

Perfect score: 112

Sequence: 1 NLWAAQRYGRELRLRMSDFVD 21

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A\_Geneseq\_0601.\*  
1: /SID88/gcgdata/geneseq/geneseq/AA1980.DAT.\*  
2: /SID88/gcgdata/geneseq/geneseq/AA1981.DAT.\*  
3: /SID88/gcgdata/geneseq/geneseq/AA1982.DAT.\*  
4: /SID88/gcgdata/geneseq/geneseq/AA1983.DAT.\*  
5: /SID88/gcgdata/geneseq/geneseq/AA1984.DAT.\*  
6: /SID88/gcgdata/geneseq/geneseq/AA1985.DAT.\*  
7: /SID88/gcgdata/geneseq/geneseq/AA1986.DAT.\*  
8: /SID88/gcgdata/geneseq/geneseq/AA1987.DAT.\*  
9: /SID88/gcgdata/geneseq/geneseq/AA1988.DAT.\*  
10: /SID88/gcgdata/geneseq/geneseq/AA1989.DAT.\*  
11: /SID88/gcgdata/geneseq/geneseq/AA1990.DAT.\*  
12: /SID88/gcgdata/geneseq/geneseq/AA1991.DAT.\*  
13: /SID88/gcgdata/geneseq/geneseq/AA1992.DAT.\*  
14: /SID88/gcgdata/geneseq/geneseq/AA1993.DAT.\*  
15: /SID88/gcgdata/geneseq/geneseq/AA1994.DAT.\*  
16: /SID88/gcgdata/geneseq/geneseq/AA1995.DAT.\*  
17: /SID88/gcgdata/geneseq/geneseq/AA1996.DAT.\*  
18: /SID88/gcgdata/geneseq/geneseq/AA1997.DAT.\*  
19: /SID88/gcgdata/geneseq/geneseq/AA1998.DAT.\*  
20: /SID88/gcgdata/geneseq/geneseq/AA1999.DAT.\*  
21: /SID88/gcgdata/geneseq/geneseq/AA2000.DAT.\*  
22: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	112	100.0	166	18	AAW32476
2	112	100.0	168	19	AAW55779
3	112	100.0	168	21	AAW33512
4	112	100.0	168	22	AAW70368
5	112	100.0	168	22	AAW48287
6	102	91.1	23	17	AAW95166
7	102	91.1	26	21	AAW37001
8	102	91.1	26	21	AAW37002
9	102	91.1	27	21	AAW37003
10	102	91.1	27	21	AAW37056
11	102	91.1	28	21	AAW37055

12	102	91.1	59	19	AAW61319	Mutant BCL-XL/BCL-
13	102	91.1	59	19	AAW61320	Mutant BCL-XL/BCL-
14	102	91.1	59	19	AAW61321	Mutant BCL-XL/BCL-
15	102	91.1	59	19	AAW61322	Mutant BCL-XL/BCL-
16	102	91.1	162	22	AAW70370	Shorter murine BAD
17	102	91.1	204	17	AAW95168	bcl-x(L)/bcl-2 ass
18	102	91.1	204	19	AAW61315	Murine BCL-XL/BCL-
19	102	91.1	204	19	AAW61316	Mutant BCL-XL/BCL-
20	102	91.1	204	19	AAW61317	Mutant BCL-XL/BCL-
21	102	91.1	204	19	AAW61318	Mutant BCL-XL/BCL-
22	102	91.1	204	19	AAW58832	Murine BAD protein
23	102	91.1	204	22	AAW70369	Longer murine BAD
24	91	81.2	26	21	AAW96321	Mammalian Bad Bcl-
25	91	81.2	26	22	AAW70371	BAD BH3 consensus
26	86	76.8	16	17	AAW95163	bcl-x(L)/bcl-2 ass
27	83	74.1	16	20	AAW05421	Human BAD BH3 doma
28	83	74.1	16	21	AAW37029	Bcl2 polypeptide B
29	75	67.0	18	22	AAW70379	BAD BH3 domain reg
30	75	67.0	20	22	AAW70380	BAD BH3 domain reg
31	73	65.2	16	20	AAW05422	Mouse BAD BH3 doma
32	73	65.2	16	21	AAW37028	Bcl2 polypeptide B
33	46	41.1	16	21	AAW37046	Bcl2 polypeptide B
34	46	41.1	26	21	AAW97352	Mammalian Bim Bcl-
35	46	41.1	26	22	AAW70378	BIM BH3 consensus
36	46	41.1	27	21	AAW37019	Bcl2 polypeptide B
37	46	41.1	138	20	AAW98164	Human Bim-L mutant
38	46	41.1	138	20	AAW98165	Human Bim-L mutant
39	46	41.1	138	20	AAW98166	Human Bim-L mutant
40	46	41.1	138	20	AAW98167	Human Bim-L mutant
41	46	41.1	138	20	AAW98168	Human Bim-L mutant
42	46	41.1	138	20	AAW98157	Human Bcl-2 intera
43	46	41.1	198	20	AAW98158	Human Bcl-2 intera
44	45	40.2	377	22	AAW48502	Mouse APJ polypept
45	45	40.2	380	21	AAW90660	Human mutant G pro

#### ALIGNMENTS

RESULT 1  
AAW32476  
ID AAW32476 standard; Protein; 166 AA.  
XX  
AC AAW32476;  
XX  
DT 15-JAN-1998 (first entry)  
XX  
DE BBC6 protein for regulating cell death.  
XX  
KW BBC6 gene; cell death; cell cycle; Bcl2; human.  
XX  
OS Homo sapiens.  
XX  
PN US5663316-A.  
XX  
PD 02-SEP-1997.  
XX  
PF 18-JUN-1996; 96US-0665617.  
XX  
PR 18-JUN-1996; 96US-0665617.  
XX  
PA (CLON-) CLONTECH LAB INC.  
XX  
PI Xudong Y;  
XX  
DR WPI; 1997-447980/41.  
XX  
DR N-PSDB; AAT91561.  
XX  
PT Isolated BBC6 gene - encodes a protein that regulates cell death  
PT through interaction with Bcl-2  
XX  
PS Claim 1; Column 11-12; 7pp; English.  
XX

CC The present sequence represents a protein of 166 amino acids. The  
 CC sequence is disclosed as being a protein called BBC6 which regulates  
 CC cell death through interaction with Bcl-2. The DNA may be used for the  
 CC production of the recombinant protein, which can be used in unspecified  
 CC therapeutic or diagnostic procedures, as a molecular weight marker, and  
 CC to raise antibodies that can be used in unspecified diagnostic or  
 CC therapeutic applications and to reduce or eliminate the biological  
 CC activity of the BBC6 protein in vivo.

XX Sequence 166 AA;

Query Match 100.0%; Score 112; DB 18; Length 166;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-10;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NLWAAOYRGRELRRMSDEFVD 21  
 |||||  
 Db 101 nlwaagyrgrelrrmsdefvd 121

#### RESULT 2

AAW55779  
 ID AAW55779 standard; Protein; 168 AA.

XX AAW55779;

XX 17-JUL-1998 (first entry)

XX Human Bcl-xL/Bcl-2 associated death promoting polypeptide.

XX Human; Bcl-xL/Bcl-2 associated death promoting polypeptide; Bad;  
 KW programmed cell death; apoptosis.

XX Homo sapiens.

XX WO9812328-A2.

XX 26-MAR-1998.

XX 18-SEP-1997; 97WO-US16991.

XX 20-SEP-1996; 96US-0717123.

XX (IDUN-) IDUN PHARM INC.

XX Horne WA, Oltersdorf T;

XX WPI; 1998-217267/19.

XX N-PSDB; AAV25877.

XX Bad gene mediating apoptosis - used to develop products for treating  
 XX e.g. neurodegenerative disease, cancers or autoimmune disease

XX Claim 8; Fig 1; 41pp; English.

XX The present sequence is the human Bcl-xL/Bcl-2 associated  
 CC death promoting polypeptide, Bad, the binding of which to Bcl-xL  
 CC results in the induction of programmed cell death, i.e. apoptosis.  
 CC Bad can be used in screening assays for compounds to treat or  
 CC prevent diseases characterised by apoptotic cell death, such as  
 CC neurodegenerative disorders, e.g. Alzheimer's and Parkinson's  
 CC disease, amyotrophic lateral sclerosis, retinitis pigmentosa and  
 CC cerebellar degeneration, and myelodysplastic syndromes, e.g.  
 CC aplastic anaemia and ischaemic injury including myocardial  
 CC infarction, stroke and reperfusion injury. Assays can also be  
 CC used to obtain apoptosis enhancing compounds to treat or prevent  
 CC diseases characterised by the loss of apoptotic cell death, such as  
 CC cancers, e.g. lymphoma and hormone dependent tumours, autoimmune  
 CC diseases, e.g. systemic lupus erythematosus and immune-mediated  
 CC glomerulonephritis and viral infections, e.g. herpesvirus,  
 CC poxvirus or adenovirus infection. Bad can also be used for  
 CC detection and diagnosis.

XX SQ Sequence 168 AA;

Query Match 100.0%; Score 112; DB 19; Length 168;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-10;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NLWAAOYRGRELRRMSDEFVD 21  
 |||||  
 Db 103 nlwaagyrgrelrrmsdefvd 123

#### RESULT 3

AAAB13512  
 ID AAB13512 standard; protein; 168 AA.

XX AAB13512;

XX 02-NOV-2000 (first entry)

XX Human cell proliferation protein APOP-1.

XX Human; cell proliferation; APOP-1; cancer; inflammation; infection;  
 KW trauma; neurodegenerative disease; ischaemic injury; wasting disease.

XX Homo sapiens.

XX US6080847-A.

XX 27-JUN-2000.

XX 04-DEC-1997; 97US-0985335.

XX 04-DEC-1997; 97US-0985335.

XX (INCY-) INCYTE PHARM INC.

XX Corley NC, Hillman JL, Yue H, Lal P, Shah P;

XX WPI; 2000-451230/39.

XX N-PSDB; AAA63332.

XX Novel polynucleotide and polypeptide sequences of proteins associated  
 XX with cell proliferation for diagnosis, prevention and treatment of e.g.  
 XX cancer, acquired immunodeficiency syndrome, and Parkinson's disease

XX Example 8; Fig 1; 58pp; English.

XX The present sequence is the human APOP-1 protein. This protein, which  
 CC shares structural and chemical homology with Bcl-2, is involved in cell  
 CC proliferation. Its coding sequence was isolated by screening a synovial  
 CC tissue CDNA library using a computer search for amino acid sequence  
 CC alignments. The gene and protein can be used in the treatment of various  
 CC cancers, disorders with associated inflammation such as Addison's  
 CC disease, adult respiratory distress syndrome, allergies, anaemia, asthma,  
 CC atherosclerosis, Crohn's disease, ulcerative colitis, diabetes mellitus,  
 CC emphysema, glomerulonephritis, gout, Graves' disease, irritable bowel  
 CC syndrome, lupus erythematosus, multiple sclerosis, myasthenia gravis,  
 CC myocardial or pericardial inflammation, osteoporosis, rheumatoid  
 CC arthritis, Sjogren's syndrome and autoimmune thyroiditis, complications  
 CC of cancer, haemodialysis and extracorporeal circulation, infections,  
 CC trauma, disorders with associated apoptosis including AIDS and other  
 CC infectious and genetic immunodeficiencies, neurodegenerative diseases  
 CC such as Alzheimer's disease and Parkinson's disease, ischaemic injuries  
 CC such as myocardial infarction, and wasting diseases including cachexia.

XX SQ Sequence 168 AA;

Query Match 100.0%; Score 112; DB 21; Length 168;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-10;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



DE bcl-x(L)/bcl-2 associated death promoter epitope, residues 138-160.  
 XX  
 KW Epitope; murine; bcl-x(L)/bcl-2 associated death promoter; Bad; stroke;  
 XX polypeptide; bcl-x; cell death; regulate; BH1; BH2; apoptotic cell death;  
 KW cytokine deprivation; IL-3 dependent cell line; immunodeficiency; AIDS;  
 KW neurodegenerative disease; senescence; ischaemia; neoplasia.  
 XX  
 OS Mus musculus.  
 XX  
 PN W09613614-A1.  
 XX  
 XX 09-MAY-1996.  
 PD  
 XX 31-OCT-1995; 95WO-US14246.  
 XX  
 XX 31-OCT-1994; 94US-0333565.  
 PR  
 XX (UNIW ) UNIV WASHINGTON.  
 PA  
 PI Korsmeyer SJ;  
 XX  
 XX WPI; 1996-251465/25.  
 DR  
 XX Polynucleotide encoding bcl-x(L)/bcl-2 associated death promoter -  
 PT useful to treat neoplasia and apoptosis and to identify agents  
 PT inhibiting its binding to bcl-2 or bcl-x(L) to form heteromultimers  
 XX  
 XX Claim 2; Page 103; 130pp; English.  
 XX  
 CC The sequences given in AAR95155-67 represent epitopes derived from the  
 CC murine bcl-x(L)/bcl-2 associated death promoter (Bad) polypeptide (see  
 CC also AAR95168). Bad is a 22.1 kD protein which interacts with bcl-2 and  
 CC bcl-x proteins and regulates cell death. It has homology to the bcl-2-  
 CC related family clustered in the BH1 and BH2 domain. Bad has been found  
 CC to hybridize to bcl-x(L) and bcl-2 in yeast two-hybrid assays and in  
 CC vivo in mammalian cells. Overexpressed Bad counters the death  
 CC inhibitory activity of bcl-x(L), but is much less effective at countering  
 CC the death inhibitory activity of bcl-2. Bad expression can accelerate  
 CC apoptotic cell death induced by cytokine deprivation in an IL-3 dependent  
 CC cell line expressing bcl-x(L), and its also counters the death repressor  
 CC activity of bcl-x(L). Bad competes with Bax for binding to bcl-x(L).  
 CC Bad may be used to identify agents which inhibit its binding to bcl-2  
 CC or bcl-x(L) to form heterodimers. Such agents may be used to treat  
 CC neurodegenerative diseases, immunodeficiency diseases, e.g. AIDS,  
 CC senescence or ischaemia.  
 XX  
 SQ Sequence 23 AA;

Query Match 91.1%; Score 102; DB 17; Length 23;  
 Best Local Similarity 100.0%; Pred. No. 7.7e-10;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLWAAQRYGRELRRMSDEF 19  
 DB 3 nlwaaqrygrellrmsdef 21

RESULT 7

AAB37001  
 ID AAB37001 standard; peptide; 26 AA.  
 XX  
 XX AAB37001;

XX 28-FEB-2001 (first entry)  
 DT  
 XX Bcl2 polypeptide BH3 domain peptide #1.

XX Cytostatic; neuroprotective; anti-HIV; virucide; cerebroprotective;  
 KW cardiant; Bcl-2 superfamily; BH3 domain; cell death agonist; Bad;  
 KW apoptosis modulation; B cell lymphoma/leukemia 2; cancer; prostate;  
 KW colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma;  
 KW melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS;

KW stroke; myocardial infarction.

XX Homo sapiens.

XX W0200059526-A1.

XX 12-OCT-2000.

XX 06-APR-2000; 2000WO-US09352.

XX 07-APR-1999; 99US-0128202.

XX (UYJE-) UNIV JEFFERSON THOMAS.

XX Huang Z, Wang J, Zhang Z, Shan S, Lu Z;

XX WPI; 2000-679325/66.

XX New peptide conjugates for modulating apoptosis or for inhibiting B  
 PT cell lymphoma/leukemia 2 (Bcl-2) function, especially useful for  
 PT treating neurodegenerative disorders, stroke, or cancer -

XX Claim 18; Page 17; 74pp; English.

XX The invention relates to a peptide conjugate having the formula:  
 CC (R-X)n-peptide where n = 1-10; X = C=O, when the R-X group is attached  
 CC to the N-terminus of the peptide, or a side chain of the peptide where  
 CC the functional group of the side chain is NH2 or OH; or X = O or NH,  
 CC when the R-X group is attached to the C-terminus of the peptide, or a  
 CC side chain of the peptide, where the side chain functional group is COOH  
 CC or CONH2; and R = 2-18C alkyl or alkoxy, 2-14C alkenyl containing one  
 CC or two double bonds, cyclobutyl, cyclopentyl, cyclohexyl optionally  
 CC monosubstituted with a 1-5C straight or branched chain alkyl group,  
 CC phenyl optionally monosubstituted with a 1-5C straight or branched chain  
 CC alkyl group, or benzyl. The peptides AAB37001-B37058 represent examples  
 CC of the peptide portion of the conjugate. The peptides represent analogues  
 CC of a Bcl-2 superfamily polypeptide corresponding to amino acids 72-97 of  
 CC the BH3 domain of the cell death agonist Bad. The peptide conjugate is  
 CC useful for modulating apoptosis in the cells of a subject, or for  
 CC reversing B cell lymphoma/leukemia 2 (Bcl-2)-mediated blockage of  
 CC apoptosis in cancer cells. It is also useful for inhibiting Bcl-2  
 CC function. In particular, the peptide conjugate is useful for treating a  
 CC subject afflicted with a cancer characterized by cancer cells that  
 CC express Bcl-2. The cancer includes prostate, colorectal, gastric,  
 CC non-small lung, renal or thyroid cancers, neuroblastoma, melanoma, or  
 CC acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide  
 CC conjugate is also useful for treating disorders characterized by  
 CC increased apoptosis, e.g. neurodegenerative disorders, acquired  
 CC immunodeficiency syndrome (AIDS), stroke or myocardial infarction.

XX Sequence 26 AA;

Query Match 91.1%; Score 102; DB 21; Length 26;  
 Best Local Similarity 100.0%; Pred. No. 8.8e-10;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLWAAQRYGRELRRMSDEF 19  
 DB 1 nlwaaqrygrellrmsdef 19

RESULT 8

AAB37002

ID AAB37002 standard; peptide; 26 AA.

XX AAB37002;

XX 28-FEB-2001 (first entry)

XX Bcl2 polypeptide BH3 domain peptide #2.

XX Cytostatic; neuroprotective; anti-HIV; virucide; cerebroprotective;

KW cardiant; Bcl-2 superfamily; BH3 domain; cell death agonist; Bad;  
 KW apoptosis modulation; B cell lymphoma/leukemia 2; cancer; prostate;  
 KW colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma;  
 KW melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS;  
 KW stroke; myocardial infarction.  
 XX Homo sapiens.  
 OS WO2000059526-A1.  
 XX 12-OCT-2000.  
 XX 06-APR-2000; 2000WO-US09352.  
 PF 07-APR-1999; 99US-0128202.  
 XX (UYJE-) UNIV JEFFERSON THOMAS.  
 XX Huang Z, Wang J, Zhang Z, Shan S, Lu Z;  
 DR WPI; 2000-679325/66.  
 XX New peptide conjugates for modulating apoptosis or for inhibiting B  
 PT cell lymphoma/leukemia 2 (Bcl-2) function, especially useful for  
 PT treating neurodegenerative disorders, stroke, or cancer -  
 XX Claim 18; Page 17; 74pp; English.  
 CC The invention relates to a peptide conjugate having the formula:  
 CC (R-X)n-peptide where n = 1-10; X = C-O, when the R-X group is attached  
 CC to the N-terminus of the peptide, or a side chain of the peptide where  
 CC the functional group of the side chain is NH2 or OH; or X = O or NH,  
 CC when the R-X group is attached to the C-terminus of the peptide, or a  
 CC side chain of the peptide, where the side chain functional group is COOH  
 CC or CONH2; and R = 2-18C alkyl or alkoxy, 2-14C alkenyl containing one  
 CC or two double bonds, cyclobutyl, cyclopentyl, cyclohexyl optionally  
 CC monosubstituted with a 1-5C straight or branched chain alkyl group,  
 CC phenyl optionally monosubstituted with a 1-5C straight or branched chain  
 CC alkyl group, or benzyl. The peptides AAB37001-B37058 represent examples  
 CC of the peptide portion of the conjugate. The peptides represent analogues  
 CC of a Bcl-2 superfamily polypeptide corresponding to amino acids 72-97 of  
 CC the BH3 domain of the cell death agonist Bad. The peptide conjugate is  
 CC useful for modulating apoptosis in the cells of a subject, or for  
 CC reversing B cell lymphoma/leukemia 2 (Bcl-2)-mediated blockage of  
 CC apoptosis in cancer cells. It is also useful for inhibiting Bcl-2  
 CC function. In particular, the peptide conjugate is useful for treating a  
 CC subject afflicted with a cancer characterized by cancer cells that  
 CC express Bcl-2. The cancer includes prostate, colorectal, gastric,  
 CC non-small lung, renal or thyroid cancers, neuroblastoma, melanoma, or  
 CC acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide  
 CC conjugate is also useful for treating disorders characterized by  
 CC increased apoptosis, e.g. neurodegenerative disorders, acquired  
 CC immunodeficiency syndrome (AIDS), stroke or myocardial infarction.  
 XX Sequence 26 AA;  
 SQ  
 Query Match 91.1%; Score 102; DB 21; Length 26;  
 Best Local Similarity 100.0%; Pred. No. 8.8e-10;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 NLWAAQRYGRELRRMSDEF 19  
 DB 1 nlwaaqrygrellrmsdef 19  
 RESULT 9  
 AAB37003  
 ID AAB37003 standard; peptide; 27 AA.  
 XX AAB37003;  
 AC AAB37003;  
 XX 28-FEB-2001 (first entry)  
 DT

XX Bcl2 polypeptide BH3 domain peptide #3.  
 DE cardiant; neuroprotective; anti-HIV; virucide; cerebroprotective;  
 XX cardiant; Bcl-2 superfamily; BH3 domain; cell death agonist; Bad;  
 KW apoptosis modulation; B cell lymphoma/leukemia 2; cancer; prostate;  
 KW colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma;  
 KW melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS;  
 KW stroke; myocardial infarction.  
 XX Homo sapiens.  
 OS WO2000059526-A1.  
 XX 12-OCT-2000.  
 XX 06-APR-2000; 2000WO-US09352.  
 PF 07-APR-1999; 99US-0128202.  
 XX (UYJE-) UNIV JEFFERSON THOMAS.  
 XX Huang Z, Wang J, Zhang Z, Shan S, Lu Z;  
 DR WPI; 2000-679325/66.  
 XX New peptide conjugates for modulating apoptosis or for inhibiting B  
 PT cell lymphoma/leukemia 2 (Bcl-2) function, especially useful for  
 PT treating neurodegenerative disorders, stroke, or cancer -  
 XX Claim 18; Page 17; 74pp; English.  
 CC The invention relates to a peptide conjugate having the formula:  
 CC (R-X)n-peptide where n = 1-10; X = C-O, when the R-X group is attached  
 CC to the N-terminus of the peptide, or a side chain of the peptide where  
 CC the functional group of the side chain is NH2 or OH; or X = O or NH,  
 CC when the R-X group is attached to the C-terminus of the peptide, or a  
 CC side chain of the peptide, where the side chain functional group is COOH  
 CC or CONH2; and R = 2-18C alkyl or alkoxy, 2-14C alkenyl containing one  
 CC or two double bonds, cyclobutyl, cyclopentyl, cyclohexyl optionally  
 CC monosubstituted with a 1-5C straight or branched chain alkyl group,  
 CC phenyl optionally monosubstituted with a 1-5C straight or branched chain  
 CC alkyl group, or benzyl. The peptides AAB37001-B37058 represent examples  
 CC of the peptide portion of the conjugate. The peptides represent analogues  
 CC of a Bcl-2 superfamily polypeptide corresponding to amino acids 72-97 of  
 CC the BH3 domain of the cell death agonist Bad. The peptide conjugate is  
 CC useful for modulating apoptosis in the cells of a subject, or for  
 CC reversing B cell lymphoma/leukemia 2 (Bcl-2)-mediated blockage of  
 CC apoptosis in cancer cells. It is also useful for inhibiting Bcl-2  
 CC function. In particular, the peptide conjugate is useful for treating a  
 CC subject afflicted with a cancer characterized by cancer cells that  
 CC express Bcl-2. The cancer includes prostate, colorectal, gastric,  
 CC non-small lung, renal or thyroid cancers, neuroblastoma, melanoma, or  
 CC acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide  
 CC conjugate is also useful for treating disorders characterized by  
 CC increased apoptosis, e.g. neurodegenerative disorders, acquired  
 CC immunodeficiency syndrome (AIDS), stroke or myocardial infarction.  
 XX Sequence 27 AA;  
 SQ  
 Query Match 91.1%; Score 102; DB 21; Length 27;  
 Best Local Similarity 100.0%; Pred. No. 9.2e-10;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 NLWAAQRYGRELRRMSDEF 19  
 DB 1 nlwaaqrygrellrmsdef 19  
 RESULT 10  
 AAB37056  
 ID AAB37056 standard; peptide; 27 AA.



OY 1 NLWAAQRYGRELRRMSDEF 19  
Db 2 nlwaaqrygrellrmsdef 20

RESULT 12  
AAW61319  
ID AAW61319 standard; Protein; 59 AA.

XX AC AAW61319;

XX 07-OCT-1998 (first entry)

XX Mutant BCL-XL/BCL-2 associated cell death regulator #4.

XX Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein;  
KW serine substituted mutant; apoptosis; cancer; viral infection.

XX OS Mus sp.  
OS Synthetic.

XX WO9817682-A1.

XX 30-APR-1998.

XX 17-OCT-1997; 97WO-US19175.

XX 18-OCT-1996; 96US-0733505.

XX (UNIW ) UNIV WASHINGTON.

XX Korsmeyer SJ;

XX WPI; 1998-261422/23.

XX N-PSDB; AAV27837.

PT New mutant BAD polypeptide with phosphorylatable serine replaced -  
PT useful for, e.g. treating reduced apoptosis such as in cancer or  
PT viral infection

PS Claim 8; Page 73; 95pp; English.

XX The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell  
CC death regulator) proteins, having an amino acid other than Ser at  
CC position 112 and/or 136, relative to the murine BAD 204 aa sequence. The  
CC present sequence represents a mutant BAD protein. Also described are: (1)  
CC fragments of mutant BAD protein able to decrease cell viability; (2)  
CC fusion proteins of mutant BAD with a heterologous polypeptide that  
CC increases intracellular delivery. Mutant BAD proteins are used to treat  
CC or prevent diseases associated with reduced apoptosis, e.g. cancer,  
CC viral infection, lymphoproliferation, arthritis, infertility,  
CC inflammation and autoimmune disease. Polynucleotide sequences encoding  
CC mutant BAD proteins can be used similarly by gene therapy or to produce  
CC transgenic animals for use as disease models or in drug screening. BAD  
CC proteins phosphorylated at specified Ser are used to screen for enhancers  
CC and inhibitors of serine-phosphatase. Inhibitors are potentially useful  
CC in treatment of excessive apoptosis such as AIDS, neurodegeneration,  
CC aging or ischaemic cell death. The apoptotic status of cells is  
CC determined by measuring relative amounts of phosphorylated and non-  
CC phosphorylated BAD, by usual immunoassays. Mutant BAD proteins have  
CC greater death-promoting activity than wild-type BAD which can become  
CC phosphorylated on the specified Ser, forming a product that does not  
CC heterodimerise with BCL-2 or BCL-XL but instead binds to 14-3-3 family  
CC proteins in the cytosol, thus promoting cell survival. The mutants with  
CC Ser substituted cannot bind 14-3-3.

XX Sequence 59 AA;

Query Match 91.1%; Score 102; DB 19; Length 59;  
Best Local Similarity 100.0%; Pred. No. 2.le-09;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NLWAAQRYGRELRRMSDEF 19  
Db 41 nlwaaqrygrellrmsdef 59

RESULT 13  
AAW61320  
ID AAW61320 standard; Protein; 59 AA.

XX AC AAW61320;

XX 07-OCT-1998 (first entry)

XX Mutant BCL-XL/BCL-2 associated cell death regulator #5.

XX Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein;  
KW serine substituted mutant; apoptosis; cancer; viral infection.

XX OS Mus sp.  
OS Synthetic.

XX WO9817682-A1.

XX 30-APR-1998.

XX 17-OCT-1997; 97WO-US19175.

XX 18-OCT-1996; 96US-0733505.

XX (UNIW ) UNIV WASHINGTON.

XX Korsmeyer SJ;

XX WPI; 1998-261422/23.

XX N-PSDB; AAV27838.

PT New mutant BAD polypeptide with phosphorylatable serine replaced -  
PT useful for, e.g. treating reduced apoptosis such as in cancer or  
PT viral infection

PS Claim 8; Page 73; 95pp; English.

XX The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell  
CC death regulator) proteins, having an amino acid other than Ser at  
CC position 112 and/or 136, relative to the murine BAD 204 aa sequence. The  
CC present sequence represents a mutant BAD protein. Also described are: (1)  
CC fragments of mutant BAD protein able to decrease cell viability; (2)  
CC fusion proteins of mutant BAD with a heterologous polypeptide that  
CC increases intracellular delivery. Mutant BAD proteins are used to treat  
CC or prevent diseases associated with reduced apoptosis, e.g. cancer,  
CC viral infection, lymphoproliferation, arthritis, infertility,  
CC inflammation and autoimmune disease. Polynucleotide sequences encoding  
CC mutant BAD proteins can be used similarly by gene therapy or to produce  
CC transgenic animals for use as disease models or in drug screening. BAD  
CC proteins phosphorylated at specified Ser are used to screen for enhancers  
CC and inhibitors of serine-phosphatase. Inhibitors are potentially useful  
CC in treatment of excessive apoptosis such as AIDS, neurodegeneration,  
CC aging or ischaemic cell death. The apoptotic status of cells is  
CC determined by measuring relative amounts of phosphorylated and non-  
CC phosphorylated BAD, by usual immunoassays. Mutant BAD proteins have  
CC greater death-promoting activity than wild-type BAD which can become  
CC phosphorylated on the specified Ser, forming a product that does not  
CC heterodimerise with BCL-2 or BCL-XL but instead binds to 14-3-3 family  
CC proteins in the cytosol, thus promoting cell survival. The mutants with  
CC Ser substituted cannot bind 14-3-3.

XX Sequence 59 AA;

Query Match 91.1%; Score 102; DB 19; Length 59;  
Best Local Similarity 100.0%; Pred. No. 2.le-09;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLWAAQRYGRELRRMSDEF 19  
| | | | | | | | | | | | | | | | | |  
Db 41 nlwaaqrygrellrmsdef 59

RESULT 14  
AAW61321  
ID AAW61321 standard; Protein; 59 AA.

XX AC AAW61321;  
XX DT 07-OCT-1998 (first entry)  
XX DE Mutant BCL-XL/BCL-2 associated cell death regulator #6.  
XX Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein;  
KW serine substituted mutant; apoptosis; cancer; viral infection.  
XX Mus sp.  
OS Synthetic.  
XX WO9817682-A1.  
XX PN 30-APR-1998.  
XX PD 17-OCT-1997; 97WO-US19175.  
XX PF 18-OCT-1996; 96US-0733505.  
XX PR (UNIW ) UNIV WASHINGTON.  
XX PA Korsmeyer SJ;  
XX PI WPI: 1998-261422/23.  
XX DR N-PSDB; AAV27839.

XX New mutant BAD polypeptide with phosphorylatable serine replaced -  
PT useful for, e.g. treating reduced apoptosis such as in cancer or  
PT viral infection  
XX Claim 8; Page 73-74; 95pp; English.

XX The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell  
CC death regulator) proteins, having an amino acid other than Ser at  
CC position 112 and/or 136, relative to the murine BAD 204 aa sequence. The  
CC present sequence represents a mutant BAD protein. Also described are: (1)  
CC fragments of mutant BAD protein able to decrease cell viability; (2)  
CC fusion proteins of mutant BAD with a heterologous polypeptide that  
CC increases intracellular delivery. Mutant BAD proteins are used to treat  
CC or prevent diseases associated with reduced apoptosis, e.g. cancer,  
CC viral infection, lymphoproliferation, arthritis, infertility,  
CC inflammation and autoimmune disease. Polynucleotide sequences encoding  
CC mutant BAD proteins can be used similarly by gene therapy or to produce  
CC transgenic animals for use as disease models or in drug screening. BAD  
CC proteins phosphorylated at specified Ser are used to screen for enhancers  
CC and inhibitors of serine-phosphatase. Inhibitors are potentially useful  
CC in treatment of excessive apoptosis such as AIDS, neurodegeneration,  
CC aging or ischaemic cell death. The apoptotic status of cells is  
CC determined by measuring relative amounts of phosphorylated and non-  
CC phosphorylated BAD, by usual immunoassays. Mutant BAD proteins have  
CC greater death-promoting activity than wild-type BAD which can become  
CC phosphorylated on the specified Ser, forming a product that does not  
CC heterodimerise with BCL-2 or BCL-XL but instead binds to 14-3-3 family  
CC proteins in the cytosol, thus promoting cell survival. The mutants with  
CC Ser substituted cannot bind 14-3-3.

XX Sequence 59 AA;

Query Match 91.1%; Score 102; DB 19; Length 59;  
Best Local Similarity 100.0%; Pred. No. 2.1e-09;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLWAAQRYGRELRRMSDEF 19  
| | | | | | | | | | | | | | | | | |  
Db 41 nlwaaqrygrellrmsdef 59

RESULT 15  
AAW61322  
ID AAW61322 standard; Protein; 59 AA.

XX AC AAW61322;  
XX DT 07-OCT-1998 (first entry)  
XX DE Mutant BCL-XL/BCL-2 associated cell death regulator #7.  
XX Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein;  
KW serine substituted mutant; apoptosis; cancer; viral infection.  
XX Mus sp.  
OS Synthetic.  
XX WO9817682-A1.  
XX PN 30-APR-1998.  
XX PD 17-OCT-1997; 97WO-US19175.  
XX PF 18-OCT-1996; 96US-0733505.  
XX PR (UNIW ) UNIV WASHINGTON.  
XX PA Korsmeyer SJ;  
XX PI WPI: 1998-261422/23.  
XX DR N-PSDB; AAV27840.

XX New mutant BAD polypeptide with phosphorylatable serine replaced -  
PT useful for, e.g. treating reduced apoptosis such as in cancer or  
PT viral infection  
XX Claim 24; Page 74; 95pp; English.

XX The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell  
CC death regulator) proteins, having an amino acid other than Ser at  
CC position 112 and/or 136, relative to the murine BAD 204 aa sequence. The  
CC present sequence represents a mutant BAD protein. Also described are: (1)  
CC fragments of mutant BAD protein able to decrease cell viability; (2)  
CC fusion proteins of mutant BAD with a heterologous polypeptide that  
CC increases intracellular delivery. Mutant BAD proteins are used to treat  
CC or prevent diseases associated with reduced apoptosis, e.g. cancer,  
CC viral infection, lymphoproliferation, arthritis, infertility,  
CC inflammation and autoimmune disease. Polynucleotide sequences encoding  
CC mutant BAD proteins can be used similarly by gene therapy or to produce  
CC transgenic animals for use as disease models or in drug screening. BAD  
CC proteins phosphorylated at specified Ser are used to screen for enhancers  
CC and inhibitors of serine-phosphatase. Inhibitors are potentially useful  
CC in treatment of excessive apoptosis such as AIDS, neurodegeneration,  
CC aging or ischaemic cell death. The apoptotic status of cells is  
CC determined by measuring relative amounts of phosphorylated and non-  
CC phosphorylated BAD, by usual immunoassays. Mutant BAD proteins have  
CC greater death-promoting activity than wild-type BAD which can become  
CC phosphorylated on the specified Ser, forming a product that does not  
CC heterodimerise with BCL-2 or BCL-XL but instead binds to 14-3-3 family  
CC proteins in the cytosol, thus promoting cell survival. The mutants with  
CC Ser substituted cannot bind 14-3-3.

XX Sequence 59 AA;

Query Match 91.1%; Score 102; DB 19; Length 59;  
Best Local Similarity 100.0%; Pred. No. 2.1e-09;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;







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OM protein - protein search, using sw model

Run on: October 9, 2001, 16:07:48 ; Search time 239.36 seconds  
(without alignments)  
19.464 Million cell updates/sec

Title: US-09-580-523-1-copy\_103\_123  
Sequence: 1 NLWAAQRYGRELRRMSDEVD 21

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2803329 seqs, 221847457 residues  
Total number of hits satisfying chosen parameters: 2803329

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending\_Patents\_AA\_Main:\*

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2: /cgn2\_6/ptodata/2/paa/US06\_COMB.pep.\*  
3: /cgn2\_6/ptodata/2/paa/US07\_COMB.pep.\*  
4: /cgn2\_6/ptodata/2/paa/US080\_COMB.pep.\*  
5: /cgn2\_6/ptodata/2/paa/US081\_COMB.pep.\*  
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11: /cgn2\_6/ptodata/2/paa/US087\_COMB.pep.\*  
12: /cgn2\_6/ptodata/2/paa/US088\_COMB.pep.\*  
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22: /cgn2\_6/ptodata/2/paa/US098\_COMB.pep.\*  
23: /cgn2\_6/ptodata/2/paa/US060\_COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	112	100.0	21	20	US-09-656-399-30
2	112	100.0	21	20	US-09-656-399A-30
3	112	100.0	21	21	US-09-716-395-36
4	112	100.0	22	20	US-09-656-399-29
5	112	100.0	22	20	US-09-656-399A-29
6	112	100.0	23	20	US-09-656-399-28
7	112	100.0	23	20	US-09-656-399A-28
8	112	100.0	24	20	US-09-656-399-27
9	112	100.0	24	20	US-09-656-399A-27
10	112	100.0	25	20	US-09-656-399-10

11	112	100.0	25	20	US-09-656-399-17	Sequence 17, Appl
12	112	100.0	25	20	US-09-656-399-18	Sequence 18, Appl
13	112	100.0	25	20	US-09-656-399-19	Sequence 19, Appl
14	112	100.0	25	20	US-09-656-399-20	Sequence 20, Appl
15	112	100.0	25	20	US-09-656-399A-10	Sequence 10, Appl
16	112	100.0	25	20	US-09-656-399A-17	Sequence 17, Appl
17	112	100.0	25	20	US-09-656-399A-18	Sequence 18, Appl
18	112	100.0	25	20	US-09-656-399A-19	Sequence 19, Appl
19	112	100.0	25	20	US-09-656-399A-20	Sequence 20, Appl
20	112	100.0	25	21	US-09-716-395-20	Sequence 20, Appl
21	112	100.0	25	21	US-09-716-395-26	Sequence 26, Appl
22	112	100.0	25	21	US-09-716-395-27	Sequence 27, Appl
23	112	100.0	25	21	US-09-716-395-28	Sequence 28, Appl
24	112	100.0	25	21	US-09-716-395-29	Sequence 29, Appl
25	112	100.0	63	1	PCT-US97-15871A-12	Sequence 12, Appl
26	112	100.0	63	1	PCT-US98-19765-42	Sequence 42, Appl
27	112	100.0	125	13	US-08-946-039-42	Sequence 42, Appl
28	112	100.0	125	23	US-60-197-873-16338	Sequence 16338, A
29	112	100.0	168	1	PCT-US00-11864-1	Sequence 1, Appl
30	112	100.0	168	12	US-08-883-731-2	Sequence 2, Appl
31	112	100.0	168	17	US-09-375-257-2	Sequence 2, Appl
32	112	100.0	168	17	US-09-376-154-2	Sequence 2, Appl
33	112	100.0	168	18	US-09-410-372-1	Sequence 1, Appl
34	112	100.0	168	18	US-09-410-372-7	Sequence 7, Appl
35	112	100.0	168	18	US-09-456-357-32	Sequence 32, Appl
36	112	100.0	168	19	US-09-580-523-1	Sequence 1, Appl
37	112	100.0	168	19	US-09-587-473-21	Sequence 21, Appl
38	108	96.4	21	20	US-09-656-399-7	Sequence 7, Appl
39	108	96.4	21	20	US-09-656-399A-7	Sequence 7, Appl
40	108	96.4	25	20	US-09-656-399-15	Sequence 15, Appl
41	108	96.4	25	20	US-09-656-399-16	Sequence 16, Appl
42	108	96.4	25	20	US-09-656-399A-15	Sequence 15, Appl
43	108	96.4	25	20	US-09-656-399A-16	Sequence 16, Appl
44	108	96.4	25	21	US-09-716-395-24	Sequence 24, Appl
45	108	96.4	25	21	US-09-716-395-25	Sequence 25, Appl

ALIGNMENTS

RESULT 1  
US-09-656-399-30  
; Sequence 30, Application US/09656399  
; GENERAL INFORMATION:  
; APPLICANT: Abbott Laboratories  
; APPLICANT: Fesik, Steven  
; APPLICANT: Petros, Andrew  
; APPLICANT: Nettesheim, David  
; APPLICANT: Meadows, Bob  
; APPLICANT: Olejniczak, Ed  
; APPLICANT: Zhang, Haichao  
; APPLICANT: Ng, ShiChung  
; APPLICANT: Swift, Kerry  
; APPLICANT: Matayoshi, Ed  
; APPLICANT: Joseph, Mary K.  
; TITLE OF INVENTION: MUTANT PEPTIDES DERIVED FROM BAD AND  
; TITLE OF INVENTION: THEIR USE TO IDENTIFY SUBSTANCES WHICH BIND TO A MEMBER OF  
; TITLE OF INVENTION: THE BCL-2 FAMILY OF PROTEINS  
; FILE REFERENCE: 6370-US.OI  
; CURRENT APPLICATION NUMBER: US/09/656,399  
; CURRENT FILING DATE: 2000-09-06  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 30  
; LENGTH: 21  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Wild-type human BAB peptide  
US-09-656-399-30  
Query Match 100.0%; Score 112; DB 20; Length 21;

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; LENGTH: 22
;
; TYPE: PRT
;
; ORGANISM: Artificial Sequence
;
; FEATURE:

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; OTHER INFORMATION: synthetic peptide  
US-09-656-399A-29

Query Match 100.0%; Score 112; DB 20; Length 22;  
Best Local Similarity 100.0%; Pred. No. 2.3e-10;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLWAAQRYGRELRRMSDEFDV 21  
DB 1 NLWAAQRYGRELRRMSDEFDV 21

## RESULT 6

US-09-656-399-28

; Sequence 28, Application US/09656399

; GENERAL INFORMATION:

; APPLICANT: Abbott Laboratories

; APPLICANT: Fesik, Steven

; APPLICANT: Petros, Andrew

; APPLICANT: Nettesheim, David

; APPLICANT: Meadows, Bob

; APPLICANT: Olejniczak, Ed

; APPLICANT: Zhang, Haichao

; APPLICANT: Ng, Shichung

; APPLICANT: Swift, Kerry

; APPLICANT: Matayoshi, Ed

; APPLICANT: Joseph, Mary K.

; TITLE OF INVENTION: MUTANT PEPTIDES DERIVED FROM BAD AND

; TITLE OF INVENTION: THEIR USE TO IDENTIFY SUBSTANCES WHICH BIND TO A MEMBER OF

; TITLE OF INVENTION: THE BCL-2 FAMILY OF PROTEINS

; FILE REFERENCE: 6370.US.01

; CURRENT APPLICATION NUMBER: US/09/656,399

; CURRENT FILING DATE: 2000-09-06

; NUMBER OF SEQ ID NOS: 30

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 28

; LENGTH: 23

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Wild-type human BAD peptide

US-09-656-399-28

Query Match 100.0%; Score 112; DB 20; Length 23;  
Best Local Similarity 100.0%; Pred. No. 2.4e-10;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLWAAQRYGRELRRMSDEFDV 21  
DB 1 NLWAAQRYGRELRRMSDEFDV 21

## RESULT 7

US-09-656-399A-28

; Sequence 28, Application US/09656399A

; GENERAL INFORMATION:

; APPLICANT: Fesik, Stephen F.

; APPLICANT: Meadows, Robert P.

; APPLICANT: Joseph, Mary K.

; APPLICANT: Olejniczak, Edward T.

; APPLICANT: Petros, Andrew M.

; APPLICANT: Nettesheim, David G.

; APPLICANT: Swift, Kerry M.

; APPLICANT: Matayoshi, Edmund

; APPLICANT: Zhang, Haichao

; TITLE OF INVENTION: MUTANT PEPTIDES DERIVED FROM BAD AND

; TITLE OF INVENTION: THEIR USE TO IDENTIFY SUBSTANCES WHICH BIND TO A MEMBER OF

; TITLE OF INVENTION: THE BCL-2 FAMILY OF PROTEINS

; FILE REFERENCE: 6370.US.01

; CURRENT APPLICATION NUMBER: US/09/656,399A

; CURRENT FILING DATE: 2000-09-06

; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 28  
; LENGTH: 23  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:

; OTHER INFORMATION: synthetic peptide

US-09-656-399A-28

US-09-656-399A-28

Query Match 100.0%; Score 112; DB 20; Length 23;  
Best Local Similarity 100.0%; Pred. No. 2.4e-10;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLWAAQRYGRELRRMSDEFDV 21  
DB 1 NLWAAQRYGRELRRMSDEFDV 21

## RESULT 8

US-09-656-399-27

; Sequence 27, Application US/09656399

; GENERAL INFORMATION:

; APPLICANT: Abbott Laboratories

; APPLICANT: Fesik, Steven

; APPLICANT: Petros, Andrew

; APPLICANT: Nettesheim, David

; APPLICANT: Meadows, Bob

; APPLICANT: Olejniczak, Ed

; APPLICANT: Zhang, Haichao

; APPLICANT: Ng, Shichung

; APPLICANT: Swift, Kerry

; APPLICANT: Matayoshi, Ed

; APPLICANT: Joseph, Mary K.

; TITLE OF INVENTION: MUTANT PEPTIDES DERIVED FROM BAD AND

; TITLE OF INVENTION: THEIR USE TO IDENTIFY SUBSTANCES WHICH BIND TO A MEMBER OF

; TITLE OF INVENTION: THE BCL-2 FAMILY OF PROTEINS

; FILE REFERENCE: 6370.US.01

; CURRENT APPLICATION NUMBER: US/09/656,399

; CURRENT FILING DATE: 2000-09-06

; NUMBER OF SEQ ID NOS: 30

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 27

; LENGTH: 24

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Wild-type human BAD peptide

US-09-656-399-27

Query Match 100.0%; Score 112; DB 20; Length 24;  
Best Local Similarity 100.0%; Pred. No. 2.6e-10;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLWAAQRYGRELRRMSDEFDV 21  
DB 1 NLWAAQRYGRELRRMSDEFDV 21

## RESULT 9

US-09-656-399A-27

; Sequence 27, Application US/09656399A

; GENERAL INFORMATION:

; APPLICANT: Fesik, Stephen F.

; APPLICANT: Meadows, Robert P.

; APPLICANT: Joseph, Mary K.

; APPLICANT: Olejniczak, Edward T.

; APPLICANT: Petros, Andrew M.

; APPLICANT: Nettesheim, David G.

; APPLICANT: Swift, Kerry M.

; APPLICANT: Matayoshi, Edmund

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; APPLICANT: Zhang, Haichao
; TITLE OF INVENTION: MUTANT PEPTIDES DERIVED FROM BAD AND
; THEIR USE TO IDENTIFY SUBSTANCES WHICH BIND TO A MEMBER OF
; TITLE OF INVENTION: THE BCL-2 FAMILY OF PROTEINS
; FILE REFERENCE: 6730.US.01
; CURRENT APPLICATION NUMBER: US/09/656,399A
; CURRENT FILING DATE: 2000-09-06
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-09-656-399A-27

Query Match 100.0%; Score 112; DB 20; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.6e-10;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLWAAQRYGRELRRMSDFVD 21
| | | | | | | | | | | | | | | | | | | | | |
Db 1 NLWAAQRYGRELRRMSDFVD 21

RESULT 10
US-09-656-399-10
; Sequence 10, Application US/09656399
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Pesik, Steven
; APPLICANT: Petros, Andrew
; APPLICANT: Nettesheim, David
; APPLICANT: Meadows, Bob
; APPLICANT: Olejniczak, Ed
; APPLICANT: Zhang, Haichao
; APPLICANT: Ng, Shichung
; APPLICANT: Swift, Kerry
; APPLICANT: Matayoshi, Ed
; APPLICANT: Joseph, Mary K.
; TITLE OF INVENTION: MUTANT PEPTIDES DERIVED FROM BAD AND
; THEIR USE TO IDENTIFY SUBSTANCES WHICH BIND TO A MEMBER OF
; TITLE OF INVENTION: THE BCL-2 FAMILY OF PROTEINS
; FILE REFERENCE: 6370.US.01
; CURRENT APPLICATION NUMBER: US/09/656,399
; CURRENT FILING DATE: 2000-09-06
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: These sequences were chemically synthesized based
; OTHER INFORMATION: on the naturally occurring human BAD protein
US-09-656-399-10

Query Match 100.0%; Score 112; DB 20; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.7e-10;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLWAAQRYGRELRRMSDFVD 21
| | | | | | | | | | | | | | | | | | | | | |
Db 1 NLWAAQRYGRELRRMSDFVD 21

RESULT 11
US-09-656-399-17
; Sequence 17, Application US/09656399
; GENERAL INFORMATION:
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; APPLICANT: Abbott Laboratories
; APPLICANT: Pesik, Steven
; APPLICANT: Petros, Andrew
; APPLICANT: Nettesheim, David
; APPLICANT: Meadows, Bob
; APPLICANT: Olejniczak, Ed
; APPLICANT: Zhang, Haichao
; APPLICANT: Ng, Shichung
; APPLICANT: Swift, Kerry
; APPLICANT: Matayoshi, Ed
; APPLICANT: Joseph, Mary K.
; TITLE OF INVENTION: MUTANT PEPTIDES DERIVED FROM BAD AND
; THEIR USE TO IDENTIFY SUBSTANCES WHICH BIND TO A MEMBER OF
; TITLE OF INVENTION: THE BCL-2 FAMILY OF PROTEINS
; FILE REFERENCE: 6370.US.01
; CURRENT APPLICATION NUMBER: US/09/656,399
; CURRENT FILING DATE: 2000-09-06
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: These sequences were chemically synthesized based
; OTHER INFORMATION: on the naturally occurring human BAD protein
US-09-656-399-17

Query Match 100.0%; Score 112; DB 20; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.7e-10;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLWAAQRYGRELRRMSDFVD 21
| | | | | | | | | | | | | | | | | | | | | |
Db 1 NLWAAQRYGRELRRMSDFVD 21

RESULT 12
US-09-656-399-18
; Sequence 18, Application US/09656399
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Pesik, Steven
; APPLICANT: Petros, Andrew
; APPLICANT: Nettesheim, David
; APPLICANT: Meadows, Bob
; APPLICANT: Olejniczak, Ed
; APPLICANT: Zhang, Haichao
; APPLICANT: Ng, Shichung
; APPLICANT: Swift, Kerry
; APPLICANT: Matayoshi, Ed
; APPLICANT: Joseph, Mary K.
; TITLE OF INVENTION: MUTANT PEPTIDES DERIVED FROM BAD AND
; THEIR USE TO IDENTIFY SUBSTANCES WHICH BIND TO A MEMBER OF
; TITLE OF INVENTION: THE BCL-2 FAMILY OF PROTEINS
; FILE REFERENCE: 6370.US.01
; CURRENT APPLICATION NUMBER: US/09/656,399
; CURRENT FILING DATE: 2000-09-06
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: These sequences were chemically synthesized based
; OTHER INFORMATION: on the naturally occurring human BAD protein
US-09-656-399-18

Query Match 100.0%; Score 112; DB 20; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.7e-10;
```

```
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NLWAAQRYGRELRRMSDEFVD 21
   |||||
Db 1 NLWAAQRYGRELRRMSDEFVD 21

RESULT 13
US-09-656-399-19
; Sequence 19, Application US/09656399
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Fesik, Steven
; APPLICANT: Petros, Andrew
; APPLICANT: Nettesheim, David
; APPLICANT: Meadows, Bob
; APPLICANT: Olejniczak, Ed
; APPLICANT: Zhang, Haichao
; APPLICANT: Ng, ShiChung
; APPLICANT: Swift, Kerry
; APPLICANT: Matayoshi, Ed
; APPLICANT: Joseph, Mary K.
; TITLE OF INVENTION: MUTANT PEPTIDES DERIVED FROM BAD AND
; TITLE OF INVENTION: THEIR USE TO IDENTIFY SUBSTANCES WHICH BIND TO A MEMBER OF
; TITLE OF INVENTION: THE BCL-2 FAMILY OF PROTEINS
; FILE REFERENCE: 6370.US.01
; CURRENT APPLICATION NUMBER: US/09/656.399
; CURRENT FILING DATE: 2000-09-06
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: These sequences were chemically synthesized based
; OTHER INFORMATION: on the naturally occurring human BAD protein
US-09-656-399-19

Query Match 100.0%; Score 112; DB 20; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.7e-10;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NLWAAQRYGRELRRMSDEFVD 21
   |||||
Db 1 NLWAAQRYGRELRRMSDEFVD 21

RESULT 14
US-09-656-399-20
; Sequence 20, Application US/09656399
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Fesik, Steven
; APPLICANT: Petros, Andrew
; APPLICANT: Nettesheim, David
; APPLICANT: Meadows, Bob
; APPLICANT: Olejniczak, Ed
; APPLICANT: Zhang, Haichao
; APPLICANT: Ng, ShiChung
; APPLICANT: Swift, Kerry
; APPLICANT: Matayoshi, Ed
; APPLICANT: Joseph, Mary K.
; TITLE OF INVENTION: MUTANT PEPTIDES DERIVED FROM BAD AND
; TITLE OF INVENTION: THEIR USE TO IDENTIFY SUBSTANCES WHICH BIND TO A MEMBER OF
; TITLE OF INVENTION: THE BCL-2 FAMILY OF PROTEINS
; FILE REFERENCE: 6370.US.01
; CURRENT APPLICATION NUMBER: US/09/656.399
; CURRENT FILING DATE: 2000-09-06
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 20
```

```
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: These sequences were chemically synthesized based
; OTHER INFORMATION: on the naturally occurring human BAD protein
US-09-656-399-20

Query Match 100.0%; Score 112; DB 20; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.7e-10;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NLWAAQRYGRELRRMSDEFVD 21
   |||||
Db 1 NLWAAQRYGRELRRMSDEFVD 21

RESULT 15
US-09-656-399A-10
; Sequence 10, Application US/09656399A
; GENERAL INFORMATION:
; APPLICANT: Fesik, Stephen F.
; APPLICANT: Meadows, Robert P.
; APPLICANT: Joseph, Mary K.
; APPLICANT: Olejniczak, Edward T.
; APPLICANT: Petros, Andrew M.
; APPLICANT: Nettesheim, David G.
; APPLICANT: Swift, Kerry M.
; APPLICANT: Matayoshi, Edmund
; APPLICANT: Zhang, Haichao
; TITLE OF INVENTION: MUTANT PEPTIDES DERIVED FROM BAD AND
; TITLE OF INVENTION: THEIR USE TO IDENTIFY SUBSTANCES WHICH BIND TO A MEMBER OF
; TITLE OF INVENTION: THE BCL-2 FAMILY OF PROTEINS
; FILE REFERENCE: 6730.US.01
; CURRENT APPLICATION NUMBER: US/09/656.399A
; CURRENT FILING DATE: 2000-09-06
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-09-656-399A-10

Query Match 100.0%; Score 112; DB 20; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.7e-10;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NLWAAQRYGRELRRMSDEFVD 21
   |||||
Db 1 NLWAAQRYGRELRRMSDEFVD 21
```

Search completed: October 9, 2001, 16:07:48  
Job time: 498 sec





GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 9, 2001, 15:55:20 ; Search time 17.79 Seconds  
(without alignments)  
40.436 Million cell updates/sec

Title: US-09-580-523-1\_COPY\_103\_123  
Perfect score: 112  
Sequence: 1 NLWAAQRYGRELRRMSDEFVD 21

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	112	100.0	168	1	BAD_HUMAN
2	102	91.1	204	1	BAD_MOUSE
3	47.5	42.4	595	1	VGL1_BPMD2
4	46.5	41.5	503	1	MTBR_BPRH1
5	45	40.2	287	1	PRFA_POLPE
6	45	40.2	370	1	AROG_YEAST
7	45	40.2	377	1	APJ_MOUSE
8	45	40.2	380	1	APJ_HUMAN
9	45	40.2	380	1	APJ_MACMU
10	44	39.3	1008	1	DPOL_HSV2
11	43	38.4	220	1	6PGL_THENA
12	43	38.4	370	1	AROG_CANAL
13	43	38.4	463	1	Y030_NPVAC
14	43	38.4	905	1	Z03_MOUSE
15	43	38.4	1557	1	LML1_CAEEL
16	42	37.5	185	1	RRF_THEMEA
17	42	37.5	432	1	TIG_ECOLI
18	42	37.5	501	1	TDT_ONCMY
19	42	37.5	653	1	HT2A_HUMAN
20	42	37.5	715	1	DCLY_SALTY
21	42	37.5	752	1	NECL1_RAT
22	41	36.6	391	1	UBIF_ECOLI
23	41	36.6	629	1	DNAK_HALCU
24	41	36.6	704	1	KPC1_CAEEL
25	41	36.6	861	1	GCR3_YEAST
26	41	36.6	883	1	CAPP_ECOLI
27	41	36.6	4466	1	DYHC_ANTCR
28	40.5	36.2	143	1	YXAD_BACSU
29	40.5	36.2	659	1	YYBT_BACSU
30	40	35.7	188	1	ADML_BOVIN
31	40	35.7	205	1	TEN1_BACSU
32	40	35.7	261	1	YGF6_ECOLI
33	40	35.7	380	1	PHLC_TRYCR

34	40	35.7	494	1	CAT2_HORVU	P55308 hordeum vul
35	40	35.7	578	1	ACEK_ECOLI	P11071 escherichia
36	40	35.7	583	1	ACEK_SALTY	P51067 salmonella
37	40	35.7	631	1	RPSD_BORBU	P52323 borrelia bu
38	39	34.8	125	1	VSIS_REOVJ	P32868 reovirus (t
39	39	34.8	185	1	ADML_HUMAN	P33318 homo sapien
40	39	34.8	282	1	HBD_CLOAB	P52041 clostridium
41	39	34.8	312	1	CELF_PVRKA	O85230 pseudorabie
42	39	34.8	331	1	OTCC_NEIMA	O91c14 neisseria m
43	39	34.8	331	1	OTCC_NEIMA	O91y13 neisseria m
44	39	34.8	365	1	RA51_SCHPO	P36601 schizosacch
45	39	34.8	418	1	VS12_REOVD	P03525 reovirus (t

ALIGNMENTS

RESULT 1  
BAD\_HUMAN STANDARD; PRT; 168 AA.  
AC Q92934;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 01-OCT-2000 (Rel. 40, Last annotation update)  
DE BAD PROTEIN (BCL-2 BINDING COMPONENT 6).  
GN BAD OR BCL2 OR BCL2L8.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Yin D.X., Li Z., Huang B., Chen S., Zhou H.;  
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: PROMOTES CELL DEATH. SUCCESSFULLY COMPETES FOR THE  
CC BINDING TO BCL-X(L) AND BCL-2, THEREBY AFFECTING THE LEVEL  
CC HETERODIMERIZATION OF BOTH THESE PROTEINS WITH BAX. CAN REVERSE  
CC THE DEATH REPRESSOR ACTIVITY OF BCL-X(L), BUT NOT THAT OF BCL-2  
CC (BY SIMILARITY).  
CC -!- SUBUNIT: FORMS HETERODIMERS WITH BCL-X(L) AND BCL-2, BUT NOT WITH  
CC BAX, MCL-1, A1, OR BCL-X(S) (BY SIMILARITY).  
CC -!- TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES.  
CC -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 1 (BH1).  
CC -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 2 (BH2).  
CC -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.  
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CC -----  
DR EMBL; U66879; AAB36516.1; -  
DR MIM; 603167; -  
KW Apoptosis.  
FT DOMAIN 101 121 BH1.  
FT DOMAIN 146 163 BH2.  
SQ SEQUENCE 168 AA; 18408 MW; BDF3D99587C2222BE CRC64;  
Query Match 100.0%; Score 112; DB 1; Length 168;  
Best Local Similarity 100.0%; Pred. No. 7.9e-11;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLWAAQRYGRELRRMSDEFVD 21  
DB 103 NLWAAQRYGRELRRMSDEFVD 123  
RESULT 2  
BAD\_MOUSE

[illegible]

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CC -----
DR EMBL; AF022214; AAC18453.1; -.
SQ SEQUENCE 595 AA; 66397 MW; AFD123ED5371E263 CRC64;

Query Match      42.4%; Score 47.5; DB 1; Length 595;
Best Local Similarity 47.6%; Pred. No. 5.5;
Matches 10; Conservative 4; Mismatches 4; Indels 3; Gaps 1;

QY 1 NLWAAORYGRELRRMSDEFVD 21          :| | | | | | |
Db 435 DIWDPOKYGGEVPR--EFVD 452       |||||

RESULT 4
MTBR_BPRH1
ID MTBR_BPRH1 STANDARD; PRT; 503 AA.
AC P09915;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE MODIFICATION METHYLASE RHOLLISI (EC 2.1.1.73) (CYTOSINE-SPECIFIC
DE METHYLTRANSFERASE RHOLLISI) (BSU PLIS) (M.RHO1LSI).
OS Bacteriophage rho-lls.
OC Viruses; dsDNA viruses, no RNA stage; Tailed phages; Siphoviridae;
OC Lambda phage group.
OX NCBI_TaxID=10735;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87246516; PubMed=3109889;
RA Behrens B., Noyer-Weidner M., Pawlek B., Lauster R., Balganesch T.S.,
RA Trautner T.A.;
RT "Organization of multispecific DNA methyltransferases encoded by
RT temperate Bacillus subtilis phages.";
RL EMBO J. 6:1137-1142(1987).
RN [2]
RP REVISION TO 476.
RA Trautner T.A.;
RL Submitted (SEP-1987) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: THIS ENZYME METHYLATES CYTOSINE WITHIN THE SEQUENCES
CC GGCC AND GAGTC.
CC -1- CATALYTIC ACTIVITY: S-ADENOSYL-L-METHIONINE + DNA CYTOSINE =
CC S-ADENOSYL-L-HOMOCYSTEINE + DNA 5-METHYLCYTOSINE.
CC -1- SIMILARITY: STRONG, TO OTHER C5-DNA METHYLASES.
CC -----
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CC -----
DR EMBL; X05242; CAA28869.1; -.
DR PIR; A28137; CTBPRH.
DR HSP; P05102; 5MHT.
DR REBASE; 2835; M.Rho1LSI.
DR InterPro; IPR001525; -.
DR Pfam; PF00145; DNA_methylase. 1.
DR PRINTS; PR00105; C5METTRFAS.
DR PROSITE; PS00094; C5_MTASE_1. 1.
DR PROSITE; PS00095; C5_MTASE_2. 1.
DR Transfaser; Methyltransferase; Restriction system.
KW TRANSFERASE 78 78 BY SIMILARITY.
SQ SEQUENCE 503 AA; 57129 MW; AAAFB8FE0188129E CRC64;

```



```

RL Yeast 9:1131-1137(1993).
RN [14]
RP SEQUENCE FROM N.A.
RC STRAIN=5288C;
RA Aljinovic G., Pohl F.M., Pohl T.M.;
RL Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: STEREOSPECIFIC CONDENSATION OF PHOSPHOENOLPYRUVATE (PEP)
CC AND D-ERYTHROSE-4-PHOSPHATE (EAP) GIVING RISE TO 3-DEOXY-D-
CC ARABINO-HEPTULOSONATE-7-PHOSPHATE (DAHP).
CC CATALYTIC ACTIVITY: 7-PHOSPHO-2-DEHYDRO-3-DEOXY-D-ARABINO-
CC HEPTONATE + ORTHOPHOSPHATE = PHOSPHOENOLPYRUVATE + D-ERYTHROSE
CC 4-PHOSPHATE + H(2)O.
CC -1- ENZYME REGULATION: INHIBITED BY TYROSINE.
CC -1- PATHWAY: FIRST STEP IN THE BIOSYNTHESIS OF CHORISMATE WITHIN
CC THE BIOSYNTHESIS OF AROMATIC AMINO ACIDS (THE SHIKIMATE PATHWAY).
CC -1- INDUCTION: BY AMINO ACID STARVATION.
CC -1- SIMILARITY: BELONGS TO CLASS-I DAHP SYNTHETASE FAMILY.
CC
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CC
CC EMBL; X61107; CAA43419.1; -
CC EMBL; L20296; AAA65607.1; -
CC EMBL; Z36118; CAA85212.1; -
CC PIR; S38185; S38185.
CC SGD; S0000453; ARO4.
CC InterPro; IPR001785; -
CC Pfam; PF00793; DAHP_synth.1; 1.
CC Aromatic amino acid biosynthesis; Lyase; Multigene family.
KW SEQUENCE 370 AA; 39749 MW; 594ED48F24175979 CRC64;
SQ

```

Query Match 40.2%; Score 45; DB 1; Length 370;  
Best Local Similarity 50.0%; Pred. No. 8;  
Matches 9; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

```

OY 1 NLWAAQRYGRELRRMSDE 18
DB 80 DLEAAQAEYALRLAKLSDE 97

```

RESULT 7  
APJ\_MOUSE  
ID APJ\_MOUSE STANDARD; PRT; 377 AA.  
AC Q9WV08;  
DT 01-OCT-2000 (Rel. 40, Created)  
DT 01-OCT-2000 (Rel. 40, Last sequence update)  
DT 01-OCT-2000 (Rel. 40, Last annotation update)  
DE PROBABLE G PROTEIN-COUPLED RECEPTOR APJ (MSR).  
GN AGTRL1 OR APJ.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Rizzoti K.;  
RT "The G protein-coupled receptor msr/APJ is expressed in endothelial precursors".  
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.  
CC -1- FUNCTION: ORPHAN RECEPTOR.  
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
CC
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CC
CC EMBL; X61107; CAA43419.1; -
CC EMBL; L20296; AAA65607.1; -
CC EMBL; Z36118; CAA85212.1; -
CC PIR; S38185; S38185.
CC SGD; S0000453; ARO4.
CC InterPro; IPR001785; -
CC Pfam; PF00793; DAHP\_synth.1; 1.
CC Aromatic amino acid biosynthesis; Lyase; Multigene family.
KW SEQUENCE 370 AA; 39749 MW; 594ED48F24175979 CRC64;
SQ

Query Match 40.2%; Score 45; DB 1; Length 377;  
Best Local Similarity 47.4%; Pred. No. 8.2;  
Matches 9; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

```

OY 2 LWAAQRYGRELRRMSDEFV 20
DB 48 LMTVFTSRKRSADIFI 66

```

RESULT 8  
APJ\_HUMAN  
ID APJ\_HUMAN STANDARD; PRT; 380 AA.  
AC P35414;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 01-OCT-2000 (Rel. 40, Last annotation update)  
DE PROBABLE G PROTEIN-COUPLED RECEPTOR APJ.  
GN AGTRL1 OR APJ.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=94124031; PubMed=8294032;  
RA O'Dowd B.F., Heiber M., Chan A., Heng H.H., Tsui L.-C., Kennedy J.L.,  
RA Shi X., Petronis A., George S.R., Nguyen T.;  
RT "A human gene that shows identity with the gene encoding the  
RT angiotensin receptor is located on chromosome 11.";  
RL Gene 136:355-360(1993).  
CC -1- FUNCTION: ORPHAN RECEPTOR.  
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
CC -1- HIGHLY RELATED TO ANGIOTENSIN RECEPTOR 1.  
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CC
CC EMBL; AJ007612; CAB50696.1; -
CC MGD; MGI:1346086; Agtr1l.  
CC InterPro; IPR000276; -
CC Pfam; PF00001; 7tm.1; 1.  
CC PRINTS; PR00237; GPCRHHODPSN.  
CC PROSITE; PS00237; G-PROTEIN\_RECEPTOR\_F1\_1; 1.  
CC PROSITE; PS00262; G-PROTEIN\_RECEPTOR\_F1\_2; 1.  
KW G-protein coupled receptor; Transmembrane; Glycoprotein.  
FT DOMAIN 1 24 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 25 49 1 (POTENTIAL).  
FT DOMAIN 50 64 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 65 89 2 (POTENTIAL).  
FT DOMAIN 90 98 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 99 123 3 (POTENTIAL).  
FT DOMAIN 124 142 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 143 164 4 (POTENTIAL).  
FT DOMAIN 165 198 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 199 219 5 (POTENTIAL).  
FT DOMAIN 220 242 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 243 269 6 (POTENTIAL).  
FT DOMAIN 270 282 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 283 306 7 (POTENTIAL).  
FT DOMAIN 307 377 CYTOPLASMIC (POTENTIAL).  
FT CARBOHYD 13 13 N-LINKED (GLCNAC... ) (POTENTIAL).  
FT CARBOHYD 173 173 N-LINKED (GLCNAC... ) (POTENTIAL).  
SQ SEQUENCE 377 AA; 42266 MW; AA437A800A24E0B CRC64;

Query Match 40.2%; Score 45; DB 1; Length 377;  
Best Local Similarity 47.4%; Pred. No. 8.2;  
Matches 9; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

```

OY 2 LWAAQRYGRELRRMSDEFV 20
DB 48 LMTVFTSRKRSADIFI 66

```

RESULT 8  
APJ\_HUMAN  
ID APJ\_HUMAN STANDARD; PRT; 380 AA.  
AC P35414;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 01-OCT-2000 (Rel. 40, Last annotation update)  
DE PROBABLE G PROTEIN-COUPLED RECEPTOR APJ.  
GN AGTRL1 OR APJ.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=94124031; PubMed=8294032;  
RA O'Dowd B.F., Heiber M., Chan A., Heng H.H., Tsui L.-C., Kennedy J.L.,  
RA Shi X., Petronis A., George S.R., Nguyen T.;  
RT "A human gene that shows identity with the gene encoding the  
RT angiotensin receptor is located on chromosome 11.";  
RL Gene 136:355-360(1993).  
CC -1- FUNCTION: ORPHAN RECEPTOR.  
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
CC -1- HIGHLY RELATED TO ANGIOTENSIN RECEPTOR 1.  
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AJ007612; CAB50696.1; -
CC MGD; MGI:1346086; Agtr1l.  
CC InterPro; IPR000276; -
CC Pfam; PF00001; 7tm.1; 1.  
CC PRINTS; PR00237; GPCRHHODPSN.  
CC PROSITE; PS00237; G-PROTEIN\_RECEPTOR\_F1\_1; 1.  
CC PROSITE; PS00262; G-PROTEIN\_RECEPTOR\_F1\_2; 1.  
KW G-protein coupled receptor; Transmembrane; Glycoprotein.  
FT DOMAIN 1 24 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 25 49 1 (POTENTIAL).  
FT DOMAIN 50 64 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 65 89 2 (POTENTIAL).  
FT DOMAIN 90 98 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 99 123 3 (POTENTIAL).  
FT DOMAIN 124 142 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 143 164 4 (POTENTIAL).  
FT DOMAIN 165 198 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 199 219 5 (POTENTIAL).  
FT DOMAIN 220 242 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 243 269 6 (POTENTIAL).  
FT DOMAIN 270 282 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 283 306 7 (POTENTIAL).  
FT DOMAIN 307 377 CYTOPLASMIC (POTENTIAL).  
FT CARBOHYD 13 13 N-LINKED (GLCNAC... ) (POTENTIAL).  
FT CARBOHYD 173 173 N-LINKED (GLCNAC... ) (POTENTIAL).  
SQ SEQUENCE 377 AA; 42266 MW; AA437A800A24E0B CRC64;

Query Match 40.2%; Score 45; DB 1; Length 377;  
Best Local Similarity 47.4%; Pred. No. 8.2;  
Matches 9; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

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CC EMBL; U03642; AAA18954.1; -
CC GCRdb; GCR_0806; -
CC MIM; 600052; -
CC InterPro; IPR000276; -
CC Pfam; PF00001; 7tm_1; 1.
CC PRINTS; PR00237; GPCRHHODPSN.
CC PROSITE; PS00237; G_PROTEIN_RECF_F1_1; 1.
CC PROSITE; PS0262; G_PROTEIN_RECF_F1_2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein.
KW DOMAIN 1 26
FT EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 27 51
FT DOMAIN 52 66
FT TRANSMEM 67 91
FT DOMAIN 92 100
FT TRANSMEM 101 125
FT DOMAIN 126 144
FT TRANSMEM 145 166
FT DOMAIN 167 200
FT TRANSMEM 201 221
FT DOMAIN 222 244
FT TRANSMEM 245 271
FT DOMAIN 272 284
FT TRANSMEM 285 308
FT DOMAIN 309 380
FT TRANSMEM 380 AA; 42660 MW; 78DB18BEA6D2B2E4 CRC64;
FT CARBOHYD 15 15
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT SEQUENCE 380 AA; 42660 MW; 78DB18BEA6D2B2E4 CRC64;
SQ

Query Match 40.2%; Score 45; DB 1; Length 380;
Best Local Similarity 47.4%; Pred. No. 8.3;
Matches 9; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

Qy 2 LWAQRYGRELRRMSDEFV 20
|| | | | | | | |
Db 50 LMTVFRSSREKRRSADIFI 68

RESULT 9
APJ_MACMU STANDARD; PRT; 380 AA.
AC O97666;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE PROBABLE G PROTEIN-COUPLED RECEPTOR APJ.
GN AGTRL1 OR APJ.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OC NCBI_TaxID=9544;
OX [1]
RN SEQUENCE FROM N.A.
RP TISSUE-Spleen;
RA Margulies B.J., Haver D.A., Clements J.E.;
RT "Identification and characterization of thirteen rhesus macaque
chemokine receptors and chemokine receptor homologues.";
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: ORPHAN RECEPTOR.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -!- HIGHLY RELATED TO ANGIOTENSIN RECEPTOR 1.
-----
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CC EMBL; AF100206; AAC72404.1; -
CC InterPro; IPR000276; -
CC Pfam; PF00001; 7tm_1; 1.
CC PRINTS; PR00237; GPCRHHODPSN.
CC PROSITE; PS00237; G_PROTEIN_RECF_F1_1; 1.
CC PROSITE; PS0262; G_PROTEIN_RECF_F1_2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein.
KW DOMAIN 1 26
FT EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 27 51
FT DOMAIN 52 66
FT TRANSMEM 67 91
FT DOMAIN 92 100
FT TRANSMEM 101 125
FT DOMAIN 126 144
FT TRANSMEM 145 166
FT DOMAIN 167 200
FT TRANSMEM 201 221
FT DOMAIN 222 244
FT TRANSMEM 245 271
FT DOMAIN 272 284
FT TRANSMEM 285 308
FT DOMAIN 309 380
FT TRANSMEM 380 AA; 42606 MW; E84F03E31FABF7ED CRC64;
FT CARBOHYD 15 15
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT SEQUENCE 380 AA; 42606 MW; E84F03E31FABF7ED CRC64;
SQ

Query Match 40.2%; Score 45; DB 1; Length 380;
Best Local Similarity 47.4%; Pred. No. 8.3;
Matches 9; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

Qy 2 LWAQRYGRELRRMSDEFV 20
|| | | | | | | |
Db 50 LMTVFRSSREKRRSADIFI 68

RESULT 10
DPOL_HSVE2 STANDARD; PRT; 1008 AA.
AC P52367;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE DNA POLYMERASE (EC 2.7.7.7).
GN 9.
OS Equine herpesvirus type 2 (strain 86/87) (EHV-2).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Gammaherpesvirinae.
OC NCBI_TaxID=82831;
OX [1]
RN SEQUENCE FROM N.A.
RP MEDLINE-95302501; PubMed-7783207;
RA Telford E.A., Watson M.S., Aird H.C., Perry J., Davison A.J.;
RT "The DNA sequence of equine herpesvirus 2.";
RL J. Mol. Biol. 249:520-528(1995).
CC -!- CATALYTIC ACTIVITY: N DEOXYNUCLEOSIDE TRIPHOSPHATE =
N PYROPHOSPHATE + DNA(N).
CC -!- SUBCELLULAR LOCATION: NUCLEAR.
CC -!- SIMILARITY: BELONGS TO DNA POLYMERASE TYPE-B FAMILY.
-----
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```

OX NCBI\_TaxID=46015;  
RN [1]

```
RP SEQUENCE FROM N.A.
RC STRAIN=C6;
RX MEDLINE=94303173; PubMed=8030224;
RA Ayres M.D., Howard S.C., Kuzio J., Lopez-Ferber M., Possee R.D.;
RT "The complete DNA sequence of Autographa californica nuclear
RT polyhedrosis virus.";
RL Virology 202:586-605(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=E2;
RX MEDLINE=93079853; PubMed=1333113;
RA Braunagel S.C., Daniel K.D., Reilly L.M., Guarino L.A., Hong T.,
RA Summers M.D.;
RX "Sequence, genomic organization of the EcoRI-A fragment of Autographa
RT californica nuclear polyhedrosis virus, and identification of a
RT viral-encoded protein resembling the outer capsid protein VP8 of
RT rotavirus.";
RL Virology 191:1003-1008(1992).
CC -1- SIMILARITY: TO CORRESPONDING ORF IN OPNPV.
CC -1- CAUTION: REF.2 SEQUENCE DIFFERS FROM THAT SHOWN FROM POSITION 294
CC ONWARD AND IS SHORTER (354 AA) DUE TO A FRAMESHIFT.
CC -----
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CC -----
CC L22858; AAA66660.1; -
DR EMBL;
DR PIR; F36828; F36828.
KW Hypothetical protein.
FT CONFLICT 254 262 AYYIRHMF -> GTTLDTCLL (IN REF. 2).
SQ SEQUENCE 463 AA; 54688 MW; D3643E87E2C6D373 CRC64;

Query Match 38.4%; Score 43; DB 1; Length 463;
Best Local Similarity 55.08; Pred. No. 21;
Matches 11; Conservative 1; Mismatches 6; Indels 2; Gaps 1;

Qy 2 LWAAQRYGRELMSDFVD 21
Db 347 LWKA--YGRHLKNSDECDD 364
||| ||| | ||| |
||| ||| | ||| |

RESULT 14
Z03_MOUSE
ID Z03_MOUSE STANDARD; PRT; 905 AA.
AC Q90XY1;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE TIGHT JUNCTION PROTEIN ZO-3 (ZONA OCCLUDENS 3 PROTEIN) (TIGHT JUNCTION
DE PROTEIN 3).
GN TJP3 OR ZO3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RX MEDLINE=20069797; PubMed=10601346;
RA Itoh M., Furuse M., Morita K., Kubota K., Saitou M., Tsukita S.;
RT "Direct binding of three tight junction-associated MAGUKs, ZO-1, ZO-2,
RT and ZO-3, with the COOH termini of claudins.";
RL J. Cell Biol. 147:1351-1363(1999).
CC -1- SUBUNIT: INTERACTS WITH OCCLUDIN, CLAUDINS AND ZO-1.
CC -1- SIMILARITY: CONTAINS 3 PDZ/DHR DOMAINS.
CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
CC -1- SIMILARITY: CONTAINS A GUANYLATE KINASE-LIKE DOMAIN.
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CC -1- SIMILARITY: BELONGS TO THE MAGUK FAMILY OF CELL JUNCTION PROTEINS.
CC -----
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CC -----
CC EMBL; AF157006; AAF24175.1; -
DR HSSP; P31016; IBFE.
DR MGD; MG1:1351650; Tjp3.
DR InterPro; IPR000619; -
DR InterPro; IPR001478; -
DR Pfam; PF00595; PDZ 3.
DR Pfam; PF00625; Guanylate_kin; 1.
DR PROSITE; PS00856; GUANYLATE_KINASE_1; FALSE_NEG.
DR PROSITE; PS00502; GUANYLATE_KINASE_2; 1.
DR PROSITE; PS0106; PDZ 3.
KW Tight junction; SH3 domain; Repeat; Membrane.
FT DOMAIN 11 93
FT DOMAIN 187 264 PDZ 1.
FT DOMAIN 368 434 PDZ 2.
FT DOMAIN ? ? SH3.
FT DOMAIN 654 754 GUANYLATE KINASE.
SQ SEQUENCE 905 AA; 99324 MW; B787BA1592661FEE CRC64;

Query Match 38.4%; Score 43; DB 1; Length 905;
Best Local Similarity 66.7%; Pred. No. 45;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 LWAAQRYGRELR 13
Db 513 LWLAARMGRDLR 524
||| | ||| |
||| | ||| |

RESULT 15
LWML_CAEEL
ID LWML_CAEEL STANDARD; PRT; 1557 AA.
AC Q18823;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE LAMININ-LIKE PROTEIN C54D1.5 PRECURSOR.
GN C54D1.5.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoides;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Minx P.;
RL Submitted (JAN-1996) to the EMBL/Genbank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 LAMININ N-TERMINAL DOMAIN (DOMAIN VI).
CC -1- SIMILARITY: CONTAINS 10.5 LAMININ EGF-LIKE DOMAINS.
CC -1- SIMILARITY: CONTAINS 1 LAMININ DOMAIN IV.
CC -----
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CC -----
CC EMBL; U46673; AAC48152.1; -
DR HSSP; P02468; ITLE.
DR WormPep; C54D1.5; CE06981.
DR InterPro; IPR000034; -
DR InterPro; IPR000561; -
```

DR InterPro: IPR001886; -  
DR InterPro: IPR002049; -  
DR Pfam: PF00052; laminin\_B; 1.  
DR Pfam: PF00053; laminin\_EGF; 10.  
DR Pfam: PF00055; laminin\_Nterm; 1.  
DR PRINTS: PR00011; EGF\_LAMININ.  
DR PROSITE: PS00022; EGF\_1; 8.  
DR PROSITE: PS01186; EGF\_2; 1.  
DR PROSITE: PS01248; LAMININ\_TYPE\_EGF; 11.  
KW Hypothetical protein; Laminin EGF-like domain; Signal; Repeat.  
FT SIGNAL 1 ? POTENTIAL.  
FT CHAIN ? 1557 LAMININ-LIKE PROTEIN C54D1.5.  
FT DOMAIN ? 271 LAMININ N-TERMINAL (DOMAIN VI).  
FT DOMAIN 272 331 LAMININ EGF-LIKE 1.  
FT DOMAIN 332 387 LAMININ EGF-LIKE 2.  
FT DOMAIN 388 434 LAMININ EGF-LIKE 3.  
FT DOMAIN 435 487 LAMININ EGF-LIKE 4.  
FT DOMAIN 488 497 LAMININ EGF-LIKE 5 (N-TERMINAL).  
FT DOMAIN 498 688 LAMININ DOMAIN IV.  
FT DOMAIN 687 732 LAMININ EGF-LIKE 5 (C-TERMINAL).  
FT DOMAIN 737 769 LAMININ EGF-LIKE 6 (INCOMPLETE).  
FT DOMAIN 770 819 LAMININ EGF-LIKE 7.  
FT DOMAIN 820 874 LAMININ EGF-LIKE 8.  
FT DOMAIN 875 930 LAMININ EGF-LIKE 9.  
FT DOMAIN 931 978 LAMININ EGF-LIKE 10.  
FT DOMAIN 979 1025 LAMININ EGF-LIKE 11.  
FT DISULFID 272 281 BY SIMILARITY.  
FT DISULFID 274 295 BY SIMILARITY.  
FT DISULFID 297 306 BY SIMILARITY.  
FT DISULFID 309 329 BY SIMILARITY.  
FT DISULFID 332 341 BY SIMILARITY.  
FT DISULFID 334 357 BY SIMILARITY.  
FT DISULFID 360 369 BY SIMILARITY.  
FT DISULFID 372 385 BY SIMILARITY.  
FT DISULFID 388 400 BY SIMILARITY.  
FT DISULFID 390 406 BY SIMILARITY.  
FT DISULFID 408 417 BY SIMILARITY.  
FT DISULFID 420 432 BY SIMILARITY.  
FT DISULFID 435 449 BY SIMILARITY.  
FT DISULFID 437 456 BY SIMILARITY.  
FT DISULFID 458 467 BY SIMILARITY.  
FT DISULFID 470 485 BY SIMILARITY.  
FT DISULFID 770 778 BY SIMILARITY.  
FT DISULFID 772 788 BY SIMILARITY.  
FT DISULFID 791 800 BY SIMILARITY.  
FT DISULFID 803 817 BY SIMILARITY.  
FT DISULFID 820 834 BY SIMILARITY.  
FT DISULFID 822 841 BY SIMILARITY.  
FT DISULFID 844 853 BY SIMILARITY.  
FT DISULFID 856 872 BY SIMILARITY.  
FT DISULFID 875 894 BY SIMILARITY.  
FT DISULFID 877 901 BY SIMILARITY.  
FT DISULFID 903 912 BY SIMILARITY.  
FT DISULFID 915 928 BY SIMILARITY.  
FT DISULFID 931 943 BY SIMILARITY.  
FT DISULFID 933 950 BY SIMILARITY.  
FT DISULFID 952 961 BY SIMILARITY.  
FT DISULFID 964 976 BY SIMILARITY.  
FT DISULFID 979 991 BY SIMILARITY.  
FT DISULFID 981 998 BY SIMILARITY.  
FT DISULFID 1000 1009 BY SIMILARITY.  
FT DISULFID 1012 1023 BY SIMILARITY.  
FT CARBOHYD 101 101 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 121 121 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 333 333 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 507 507 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 643 643 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 725 725 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 921 921 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 1062 1062 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 1168 1168 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 1211 1211 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 1244 1244 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 1321 1321 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 1437 1437 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 1557 AA; 172723 MW; CAF0B51F8D5E8D2F CRC64;

Query Match 38.4%; Score 43; DB 1; Length 1557;  
Best Local Similarity 50.0%; Pred. No. 82;  
Matches 7; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 4 AAORYGRELRRMSD 17

Db 1169 ASQYGEQSKRMSE 1182

Search completed: October 9, 2001, 15:55:21  
Job time: 196 sec



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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: October 9, 2001, 15:54:56 ; Search time 46.39 Seconds  
(without alignments)  
59.892 Million cell updates/sec

Title: US-09-580-523-1\_COPY\_103\_123

Perfect score: 112

Sequence: 1 NLWAAQRYGRELRRMSDEFVD 21

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_16:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phase:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_unclassified:\*
- 13: sp\_vertebrate:\*
- 14: sp\_virus:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	112	100.0	168	4	014803
2	102	91.1	205	11	035147
3	102	91.1	205	11	070256
4	102	91.1	220	11	09JHX1
5	82	73.2	95	13	09I9N2
6	53	47.3	223	2	Q10843
7	49	43.8	453	2	Q91403
8	49	43.8	1248	2	Q9HZQ3
9	47	42.0	295	2	Q9HY62
10	47	42.0	339	10	Q9F005
11	46.5	41.5	486	5	Q9VVM1
12	46	41.1	198	4	043521
13	45	40.2	564	2	Q9RUK9
14	45	40.2	574	2	069125
15	45	40.2	848	5	094419
16	45	40.2	1303	5	09U172
17	44	39.3	226	5	044466
18	44	39.3	335	10	064692
19	44	39.3	516	10	Q9SSP5

20	43.5	38.8	503	9	Q02778
21	43	38.4	156	2	Q9JTL8
22	43	38.4	186	2	Q9X5V5
23	43	38.4	232	2	024956
24	43	38.4	232	2	087194
25	43	38.4	232	2	Q9ZMT5
26	43	38.4	276	10	Q9FJV5
27	43	38.4	302	13	012968
28	43	38.4	314	2	Q9F2J4
29	43	38.4	325	2	007600
30	43	38.4	363	10	Q9LWN7
31	43	38.4	375	2	Q9L395
32	43	38.4	463	14	Q9JAD7
33	43	38.4	472	14	092397
34	43	38.4	5635	5	Q9N9N1
35	42	37.5	196	11	054918
36	42	37.5	196	11	088498
37	42	37.5	202	2	Q9I3G1
38	42	37.5	361	10	Q9FIC1
39	42	37.5	415	5	Q9V7Y6
40	42	37.5	461	2	Q9KR33
41	42	37.5	519	8	Q9WT28
42	42	37.5	520	4	Q9H239
43	42	37.5	525	10	Q9I144
44	42	37.5	526	10	Q9S7B5
45	42	37.5	548	2	P71029

#### ALIGNMENTS

RESULT 1  
014803  
ID 014803 PRELIMINARY; PRT; 168 AA.  
AC 014803;  
DT 01-JAN-1998 (TREMBlrel. 05, Created)  
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)  
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)  
DE BCL-X/BCL-2 BINDING PROTEIN (FRAGMENT).  
GN BAD.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=97083574; PubMed=8929532;  
RA Wang H.G., Rapp U.R., Reed J.C.;  
RT "Bcl-2 targets the protein kinase Raf-1 to mitochondria.";  
RL Cell 87:629-638(1996).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Takayama S., Reed J.C.;  
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RA Otilie S., Diaz J.L., Horne W., Chang J., Wang Y., Wilson G.,  
RA Weeks S., McConnell M., Chang S., Fritz L.C., Oltersdorf T.,  
RL J. Biol. Chem. 0:0-0(1997).  
DR EMBL; AF021792; AAB72092.1; -.  
DR EMBL; AF031523; AAB88124.1; -.  
FT NON\_TER 1  
SQ SEQUENCE 168 AA; 18392 MW; 69FD8D27DDEE3241 CRC64;

Query Match 100.0%; Score 112; DB 4; Length 168;  
Best Local Similarity 100.0%; Pred. No. 2.4e-09;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLWAAQRYGRELRRMSDEFVD 21  
DB 103 NLWAAQRYGRELRRMSDEFVD 123

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RESULT 2
Q35147
ID Q35147 PRELIMINARY; PRT; 205 AA.
AC Q35147;
DT 01-JAN-1998 (TEMBLrel. 05, Created)
DT 01-JAN-1998 (TEMBLrel. 05, Last sequence update)
DT 01-NOV-1998 (TEMBLrel. 08, Last annotation update)
DE BCL-2 ASSOCIATED DEATH PROMOTER.
GN BAD.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Ovary;
RX MEDLINE=98034386; PubMed=9369453;
RZ Hsu S.Y., Hsueh A.J.W.;
RT "Interference of BAD (Bcl-xL/Bcl-2-associated death promoter)-induced
RT apoptosis in mammalian cells by 14-3-3 isoforms and P11.";
RL Mol. Endocrinol. 11:1858-1867(1997).
DR EMBL; AF003523; AAC53374.1; -.
SQ SEQUENCE 205 AA; 22468 MW; 04DD3EBA03B11168 CRC64;

Query Match 91.1%; Score 102; DB 11; Length 205;
Best Local Similarity 100.0%; Pred. No. 9.5e-08; Indels 0; Gaps 0;
Matches 19; Conservative 0; Mismatches 0;

QY 1 NLWAAQRYGRELRRMSDEF 19
|
Db 141 NLWAAQRYGRELRRMSDEF 159

RESULT 3
Q70256
ID Q70256 PRELIMINARY; PRT; 205 AA.
AC Q70256;
DT 01-AUG-1998 (TEMBLrel. 07, Created)
DT 01-AUG-1998 (TEMBLrel. 07, Last sequence update)
DT 01-OCT-2000 (TEMBLrel. 15, Last annotation update)
DE BCL-2 ASSOCIATED DEATH PROMOTER BAD (BCL-2 ASSOCIATED DEATH AGONIST
DE ALPHA).
GN BAD OR BAD-ALPHA.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=98194755; PubMed=9535132;
RA D'Agata V., Magro G., Travali S., Musco S., Cavallaro S.;
RT "Cloning and expression of the programmed cell death regulator Bad in
RT the rat brain.";
RL Neurosci. Lett. 243:137-140(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Hamner S., Arumne U., Li-Ying Y., Sun Y.-F., Saarma M., Lindholm D.;
RT "Functional characterization of two splice variants of rat bad and
RT their interaction with bcl-w in sympathetic neurons.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF031227; AAC15100.1; -.
DR EMBL; AF279910; AAF91427.1; -.
SQ SEQUENCE 205 AA; 22228 MW; 7AFA71DAE9CF4A81 CRC64;

Query Match 91.1%; Score 102; DB 11; Length 205;
Best Local Similarity 100.0%; Pred. No. 9.5e-08; Indels 0; Gaps 0;
Matches 19; Conservative 0; Mismatches 0;

QY 1 NLWAAQRYGRELRRMSDEF 19
|
Db 141 NLWAAQRYGRELRRMSDEF 159
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Db 141 NLWAAQRYGRELRRMSDEF 159
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RESULT 4
Q9JHX1
ID Q9JHX1 PRELIMINARY; PRT; 220 AA.
AC Q9JHX1;
DT 01-OCT-2000 (TEMBLrel. 15, Created)
DT 01-OCT-2000 (TEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TEMBLrel. 15, Last annotation update)
DE BCL-2 ASSOCIATED DEATH AGONIST BETA.
GN BAD-BETA.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Hamner S., Arumne U., Li-Ying Y., Sun Y.-F., Saarma M., Lindholm D.;
RT "Functional characterization of two splice variants of rat bad and
RT their interaction with bcl-w in sympathetic neurons.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF279911; AAF91428.1; -.
SQ SEQUENCE 220 AA; 24278 MW; E27BCCD7C969E90F CRC64;

Query Match 91.1%; Score 102; DB 11; Length 220;
Best Local Similarity 100.0%; Pred. No. 1e-07; Indels 0; Gaps 0;
Matches 19; Conservative 0; Mismatches 0;

QY 1 NLWAAQRYGRELRRMSDEF 19
|
Db 141 NLWAAQRYGRELRRMSDEF 159

RESULT 5
Q9I9N2
ID Q9I9N2 PRELIMINARY; PRT; 95 AA.
AC Q9I9N2;
DT 01-OCT-2000 (TEMBLrel. 15, Created)
DT 01-OCT-2000 (TEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TEMBLrel. 16, Last annotation update)
DE BAD (FRAGMENT).
GN BAD.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Rasbora; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20373792; PubMed=10917738;
RA Inohara N., Nunez G.;
RT "Genes with Homology to Mammalian Apoptosis Regulators Identified in
RT Zebrafish.";
RL Cell Death Differ. 7:509-510(2000).
DR EMBL; AF231017; AAF66962.1; -.
FT NON_TER 1
SQ SEQUENCE 95 AA; 10804 MW; 77F5CDE879E69FF7 CRC64;

Query Match 73.2%; Score 82; DB 13; Length 95;
Best Local Similarity 77.8%; Pred. No. 4.2e-05; Indels 0; Gaps 0;
Matches 14; Conservative 4; Mismatches 0;

QY 2 LWAAQRYGRELRRMSDEF 19
|
Db 38 LWAAQRYGRELRRMSDEF 55

RESULT 6
Q10843
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ID Q10843 PRELIMINARY; PRT; 223 AA.
AC Q10843;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE HYPOTHETICAL 24.1 KDA PROTEIN CY39.03C.
GN RV2014 OR MTCY39.03C.
OS Mycobacterium tuberculosis.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H37RV;
RX MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eigmeier K., Gas S., Barry C.E. III, Tekala F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squires R., Sulston J.E.,
RA Taylor K., Whitehead S., Barrett B.G.;
RL Nature 393:537-544(1998);
CC -|- SIMILARITY: TO M.PARATUBERCULOSIS IS900.
DR EMBL; 274025; CAA98415.1; -
DR TuberculList; RV2014; -
DR InterPro; IPR003346; -
DR Pfam; PF02371; Transposase_20; 1.
KW Hypothetical protein.
SQ SEQUENCE 223 AA; 24132 MW; 70456750017F8F37 CRC64;

Query Match 47.3%; Score 53; DB 2; Length 223;
Best Local Similarity 58.8%; Pred. No. 2.6;
Matches 10; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 NLWAAQRYGRELRRMSD 17
| | | | | | | | | | |
Db 165 NLWAAADRYNRAIARGHD 181

RESULT 7
QY14U3 PRELIMINARY; PRT; 453 AA.
AC QY14U3;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE HYPOTHETICAL PROTEIN PA1031.
GN PA1031.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PA01;
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltzy L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
RT opportunistic pathogen.";
RL Nature 406:959-964(2000).
DR EMBL; AE004535; AAG04420.1; -
DR InterPro; IPR000049; -
DR ProDom; PD003528; -; 1.
DR PROSITE; PS00626; RC01_2; UNKNOWN_1.
SQ SEQUENCE 453 AA; 51539 MW; 1E7EA97E82EC5E4B CRC64;

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Query Match 43.8%; Score 49; DB 2; Length 453;
Best Local Similarity 55.6%; Pred. No. 23;
Matches 10; Conservative 4; Mismatches 2; Indels 2; Gaps 1;

QY 3 WAAQRYGR--ELRRMSDE 18
| | | | | | | | | | |
Db 65 WASERQGREELRLRLASE 82

RESULT 8
QYHZQ3 PRELIMINARY; PRT; 1248 AA.
AC QYHZQ3;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE COBALAMIN BIOSYNTHETIC PROTEIN COBN.
GN COBN OR PA2944.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PA01;
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltzy L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
RT opportunistic pathogen.";
RL Nature 406:959-964(2000).
DR EMBL; AE004720; AAG06332.1; -
DR InterPro; IPR000049; -
DR ProDom; PD003528; -; 1.
DR PROSITE; PS00626; RC01_2; UNKNOWN_1.
SQ SEQUENCE 1248 AA; 138499 MW; C3D3DBFEE6736C7A CRC64;

Query Match 43.8%; Score 49; DB 2; Length 1248;
Best Local Similarity 50.0%; Pred. No. 69;
Matches 11; Conservative 4; Mismatches 5; Indels 2; Gaps 1;

QY 2 LWAAQRYG--RELRRMSDEFVD 21
| | | | | | | | | | |
Db 611 LTRAESYGLRLDLRLADEFYD 632

RESULT 9
QYHY62 PRELIMINARY; PRT; 295 AA.
AC QYHY62;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE HYPOTHETICAL PROTEIN PA3555.
GN PA3555.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PA01;
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltzy L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,

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RA	Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA	Reizer J., Saier M.H., Hancock R.F.W., Lory S., Olson M.V.,
RT	*Complete genome sequence of <i>Pseudomonas aeruginosa</i> PA01, an
RT	opportunistic pathogen. "
RL	Nature 406:959-964 (2000).
DR	EMBL: AE004776; AAC06943.1; -.
DR	Hypothetical protein.
SW	SEQUENCE 295 AA: 5395218A63FB360 CRC64:

Query Match 42.0%; Score 47; DB 2; Length 295;  
Best Local Similarity 40.0%; Pred. No. 28;  
Matches 8; Conservative 5; Mismatches 7; Indels

QY 2 LWAAQRYGRELRRMSDEFVD 21  
:|:|:|:|:|:|  
Db 120 VMSVQQLGEQIRRGSDCLAD 139

RESULT	10
Q9FQ05	
ID	Q9FQ05
AC	PRELIMINARY; PRT; 339 AA.
DT	Q9FQ05;
DT	01-WAR-2001 (TrenBrel. 16, Created)
DT	01-WAR-2001 (TrenBrel. 16, Last sequence update)
DT	01-WAR-2001 (TrenBrel. 16, Last annotation update)
DE	ATRAF1Q2 PROTEIN (FRAGMENT).

OS *Atrichum angustatum*.  
OC Eukaryota; Viridiplantae; Embryophyta; Bryophyta; Polytrichopsida;  
OC Polytrichales; Polytrichaceae; Atrichum.

RN	[1]	RP
		SEQUENCE FROM N.A.

RA Fröhlich M.W., Estabrook G.F.;  
RT "Wilkinson Support Calculated with Exact Probabilities: An Example  
RT using Floricaula/LEAFY Amino Acid Sequences that Compares Three  
RT Hypotheses Involving Gene Gain/Loss in Seed Plants."; *Mol. Biol. Evol.* 17:1914-1925(2000).

FT	NON_TER	1	1
SQ	SEQUENCE	339 AA;	38764 MW; A978F91BD8C912CA CRC64;

Query Match 42.0%; Score 47; DB 10; Length 339;  
Best Local Similarity 61.1%; Pred. No. 33;  
Matches 11; Conservative 0; Mismatches 7; Indels

QY 4 AAQRYGRELRRMSDEFVD 21  
11 1111111111  
Db 18 AAASVGRESRRMKDLEKD 35

RESULT	11
Q9VVM1	
ID	Q9VVM1 PRELIMINARY; PRT; 486 AA.
AC	Q9VVM1;
DC	01-MAY-2000 (T-EMBLrel. 13, Created)
DT	01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
DT	01-OCT-2000 (T-EMBLrel. 15, Last annotation update)
DE	CG7408 PROTEIN.
GN	CG7408.
OS	Drosophila melanogaster (Fruit fly).
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;
OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomor-
OX	Ephydroidea; Drosophilidae; Drosophila.
OX	NCBI_TaxID=7227;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN-BERKELEY;
RA	MEDLINE=20196006; PubMed=10731132;
RX	Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,

Anatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 Sutton G.G., Wortman J.R., Vandell M.D., Zhang Q., Chen L.X.,  
 Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,  
 Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
 Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 Beeson K.Y., Benos P.V., Berhan B.P., Bhandari D., Bolshakov S.,  
 Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,  
 Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 Cherry J.M., Cawley S., Dahlike C., Davenport L.B., Davies P.,  
 de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 Durbin K.J., Evangelista C.G., Ferraz C., Ferriera S., Fleischmann W.,  
 Fodor C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,  
 Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
 Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
 Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.M.,  
 Palazozo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissensbach J.,  
 Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 Ye J., Yeh R.-F., Zaveri J.-S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.:  
 "The genome sequence of *Drosophila melanogaster*.  
 Science 287:2185-2195(2000).  
 DR EMBL: AF003522; AAF49290.1; -  
 DR HSSP: P15848; 1FSU  
 DR Flybase: Fgn0036765; CG7408  
 DR Interpro: IPR000917; -  
 DR Pfam: PF00884; Sulfatase 1h.  
 DR SEQ: 486 AA; 55063 MW; 4327F6726A98F524 CRC64;

Query Match	41.5%	Score 46.5;	DB 5;	Length 486;
Best Local Similarity	44.0%;	Pred. No. 58;		
Matches 11:	Conservative	4;	Mismatches	5;
			Indels	5;
			Gaps	1;

QY 1 NLWAAQRYG-----RELRRMSDEFV 20  
 |||:|:| | | : | | |  
 Db 275 NLWSALKYGYESVEREIVHVIDEV 299

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RESULT 12
043521 PRELIMINARY; PRT; 198 AA.
ID 043521
AC 043521; 043522;
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE BCL2-LIKE PROTEIN II (BCL2 INTERACTING MEDIATOR OF CELL DEATH).
OS BCL2L1L OR BIM.
GN Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., FUNCTION, AND ALTERNATIVE SPLICING.
RC TISSUE=PERIPHERAL BLOOD, AND SPLEEN;
RX MEDLINE=98094360; PubMed=9430630;
RA O'Connor L., Strasser A., O'Reilly L.A., Hausmann G., Adams J.M.
RA Cory S., Huang D.C.S.;

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RL Nature 368:32-38(1994).  
DR EMBL; Z79759; CAB02138.1; -  
DR InterPro; IPR001201; -  
DR InterPro; IPR002058; -  
DR InterPro; IPR002934; -  
DR Pfam; PF01909; NTP\_transf\_2; 1.  
SQ SEQUENCE 848 AA; 95038 MW; D4F9DA836DCFD53 CRC64;

Query Match 40.2%; Score 45; DB 5; Length 848;  
Best Local Similarity 36.8%; Pred. No. 1.8e+02;  
Matches 7; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 3 WAAQRYGRELRRMSDEFVD 21  
| :||| : : :||  
Db 43 WRRKRYGLNIQGLHEEIVD 61

Search completed: October 9, 2001, 15:54:57  
Job time: 192 sec



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: October 9, 2001, 15:54:03 ; Search time 28.81 Seconds  
(without alignments)  
55.525 Million cell updates/sec

Title: US-09-580-523-1\_COPY\_103\_123

Perfect score: 112

Sequence: 1 NLWAAQRYGRELRRMSDEFVD 21

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR\_68.\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	102	91.1	204	2 A55671	bad protein - mous
2	53	47.3	223	2 D70760	hypothetical prote
3	49	43.8	453	2 E83517	conserved hypothet
4	49	43.8	1248	2 G83278	cobalamin biosynth
5	47.5	42.4	595	2 B72801	gp13 protein - Myc
6	47	42.0	295	2 F83201	conserved hypothet
7	46.5	41.5	503	1 CTBPRH	site-specific DNA-
8	45	40.2	287	2 S43852	neuropeptide Pol-R
9	45	40.2	370	2 S38185	2-dehydro-3-deoxyp
10	45	40.2	380	2 I38435	angiotensin recept
11	45	40.2	564	2 H75403	glycosyl hydrolase
12	45	40.2	848	2 T28055	hypothetical prote
13	44	39.3	335	2 T52577	gibberellin 2beta-
14	44	39.3	516	2 A96753	probable threonine
15	44	39.3	1008	2 S55603	DNA polymerase rep
16	43.5	38.4	503	2 JQ1019	site-specific DNA-
17	43	38.4	156	2 C81868	hypothetical prote
18	43	38.4	220	2 F72289	oxidoreductase, so
19	43	38.4	232	1 A64538	cytochrome-c oxida
20	43	38.4	232	2 H71969	cytochrome oxidase
21	43	38.4	325	2 H69829	3'-oxoacyl- acyl-ca
22	43	38.4	463	2 F72853	AcOrf-30 protein -
23	43	38.4	472	2 T41775	AcMNPV orf30 - Bom
24	43	38.4	1557	2 T28811	hypothetical prote
25	42	37.5	185	2 H72259	ribosome recycling
26	42	37.5	202	2 D83450	probable cytochrom
27	42	37.5	432	1 D64773	trigger factor [va
28	42	37.5	432	2 F85340	hypothetical prote
29	42	37.5	461	2 B82155	deoxyribodipyrimid

30 42 37.5 526 2 T08545  
31 42 37.5 752 1 KXRTC1  
32 42 37.5 795 2 T05860  
33 41.5 37.1 1792 2 T13939  
34 41 36.6 69 2 T44956  
35 41 36.6 166 2 T25773  
36 41 36.6 203 2 B83452  
37 41 36.6 206 2 E82200  
38 41 36.6 352 2 T12515  
39 41 36.6 388 2 T22799  
40 41 36.6 391 1 D64801  
41 41 36.6 391 2 G85566  
42 41 36.6 395 2 A82827  
43 41 36.6 447 2 F85356  
44 41 36.6 567 2 T33400  
45 41 36.6 577 2 T40297

threonine synthase  
proprotein convert  
alpha, alpha-trehal  
myosin V - fruit f  
70K heat shock cha  
hypothetical prote  
cytochrome c oxida  
hypothetical prote  
hypothetical prote  
probable monooxyge  
hypothetical prote  
conserved hypothet  
hypothetical prote  
protein kinase C h  
membrane transport

#### ALIGNMENTS

##### RESULT 1

A55671

bad protein - mouse

C:Species: Mus musculus (house mouse)

C:Date: 03-Mar-1995 #sequence\_revision 03-Mar-1995 #text\_change 05-Nov-1999

C:Accession: A55671

R:Yang, E.; Zha, J.; Jockel, J.; Boise, L.H.; Thompson, C.B.; Korsmeyer, S.J.

Cell 80, 285-291, 1995

A:Title: Bad, a heterodimeric partner for Bcl-x-L and Bcl-2, displaces Bax and promot

A:Reference number: A55671; MUID:95136361

A:Accession: A55671

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-204 <YAN>

A:Cross-references: GB:L37296; NID:g639778; PIDN:AAA64465.1; PID:g639779

C:Keywords: heterodimer

##### Query Match

91.1%; Score 102; DB 2; Length 204;

Best Local Similarity 100.0%; Pred. No. 1.8e-08;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NLWAAQRYGRELRRMSDEF 19

|||||

Db 140 NLWAAQRYGRELRRMSDEF 158

##### RESULT 2

D70760

hypothetical protein Rv2014 - Mycobacterium tuberculosis (strain H37RV)

C:Species: Mycobacterium tuberculosis

C:Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 22-Oct-1999

C:Accession: D70760

R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon

; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holtroyd,

Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.

Nature 393, 537-544, 1998

A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete geno

A:Reference number: A70500; MUID:98295987

A:Accession: D70760

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-223 <COL>

A:Cross-references: GB:Z74025; GB:AL123456; NID:g3261586; PIDN:CAA98415.1; PID:el2999

A:Experimental source: strain H37RV

C:Genetics:

A:Gene: Rv2014

##### Query Match

Best Local Similarity 47.3%; Score 53; DB 2; Length 223;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 10; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 NLWAAORYGRELRRMSD 17  
||||| | | | | |

Db 165 NLWAAADRYNRAIARGHD 181

RESULT 3  
E83517  
conserved hypothetical protein PA1031 [imported] - Pseudomonas aeruginosa (strain PA01)

C:Species: Pseudomonas aeruginosa  
C:Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000  
C:Accession: E83517  
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.  
Nature 406, 959-964, 2000  
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen  
A:Reference number: A82950; MUID:20437337  
A:Accession: E83517  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-453 <STO>  
A:Cross-references: GB:AE004535; GB:AE004091; NID:99949032; PIDN:AAG04420.1; GSPDB:GN001  
A:Experimental source: strain PA01  
C:Genetics:  
A:Gene: PA1031

Query Match 43.8%; Score 49; DB 2; Length 453;  
Best Local Similarity 55.6%; Pred. No. 7;  
Matches 10; Conservative 4; Mismatches 2; Indels 2; Gaps 1;

QY 3 WAAORYGR--ELRRMSDE 18  
|||::|| | ||||::| |

Db 65 WASERGEEELRLRLASE 82

RESULT 4  
G83278  
cobalamin biosynthetic protein CobN PA2944 [imported] - Pseudomonas aeruginosa (strain PA01)

C:Species: Pseudomonas aeruginosa  
C:Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 02-Mar-2001  
C:Accession: G83278  
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.  
Nature 406, 959-964, 2000  
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen  
A:Reference number: A82950; MUID:20437337  
A:Accession: G83278  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1248 <STO>  
A:Cross-references: GB:AE004720; GB:AE004091; NID:99949032; PIDN:AAG06332.1; GSPDB:GN001  
A:Experimental source: strain PA01  
C:Genetics:  
A:Gene: cobN; PA2944  
C:Superfamily: Rhodobacter capsulatus magnesium-protoporphyrin O-methyltransferase

Query Match 43.8%; Score 49; DB 2; Length 1248;  
Best Local Similarity 50.0%; Pred. No. 19;  
Matches 11; Conservative 4; Mismatches 5; Indels 2; Gaps 1;

QY 2 LWAAORYG--RELRRMSDEFVD 21  
| | | | | | | | | | | | | | | |

Db 611 LTRAESTYGLRLRLRLADEFYD 632

RESULT 5  
B72801  
gp13 protein - Mycobacterium phage D29

C:Species: Mycobacterium phage D29  
C:Date: 12-Nov-1999 #sequence\_revision 12-Nov-1999 #text\_change 11-Jan-2000  
C:Accession: B72801  
R:Ford, M.E.; Sarkis, G.J.; Belanger, A.E.; Hendrix, R.W.; Hatfull, G.F.  
J. Mol. Biol. 29, 143-164, 1998  
A:Title: Genome structure of mycobacteriophage D29: Implications for phage evolution.  
A:Reference number: A72800; MUID:98300335  
A:Accession: B72801  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-595 <FOR>  
A:Cross-references: GB:AF022214; NID:g3172250; PIDN:AAC18453.1; PID:g3172260  
C:Genetics:  
A:Gene: 13  
C:Superfamily: Mycobacterium phage L5 gene 13 protein

Query Match 42.4%; Score 47.5; DB 2; Length 595;  
Best Local Similarity 47.6%; Pred. No. 16;  
Matches 10; Conservative 4; Mismatches 4; Indels 3; Gaps 1;

QY 1 NLWAAORYGRELRRMSDEFVD 21  
::| | | | | | | | | | |

Db 435 DIWDPOKYGGEVPR---EFVD 452

RESULT 6  
F83201  
conserved hypothetical protein PA3555 [imported] - Pseudomonas aeruginosa (strain PA01)

C:Species: Pseudomonas aeruginosa  
C:Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000  
C:Accession: F83201  
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lory, S.; Olson, M.V.  
Nature 406, 959-964, 2000  
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen  
A:Reference number: A82950; MUID:20437337  
A:Accession: F83201  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-295 <STO>  
A:Cross-references: GB:AE004776; GB:AE004091; NID:99949701; PIDN:AAG06943.1; GSPDB:GN001  
A:Experimental source: strain PA01  
C:Genetics:  
A:Gene: PA3555  
C:Superfamily: Escherichia coli hypothetical protein b2256

Query Match 42.0%; Score 47; DB 2; Length 295;  
Best Local Similarity 40.0%; Pred. No. 9.4;  
Matches 8; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 2 LWAAORYGRELRRMSDEFVD 21  
::| | | | | | | | | | |

Db 120 WMSVQQLGEOIRRGSDCLAD 139

RESULT 7  
CTBPRH  
site-specific DNA-methyltransferase (cytosine-specific) (EC 2.1.1.73) - phage rho-11s

N:Alternate names: DNA cytosine methylase; DNA methyltransferase  
C:Species: phage rho-11s  
A:Note: host Bacillus subtilis  
C:Date: 31-Mar-1989 #sequence\_revision 31-Mar-1989 #text\_change 24-Oct-1997  
C:Accession: A28137  
R:Behrens, B.; Moyer-Weidner, M.; Pawlek, B.; Lauster, R.; Balganes, T.S.; Trautner, E.M.B. J. 6, 1137-1142, 1987  
A:Title: Organization of multispecific DNA methyltransferases encoded by temperate Ba  
A:Reference number: A91063; MUID:87246516  
A:Accession: A28137  
A:Molecule type: DNA  
A:Residues: 1-475; 'E', 477-503 <BEH>

A:Cross-references: EMBL:X05242  
R:Trautner, T.A.  
submitted to the EMBL Data Library, September 1987  
A:Reference number: A94502  
A:Contents: annotation: revision of residue 476  
C:Comment: This enzyme methylates cytosine within the sequences GGCC and GAGCTC.  
C:Superfamily: site-specific methyltransferase (cytosine-specific) EcoRII  
C:Keywords: methyltransferase; S-adenosylmethionine

Query Match 41.5%; Score 46.5; DB 1; Length 503;  
Best Local Similarity 50.0%; Pred. No.19;  
Matches 10; Conservative 4; Mismatches 5; Indels 1; Gaps 1;

Qy 3 WAAQR-VGRELRRMSDEFV 21  
I:|||||:|:|:|  
Db 207 WSAQIVGRRLRLLEEIVD 226

RESULT 8  
S43852  
neuropeptide Pol-RFamide precursor - hydromedusa (Polyorchis penicillatus)  
N:Contains: neuropeptide Pol-RFamide I; neuropeptide Pol-RFamide II  
C:Species: Polyorchis penicillatus  
C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 07-May-1999  
C:Accession: S43852; JQ2216; A30321  
R:Schmutzler, C.; Diekhoff, D.; Grimmelikhuijzen, C.J.P.  
Biochem. J. 299, 431-436, 1994  
A:Title: The primary structure of the Pol-RFamide neuropeptide precursor protein from the  
A:Reference number: S43852; MUID:94226606  
A:Accession: S43852  
A:Molecule type: mRNA  
A:Residues: 1-287 <SCH>  
A:Cross-references: EMBL:L14777; NID:9294246; PID:g294247  
R:Grimmelikhuijzen, C.J.P.; Rinehart, K.L.; Spencer, A.N.  
Biochem. Biophys. Res. Commun. 183, 375-382, 1992  
A:Title: Isolation of the neuropeptide <Glu-Trp-Leu-Lys-Gly-Phe-NH2 (PolRFamide II)>  
A:Reference number: JQ2216; MUID:92198411  
A:Accession: JQ2216  
A:Molecule type: protein  
A:Residues: 53-59 <GRI>  
A:Note: This sequence was confirmed by chemical synthesis  
R:Grimmelikhuijzen, C.J.P.; Hahn, M.; Rinehart, K.L.; Spencer, A.N.  
Brain Res. 475, 198-203, 1988  
A:Title: Isolation of <Glu-Leu-Leu-Gly-Arg-Phe-NH-2>(Pol-RFamide), a novel neuropeptide  
A:Reference number: A30321; MUID:89105774  
A:Accession: A30321  
A:Molecule type: protein  
A:Residues: 182-188 <GR2>  
A:Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have  
A:Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid  
F:1-21/Domain: signal sequence #status predicted <SIG>  
F:53-59/Product: neuropeptide Pol-RFamide II #status experimental <MI1>  
F:65-71/Product: neuropeptide Pol-RFamide II #status experimental <MI2>  
F:78-84/Product: neuropeptide Pol-RFamide II #status experimental <MI3>  
F:91-97/Product: neuropeptide Pol-RFamide II #status experimental <MI4>  
F:104-110/Product: neuropeptide Pol-RFamide II #status experimental <MI5>  
F:117-123/Product: neuropeptide Pol-RFamide II #status experimental <MI6>  
F:130-136/Product: neuropeptide Pol-RFamide II #status experimental <MI7>  
F:143-149/Product: neuropeptide Pol-RFamide II #status experimental <MI8>  
F:169-175/Product: neuropeptide Pol-RFamide II #status experimental <MI9>  
F:182-188/Product: neuropeptide Pol-RFamide I #status experimental <MA1>  
F:195-201/Product: neuropeptide #status predicted <MI11>  
F:208-214/Product: neuropeptide Pol-RFamide II #status experimental <MI1A>  
F:221-227/Product: neuropeptide Pol-RFamide II #status experimental <MI1B>  
F:53.65,78.91,104,117,130,143,169,182,208,221/Modified site: pyrrolidone carboxylic acid  
F:59,71,84,97,110,123,136,149,175,188,214,227/Modified site: amidated carboxyl end (Phe)

Query Match 40.2%; Score 45; DB 2; Length 287;  
Best Local Similarity 33.3%; Pred. No.19;  
Matches 10; Conservative 5; Mismatches 5; Indels 10; Gaps 1;

Qy 1 NLWAAQRYGREL-----RRMSDEFV 20  
I:|||||:|:|:|  
Db 64 NOWLKGREGRELSQWLKGRFGRELSQWL 93

RESULT 9  
S38185  
2-dehydro-3-deoxyphosphoheptone aldolase (EC 4.1.2.15) ARO4 - yeast (Saccharomyces  
N:Alternate names: 3-deoxy-D-arabino-heptulosonate-7-phosphate synthase; DHP synthase  
C:Species: Saccharomyces cerevisiae  
C:Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 22-Jun-1999  
C:Accession: S38185; S46126; S46130; JN0322; B48651  
R:Doignon, F.; Biteau, N.; Aigle, M.; Crouzet, M.  
Yeast 9, 1131-1137, 1993  
A:Title: The complete sequence of a 6794 bp segment located on the right arm of chrom  
A:Reference number: S38185; MUID:94078675  
A:Accession: S38185  
A:Status: translation not shown  
A:Molecule type: DNA  
A:Residues: 1-370 <DOI>  
A:Cross-references: GB:L20296; NID:g311101; PIDN:AAA65607.1; PID:g311102  
R:Aljinovic, G.; Pohl, F.M.; Pohl, T.M.  
submitted to the Protein Sequence Database, August 1994  
A:Reference number: S45906  
A:Accession: S46126  
A:Molecule type: DNA  
A:Residues: 1-370 <AL>  
A:Cross-references: EMBL:Z36118; NID:9536664; PIDN:CAA85212.1; PID:9536665; MIPS:YBR2  
R:Aigle, M.; Baclet, M.C.; Barthe, C.; Biteau, N.; Crouzet, M.; Doignon, F.  
submitted to the Protein Sequence Database, August 1994  
A:Reference number: S45940  
A:Accession: S46130  
A:Molecule type: DNA  
A:Residues: 1-370 <AIG>  
A:Cross-references: EMBL:Z36118; NID:9536664; PIDN:CAA85212.1; PID:9536665; MIPS:YBR2  
R:Kuenzler, M.; Paravicini, G.; Egli, C.M.; Irniger, S.; Braus, G.H.  
Gene 113, 67-74, 1992  
A:Title: Cloning, primary structure and regulation of the ARO4 gene, encoding the tyr  
A:Reference number: JN0322; MUID:92225349  
A:Accession: JN0322  
A:Molecule type: DNA  
A:Residues: 1-204,208-370 <ROE>  
A:Cross-references: EMBL:X61107  
R:Kuenzler, M.; Balmelli, T.; Egli, C.M.; Paravicini, G.; Braus, G.H.  
J. Bacteriol. 175, 5548-5558, 1993  
A:Title: Cloning, primary structure, and regulation of the HIS7 gene encoding a bifun  
A:Reference number: A48651; MUID:93374850  
A:Accession: B48651  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 352-370 <KU2>  
A:Cross-references: GB:X61107  
C:Comment: This enzyme catalyzes the condensation of phosphoenolpyruvate and D-erythr  
C:Genetics:  
A:Gene: SGD:ARO4  
A:Cross-references: SGD:S0000453; MIPS:YBR249c  
A:Map position: 2R  
C:Function:  
A:Description: aldehyde-lyase; carbon-carbon lyase  
A:Pathway: aromatic amino acid biosynthesis; shikimate pathway  
A:Note: first step in shikimate pathway  
C:Superfamily: phospho-2-dehydro-3-deoxyheptone aldolase  
C:Keywords: aldehyde-lyase; aromatic amino acid biosynthesis; carbon-carbon lyase; cy

Query Match 40.2%; Score 45; DB 2; Length 370;  
Best Local Similarity 50.0%; Pred. No.24;  
Matches 9; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 1 NLWAAQRYGRELRRMSDE 18  
I:|||||:|:|:|  
Db 80 DLEAAQYALRLKLSDE 97



Search completed: October 9, 2001, 15:54:04  
Job time: 234 sec

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QY 61 HCGAGAVEIRSRHSSYPAGTDEDEGMGEPPSPFRGRSRAPPNLMWAAQRYGRLRMADE 120  
|||||  
Db 61 HCGAGAVEIRSRHSSYPAGTDEDEGMGEPPSPFRGRSRAPPNLMWAAQRYGRLRMSDE 120  
|||||

QY 121 FVDSFKKGLPRPKSAGTATQMROSSWTRVFQSWMDNLRGSSAPSQ 168  
|||||  
Db 121 FVDSFKKGLPRPKSAGTATQMROSSWTRVFQSWMDNLRGSSAPSQ 168  
|||||

RESULT 2  
US-08-985-335-1  
; Sequence 1, Application US/08985335  
; Patent No. 6080847  
; GENERAL INFORMATION:  
; APPLICANT: Hillman, Jennifer L.  
; APPLICANT: Yue, Henry  
; APPLICANT: Lal, Preeti  
; APPLICANT: Shah, Purvi  
; APPLICANT: Corley, Neil C.  
; TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL  
; TITLE OF INVENTION: PROLIFERATION  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Dr.  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/985,335  
; FILING DATE: Filed Herewith  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Billings, Lucy J.  
; REGISTRATION NUMBER: 36,749  
; REFERENCE/DOCKET NUMBER: PF-0421 US  
; TELEPHONE: 650-855-0555  
; TELEFAX: 650-845-4166  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 168 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: SYNORAB01  
; CLONE: 358673  
US-08-985-335-1

Query Match 99.7%; Score 902; DB 3; Length 168;  
Best Local Similarity 99.4%; Pred. No. 2.1e-84;  
Matches 167; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFOIPEFEPSEQEDSSAERGLPGSPAGDGPSSGKHHRQAPGLLDASHQOQPTSSSH 60  
|||||  
Db 1 MFOIPEFEPSEQEDSSAERGLPGSPAGDGPSSGKHHRQAPGLLDASHQOQPTSSSH 60  
|||||

QY 61 HCGAGAVEIRSRHSSYPAGTDEDEGMGEPPSPFRGRSRAPPNLMWAAQRYGRLRMADE 120  
|||||  
Db 61 HCGAGAVEIRSRHSSYPAGTDEDEGMGEPPSPFRGRSRAPPNLMWAAQRYGRLRMSDE 120  
|||||

QY 121 FVDSFKKGLPRPKSAGTATQMROSSWTRVFQSWMDNLRGSSAPSQ 168  
|||||

Db 121 FVDSFKKGLPRPKSAGTATQMROSSWTRVFQSWMDNLRGSSAPSQ 168  
|||||

RESULT 3  
US-08-665-617-2  
; Sequence 2, Application US/08665617  
; Patent No. 5663316  
; GENERAL INFORMATION:  
; APPLICANT: Xudong, Yin  
; TITLE OF INVENTION: Gene and Protein for Regulation of Cell Death  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Saliwanchik & Saliwanchik  
; STREET: 2421 N.W. 41st Street, Suite A-1  
; CITY: Gainesville  
; STATE: Florida  
; COUNTRY: USA  
; ZIP: 32606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/665,617  
; FILING DATE:  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Saliwanchik, David R.  
; REGISTRATION NUMBER: 31,794  
; REFERENCE/DOCKET NUMBER: CL-8  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (352) 375-8100  
; TELEFAX: (352) 372-5800  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 166 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-665-617-2

Query Match 82.7%; Score 748; DB 1; Length 166;  
Best Local Similarity 83.4%; Pred. No. 9e-69;  
Matches 146; Conservative 4; Mismatches 9; Indels 16; Gaps 3;

QY 1 MFOIPEFEPSEQEDSSAERGLPGSPAGDGPSSGKHHRQAPG-----LLWDASHQOE 53  
|||||  
Db 1 MFOIPEFEPSEQEDSSAERG-WRSPAGTGP-----QAPASIIARPQVLDASHQOE 51  
|||||

QY 54 QPTSSSHHGGAGAVEIRSRHSSYPAGTDEDEGMGEPPSPFRGRSRAPPNLMWAAQRYGRE 113  
|||||  
Db 52 QPTSSSHHGGAGAVEIRSRHSSYPAGTDEDEGMGEPPSPFRGARARPPPNLMWAAQRYGRE 111  
|||||

QY 114 LRRMADEFVDSFKKGLPRPKSAGTATQMROSSWTRVFQSWMDNLRGSSAPSQ 168  
|||||  
Db 112 LRRMDEFVDSFKKGLPRPKSAGTATQMROSSWTRVFQSWMDNLRGRTAAPSQ 166  
|||||

RESULT 4  
US-08-985-335-7  
; Sequence 7, Application US/08985335  
; Patent No. 6080847  
; GENERAL INFORMATION:  
; APPLICANT: Hillman, Jennifer L.  
; APPLICANT: Yue, Henry  
; APPLICANT: Lal, Preeti  
; APPLICANT: Shah, Purvi  
; APPLICANT: Corley, Neil C.  
; TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL  
; TITLE OF INVENTION: PROLIFERATION



NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Dr.  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/985,335  
FILING DATE: Filed Herewith  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J.  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0421 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-855-0555  
TELEFAX: 650-845-4166  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 168 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: GenBank  
CLONE: 1683637  
US-08-985-335-7

Query Match 81.9%; Score 741; DB 3; Length 168;  
Best Local Similarity 84.5%; Pred. No. 4.7e-68;  
Matches 142; Conservative 1; Mismatches 25; Indels 0; Gaps 0;

QY 1 MFQIPEPESQEDSSAERGLGSPAGDGPSSGKHHQAPGLLDASHQEQPTSSSH 60  
|||||  
DB 1 MFQIPEPESQEDSSAERGLGSPAGDGPSSGKHHQAPGLLDASHQEQPTSSSH 60  
|||||  
QY 61 HGGAGAVEIRSRHSYPAGTDEDEGMGEPPFRGRSRSPAPNLWAAQRYGRELRRMADE 120  
|||||  
DB 61 HGGAGCGDPPSPQLPRGDDRRDGGGAQPPFRGRSRSPAPNLWAAQRYGRELRRMSDE 120  
|||||  
QY 121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168  
|||||  
DB 121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168  
|||||

RESULT 5  
US-08-333-565-2  
Sequence 2, Application US/08333565  
Patent No. 5622852  
GENERAL INFORMATION:  
APPLICANT: KORSMEYER, Stanley J.  
TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH  
NUMBER OF SEQUENCES: 59  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Kourie and Crew  
STREET: 379 Lytton Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: US  
ZIP: 94301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/333,565  
FILING DATE: 31-OCT-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 15726A-000700  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 326-2422  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 204 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
NAME/KEY: Protein  
LOCATION: 1..204  
OTHER INFORMATION: /note= "Deduced amino acid sequence  
of mouse BAD."  
US-08-333-565-2

Query Match 71.4%; Score 646; DB 1; Length 204;  
Best Local Similarity 75.0%; Pred. No. 2.7e-58;  
Matches 126; Conservative 13; Mismatches 23; Indels 6; Gaps 3;

QY 1 MFQIPEPESQEDSSAERGLGSPAGDGPSSGKHHQAPGLLDASHQEQPTSSSH 60  
|||||  
DB 43 MFQIPEPESQEDASATDRLGSLTQDP---GPY--LAPLLGSLNHQOQGRATNSH 97  
|||||  
QY 61 HGGAGAVEIRSRHSYPAGTDEDEGMGEPPFRGRSRSPAPNLWAAQRYGRELRRMADE 120  
|||||  
DB 98 HGGAGAMETRRHSYPAGTEDEGMEEELSPFRGRSRSPAPNLWAAQRYGRELRRMSDE 157  
|||||  
QY 121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168  
|||||  
DB 158 FEGSF-KGLPRPKSAGTATQMRQSGAGWTRIIQSWWDRNLGKGSTPSQ 204  
|||||

RESULT 6  
US-08-661-479-2  
Sequence 2, Application US/08661479  
Patent No. 5834209  
GENERAL INFORMATION:  
APPLICANT: KORSMEYER, Stanley J.  
TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH  
NUMBER OF SEQUENCES: 59  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Kourie and Crew  
STREET: 379 Lytton Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: US  
ZIP: 94301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/661,479  
FILING DATE: 11-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/333,565

```

: FILING DATE: 31-OCT-1994
: ATTORNEY/AGENT INFORMATION:
: NAME: Smith, William M
: REGISTRATION NUMBER: 30, 223
: REFERENCE/DOCKET NUMBER: 15736A-000700
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 326-2400
: TELEFAX: (415) 326-2422
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 204 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: FEATURE:
: NAME/KEY: Protein
: LOCATION: 1..204
: OTHER INFORMATION: /note= "Deduced ami
: OTHER INFORMATION: of mouse BAD."
US-08-661-479-2

```

```

Query Match      71.4%; Score 646; DB 2; Length 204;
Best local Similarity 75.0%; Pred. No. 2.7e-58;
Matches 126; Conservative 13; Mismatches 23; Indels 6; Gaps 3;

QY: 1 MFQIPEPESEQEDSSAAERGLGSPAGDGPSSGSKHHRQAPGLLWDASHOQEPTSSSH 60
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 43 MFQIPEPESEQEDASATDRLGSLSTEDQP--GPY--LAPGLLGSNIHQOGRAATNSH 97
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 HGCAGAYEIRSRHSSYPAGTDEDDGMEGEEPPFRGSRSPAPNLWAAQRYGRELRRMADE 120
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 98 HGCAGAMETRSRHSYPAGTEEDGMEHEELSPFRGSRSPAPNLWAAQRYGRELRRMSDE 157
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 121 FVDSFKGLPRPKSAGATATMRQSSSTRTVFQSWWDRNLGRGSSAPSQ 168
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 158 FEGSF-KGLPRPKSAGATATMRQSGAGVTRIIQSWWDRNLGRGGSTPQ 204.
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

```

1  RESULT 7
2  US-08-733-505A-1
3  ; Sequence 1, Application US/08733505A
4  ; Patent No. 5856445
5  ; GENERAL INFORMATION:
6  ; APPLICANT: KORSMEYER, STANLEY J.
7  ; TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
8  ; TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
9  ; NUMBER OF SEQUENCES: 60
10 ; CORRESPONDENCE ADDRESS:
11 ; ADDRESSEE: HOWELL & HAFERKAMP, L.C.
12 ; STREET: 7733 FORSYTH BLVD., SUITE 1400
13 ; CITY: ST. LOUIS
14 ; STATE: MISSOURI
15 ; COUNTRY: USA
16 ; ZIP: 63105
17 ; COMPUTER READABLE FORM:
18 ; MEDIUM TYPE: Floppy disk
19 ; COMPUTER: IBM PC compatible
20 ; OPERATING SYSTEM: PC-DOS/MS-DOS
21 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
22 ; CURRENT APPLICATION DATA:
23 ; APPLICATION NUMBER: US/08/733,505A
24 ; FILING DATE:
25 ; CLASSIFICATION: 530
26 ; ATTORNEY/AGENT INFORMATION:
27 ; NAME: HOLLAND, DONALD R.
28 ; REGISTRATION NUMBER: 35,197
29 ; REFERENCE/DOCKET NUMBER: 965458
30 ; TELECOMMUNICATION INFORMATION:
31 ; TELEPHONE: (314) 727-5188
32 ; TELEFAX: (314) 727-6092
33 ; INFORMATION FOR SEQ ID NO: 1:

```

```

;
; SEQUENCE CHARACTERISTICS:
;     LENGTH: 204 amino acids
;     TYPE: amino acid
;     STRANDEDNESS:
;     TOPOLOGY: linear
;     MOLECULE TYPE: protein
; US-08-733-505A-1

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Query Match	71.48;	Score 646;	DB 2;	Length 204;
Best Local Similarity	75.09;	Pred. No. 2.7e-58;		
Matches 126; Conservative 13; Mismatches 23; Indels 6; Gaps 3;				
Qy	1	MFQIPEFPESQEDSSAERGLGSPAGDGFSGGKKHHRQAQPLGLLDASHHQEOPTSSSH	60	
Dd	43	MFQIPEFPESQEDASATDRGLGFSLTEDQP--GPY--LAPGLLGSIHHOQGRAATWSH	97	
Qy	61	HGGAGAVEIRSRHSYSYPAGTDEDCMGEPSPFGRSRSAPPNLWAAQRYCRLRLRMADE	120	
Dd	98	HGGAGAMETRSKHSYSYPAGTEDECGMEELSPFGRSRSAPPNLWAAQRYCRLRLRMSDE	157	
Qy	121	FVDFEKKGLPPKKSAGTATQMRQSSSTRVFQSWWDRNLGRGGSAPSQ	168	
Dd	158	FEFGSF-KGLPFPKKSAGTATQMRQSGAVTRIIQSWMDRLNGKGGSPTSQ	204	

RESULT 8  
US-08-717-123-3  
Sequence 3, Application US/08717123  
Patent No. 5965703  
GENERAL INFORMATION:  
APPLICANT: Horne, William A.  
APPLICANT: Oltersdorf, Tilman  
TITLE OF INVENTION: Human BAD Polypeptides, Encoding Nucleic  
TITLE OF INVENTION: Acids and Methods of Use  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Campbell and Flores  
STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego  
STATE: California  
COUNTRY: United States  
ZIP: 92122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/717,123  
FILING DATE: 20-SEP-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-ID 1929  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 204 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-717-123-3

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Query Match      71.3%; Score 645; DB 2; Length 204;
Best Local Similarity 75.0%; Pred. No. 3.4e-58;
Matches 126; Conservative 12; Mismatches 24; Indels 6; Gaps 3;
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RESULT 12  
US-08-733-505A-55  
Sequence 55, Application US/08733505A  
Patent No. 5856445  
GENERAL INFORMATION:  
APPLICANT: KORSMEYER, STANLEY J.  
TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF  
TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR  
NUMBER OF SEQUENCES: 60  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: HOWELL & HAFERKAMP, L.C.  
STREET: 7733 FORSYTH BLVD., SUITE 1400  
CITY: ST. LOUIS  
STATE: MISSOURI  
COUNTRY: USA  
ZIP: 63105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/733,505A  
FILING DATE:  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: HOLLAND, DONALD R.  
REGISTRATION NUMBER: 35,197  
REFERENCE/DOCKET NUMBER: 965458  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (314) 727-5188

```

Query Match          34.0%; Score 308; DB 2; Length 59;
Best Local Similarity 96.6%; Pred. No. 1.1e-24;
Matches 57; Conservative 2; Mismatches 0; Indels 0; Gaps 0
QY 63 GAGAVEIRSRHSYPACTDEDEGNGEESPSPFRGRSRSPPNLWAAQRYGRELRRMADEF 121
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 GAGAVEIRSRHSAYPACTDEDEGNGEESPSPFRGRSRSPPNLWAAQRYGRELRRMSDEF 59

```

```
; Sequence 57, Application US/08733505A
; Patent No. 5856445
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, STANLEY J.
; TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
; TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWELL & HAFERKAMP, L.C.
; STREET: 7733 FORSYTH BLVD., SUITE 1400
; CITY: ST. LOUIS
; STATE: MISSOURI
; COUNTRY: USA
; ZIP: 63105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/733,505A
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: HOLLAND, DONALD R.
; REGISTRATION NUMBER: 35,197
; REFERENCE/DOCKET NUMBER: 965458
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 727-5188
; TELEFAX: (314) 727-6092
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 59 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-733-505A-57

Query Match 34.0%; Score 308; DB 2; Length 59;
Best Local Similarity 96.6%; Pred. No. 1.1e-24;
Matches 57; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 63 GAGAVEIRSRHSSYPAGTDEDEGMGEPPSPFRGRSRAPPNLWAAQRYGRELRRMADEF 121
Db 1 GAGAVEIRSRHSSYPAGTDEDEGMGEPPSPFRGRSRAPPNLWAAQRYGRELRRMSDEF 59

RESULT 15
US-08-733-505A-58
; Sequence 58, Application US/08733505A
; Patent No. 5856445
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, STANLEY J.
; TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
; TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWELL & HAFERKAMP, L.C.
; STREET: 7733 FORSYTH BLVD., SUITE 1400
; CITY: ST. LOUIS
; STATE: MISSOURI
; COUNTRY: USA
; ZIP: 63105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/733,505A
; FILING DATE:
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```
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: HOLLAND, DONALD R.
; REGISTRATION NUMBER: 35,197
; REFERENCE/DOCKET NUMBER: 965458
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 727-5188
; TELEFAX: (314) 727-6092
; INFORMATION FOR SEQ ID NO: 58:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 59 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-733-505A-58

Query Match 33.7%; Score 305; DB 2; Length 59;
Best Local Similarity 94.9%; Pred. No. 2.3e-24;
Matches 56; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 63 GAGAVEIRSRHSSYPAGTDEDEGMGEPPSPFRGRSRAPPNLWAAQRYGRELRRMADEF 121
Db 1 GAGAVEIRSRHSSYPAGTDEDEGMGEPPSPFRGRSRAPPNLWAAQRYGRELRRMSDEF 59

Search completed: October 9, 2001, 15:58:34
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QY      1 MFQTPEFEPSEQEDSSAERGLGPPAGDPSPSGKGKHHRQAPGLLWDASHQQEQPTSSSH 60
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; Patent No. 5856445
;
; GENERAL INFORMATION:
;
; APPLICANT: KORSMEYER, STANLEY J.
;
; TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
;
; TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
;
; NUMBER OF SEQUENCES: 60
;
; CORRESPONDENCE ADDRESS:
;
; ADDRESSEE: HOWELL & HAFERKAMP, L.C.
;
; STREET: 7733 FORSYTH BLVD., SUITE 1400
;
; CITY: ST. LOUIS
;
; STATE: MISSOURI
;
; COUNTRY: USA
;
; ZIP: 63105
;
; COMPUTER READABLE FORM:
;
; MEDIUM TYPE: Floppy disk
;
; COMPUTER: IBM PC compatible
;
; OPERATING SYSTEM: PC-DOS/MS-DOS
;
; SOFTWARE: Patentin Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:
;
; APPLICATION NUMBER: US/08/733,505A

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STATE: MISSOURI  
COUNTRY: USA  
ZIP: 63105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/733,505A

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; MOLECULE TYPE: peptide
US-08-733-505A-13

Query Match 71.0%; Score 643; DB 2; Length 204;
Best Local Similarity 74.4%; Pred. No. 5.4e-58;
Matches 125; Conservative 14; Mismatches 23; Indels 6; Gaps 0

1 MFQIPEPSSQEDSSAERGLGPSAGDGPSSGGRKHRRQAPGLMDASHQCEQPTSSSH
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43 MFQIPEPSSQEDASATDGLGPSLTEDQ-----GPY--LAPGLGSNTHQGRATNISH
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
61 HGGAGAVEIRSRHSSYPAGTEDEGMGEESPSPFRGSRGAPPNLWAAQRYGRELRRMADE
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
98 HGGAGAMETRSRHSSYPAGTEDEGMGEELSPSPFRGSRRAAPPNLWAAQRYGRELRRMSDE
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

DBD 158 FEGSF-KGLPRKSAGTATOMROSAGWTRIIQSWDRNLKGSGTSPQ 204

RESULT 11  
US-08-733-505A-14  
: Sequence 14, Application US/08733505A  
: Patent No. 5856445  
: GENERAL INFORMATION:  
: APPLICANT: KORMSEYER, STANLEY J.  
: TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF  
: TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR  
: NUMBER OF SEQUENCES: 60  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: HOWELL & HAFERKAMP, L.C.  
: STREET: 7733 FORSYTH BLVD., SUITE 1400

STATE: MISSOURI  
COUNTRY: USA  
ZIP: 63105  
COMPUTER READABLE FORM:

**THIS PAGE BLANK (USPTO)**

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: October 9, 2001, 15:58:34 ; Search time 18.99 Seconds  
(without alignments)  
182.158 Million cell updates/sec

Title: 09-580523-lb  
Perfect score: 905  
Sequence: 1 MFQIPEPESQEDSSAER.....RVFQSWDRNLGRSSAFSQ 168

Scoring table: BLOSUM62  
Gap 10.0 , Gapext 0.5

Searched: 197339 seqs, 20590346 residues

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA.\*  
1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep.\*  
2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	902	99.7	168	2	US-08-717-123-2
2	902	99.7	188	3	US-08-985-335-1
3	748	82.7	166	1	US-08-665-617-2
4	741	81.9	168	3	US-08-985-335-7
5	646	71.4	204	1	US-08-333-565-2
6	646	71.4	204	2	US-08-661-479-2
7	646	71.4	204	2	US-08-733-505A-1
8	645	71.3	204	2	US-08-717-123-3
9	643	71.0	204	2	US-08-733-505A-12
10	643	71.0	204	2	US-08-733-505A-13
11	640	70.7	204	2	US-08-733-505A-14
12	311	34.4	59	2	US-08-733-505A-55
13	308	34.0	59	2	US-08-733-505A-56
14	308	34.0	59	2	US-08-733-505A-57
15	305	33.7	59	2	US-08-733-505A-58
16	113	12.5	23	1	US-08-333-565-10
17	113	12.5	23	2	US-08-661-479-10
18	97	10.7	2509	2	US-08-149-097D-35
19	96.5	10.7	1182	4	US-09-041-886-21
20	90.5	10.0	393	2	US-09-026-587-3
21	90.5	10.0	393	2	US-09-227-420-3
22	90	9.9	434	1	US-08-337-602-3
23	90	9.9	434	3	US-08-558-135-3
24	90	9.9	2237	1	US-08-455-543A-48
25	90	9.9	2237	1	US-08-223-305C-48
26	90	9.9	2337	3	US-08-713-118-2
27	90	9.9	2337	4	US-09-452-007-2

28 90 9.9 2339 1 US-08-455-543A-47 Sequence 47, Appl  
29 90 9.9 2339 2 US-08-223-305C-47 Sequence 47, Appl  
30 89 9.8 418 2 US-09-026-587-1 Sequence 1, Appl  
31 89 9.8 418 2 US-09-227-420-1 Sequence 1, Appl  
32 87 9.6 575 3 US-08-922-865-2 Sequence 2, Appl  
33 85.5 9.4 378 2 US-08-986-217-6 Sequence 6, Appl  
34 85.5 9.4 1159 3 US-08-956-242-13 Sequence 13, Appl  
35 85.5 9.4 1159 3 US-09-351-215-13 Sequence 13, Appl  
36 85.5 9.4 1159 4 US-09-226-012-2 Sequence 2, Appl  
37 85.5 9.4 1159 4 US-09-226-012-4 Sequence 4, Appl  
38 84 9.3 16 1 US-08-333-565-17 Sequence 17, Appl  
39 84 9.3 16 2 US-08-661-479-17 Sequence 17, Appl  
40 84 9.3 380 2 US-09-026-587-4 Sequence 4, Appl  
41 84 9.3 380 2 US-09-227-420-4 Sequence 4, Appl  
42 83 9.2 16 1 US-08-333-565-26 Sequence 26, Appl  
43 83 9.2 16 2 US-08-661-479-26 Sequence 26, Appl  
44 83 9.2 591 3 US-09-082-737-2 Sequence 2, Appl  
45 83 9.2 696 3 US-08-906-865-4 Sequence 4, Appl

ALIGNMENTS

RESULT 1  
US-08-717-123-2  
; Sequence 2, Application US/08717123  
; Patent No. 5965703  
; GENERAL INFORMATION:  
; APPLICANT: Horne, William A.  
; APPLICANT: Oltersdorf, Tilman  
; TITLE OF INVENTION: Human BAD Polypeptides, Encoding Nucleic  
; TITLE OF INVENTION: Acids and Methods of Use  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Campbell and Flores  
; STREET: 4370 La Jolla Village Drive, Suite 700  
; CITY: San Diego  
; STATE: California  
; COUNTRY: United States  
; ZIP: 92122  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/717,123  
; FILING DATE: 20-SEP-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Campbell, Cathryn A.  
; REGISTRATION NUMBER: 31,815  
; REFERENCE/DOCKET NUMBER: P-ID 1929  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 535-9001  
; TELEFAX: (619) 535-8949  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 168 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-717-123-2

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Db 1 MFQIPEPESQEDSSAERGLGSPAGDPSGSGKHRRQAPGLLDASHHQOEPSSTSS 60

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RESULT 2  
 US-08-985-335-1  
 ; Sequence 1, Application US/08985335  
 ; Patent No. 6080847  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hillman, Jennifer L.  
 ; APPLICANT: Yue, Henry  
 ; APPLICANT: Lal, Preeti  
 ; APPLICANT: Shah, Purvi  
 ; APPLICANT: Corley, Neil C.  
 ; TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL  
 ; NUMBER OF SEQUENCES: 9  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
 ; STREET: 3174 Porter Dr.  
 ; CITY: Palo Alto  
 ; STATE: CA  
 ; COUNTRY: USA  
 ; ZIP: 94304  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: DOS  
 ; SOFTWARE: FastSeq for Windows Version 2.0  
 ; CURRENT APPLICATION DATA:  
 ; FILING DATE: US/08/985.335  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER:  
 ; FILING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Billings, Lucy J.  
 ; REGISTRATION NUMBER: 36,749  
 ; REFERENCE/DOCKET NUMBER: PF-0421 US  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 650-855-0555  
 ; TELEFAX: 650-845-4166  
 ; INFORMATION FOR SEQ ID NO: 1:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 168 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; IMMEDIATE SOURCE:  
 ; LIBRARY: SYNORAB01  
 ; CLONE: 358673  
 ; US-08-985-335-1

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US-08-985-335-1  
 ; Sequence 1, Application US/08985335  
 ; Patent No. 6080847  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hillman, Jennifer L.  
 ; APPLICANT: Yue, Henry  
 ; APPLICANT: Lal, Preeti  
 ; APPLICANT: Shah, Purvi  
 ; APPLICANT: Corley, Neil C.  
 ; TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL  
 ; NUMBER OF SEQUENCES: 9  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
 ; STREET: 3174 Porter Dr.  
 ; CITY: Palo Alto  
 ; STATE: CA  
 ; COUNTRY: USA  
 ; ZIP: 94304  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: DOS  
 ; SOFTWARE: FastSeq for Windows Version 2.0  
 ; CURRENT APPLICATION DATA:  
 ; FILING DATE: US/08/985.335  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER:  
 ; FILING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Billings, Lucy J.  
 ; REGISTRATION NUMBER: 36,749  
 ; REFERENCE/DOCKET NUMBER: PF-0421 US  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 650-855-0555  
 ; TELEFAX: 650-845-4166  
 ; INFORMATION FOR SEQ ID NO: 1:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 168 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; IMMEDIATE SOURCE:  
 ; LIBRARY: SYNORAB01  
 ; CLONE: 358673  
 ; US-08-985-335-1

Query Match 99.7%; Score 902; DB 3; Length 168;  
 Best Local Similarity 99.4%; Pred. No. 2,1e-84;  
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 QY 61 HGGAGAVEIRSRHSSYPAGTDEGMEGEPSPFRGRSRAPPNLWAAQRYGRELRRMADE 120  
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US-08-985-335-1

Db 121 FVDSFKKGLPRKSGATATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168

RESULT 3  
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 ; Sequence 2, Application US/08665617  
 ; Patent No. 5663316  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Xudong, Yin  
 ; TITLE OF INVENTION: Gene and Protein for Regulation of Cell Death  
 ; NUMBER OF SEQUENCES: 2  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Saliwanchik & Saliwanchik  
 ; STREET: 2421 N.W. 41st Street, Suite A-1  
 ; CITY: Gainesville  
 ; STATE: Florida  
 ; COUNTRY: USA  
 ; ZIP: 32606  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC Compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/665,617  
 ; FILING DATE:  
 ; CLASSIFICATION: 530  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Saliwanchik, David R.  
 ; REGISTRATION NUMBER: 31,794  
 ; REFERENCE/DOCKET NUMBER: CL-8  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (352) 375-8100  
 ; TELEFAX: (352) 372-5800  
 ; INFORMATION FOR SEQ ID NO: 2:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 166 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-08-665-617-2

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US-08-985-335-7  
 ; Sequence 7, Application US/08985335  
 ; Patent No. 6080847  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hillman, Jennifer L.  
 ; APPLICANT: Yue, Henry  
 ; APPLICANT: Lal, Preeti  
 ; APPLICANT: Shah, Purvi  
 ; APPLICANT: Corley, Neil C.  
 ; TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL  
 ; Proliferation

RESULT 4  
 US-08-985-335-7  
 ; Sequence 7, Application US/08985335  
 ; Patent No. 6080847  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hillman, Jennifer L.  
 ; APPLICANT: Yue, Henry  
 ; APPLICANT: Lal, Preeti  
 ; APPLICANT: Shah, Purvi  
 ; APPLICANT: Corley, Neil C.  
 ; TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL  
 ; Proliferation

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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 9, 2001, 15:58:34 ; Search time 18.99 Seconds  
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182.158 Million cell updates/sec

Title: 09-580523-lb  
Perfect score: 905  
Sequence: 1 MFQIPEPSEQEDSSAER.....RVFQSWDRNLGRSSAPSQ 168

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Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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6: /cgn2\_6/ptodata/2/1aa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

*Result No.	Score	Query Match %	Length	DB ID	Description
1	902	99.7	168	2	US-08-717-123-2
2	902	99.7	168	3	US-08-985-333-1
3	748	82.7	166	1	US-08-665-617-2
4	741	81.9	168	3	US-08-985-335-7
5	646	71.4	204	1	US-08-333-565-2
6	646	71.4	204	2	US-08-661-479-2
7	646	71.4	204	2	US-08-733-505A-1
8	645	71.3	204	2	US-08-717-123-3
9	643	71.0	204	2	US-08-733-505A-12
10	643	71.0	204	2	US-08-733-505A-13
11	640	70.7	204	2	US-08-733-505A-14
12	311	34.4	59	2	US-08-733-505A-55
13	308	34.0	59	2	US-08-733-505A-56
14	308	34.0	59	2	US-08-733-505A-57
15	305	33.7	59	2	US-08-733-505A-58
16	113	12.5	23	1	US-08-333-565-10
17	113	12.5	23	2	US-08-661-479-10
18	97	10.7	2509	2	US-08-149-097D-35
19	96.5	10.7	1182	4	US-09-041-886-21
20	90.5	10.0	393	2	US-09-026-587-3
21	90.5	10.0	393	2	US-09-227-420-3
22	90	9.9	434	1	US-08-337-602-3
23	90	9.9	434	3	US-08-558-135-3
24	90	9.9	2237	1	US-08-455-543A-48
25	90	9.9	2237	2	US-08-223-305C-48
26	90	9.9	2237	3	US-08-713-118-2
27	90	9.9	2337	4	US-09-452-007-2

28	90	9.9	2339	1	US-08-455-543A-47	Sequence 47, Appl
29	90	9.9	2339	2	US-08-223-305C-47	Sequence 47, Appl
30	89	9.8	418	2	US-09-026-587-1	Sequence 1, Appl
31	89	9.8	418	2	US-09-227-420-1	Sequence 1, Appl
32	87	9.6	575	3	US-08-822-865-2	Sequence 2, Appl
33	85.5	9.4	378	2	US-08-986-217-6	Sequence 6, Appl
34	85.5	9.4	1159	3	US-08-956-242-13	Sequence 13, Appl
35	85.5	9.4	1159	3	US-09-351-215-13	Sequence 2, Appl
36	85.5	9.4	1159	4	US-09-226-012-2	Sequence 2, Appl
37	85.5	9.4	1159	4	US-09-226-012-4	Sequence 4, Appl
38	84	9.3	16	1	US-08-333-565-17	Sequence 17, Appl
39	84	9.3	16	2	US-08-661-479-17	Sequence 17, Appl
40	84	9.3	380	2	US-09-026-587-4	Sequence 4, Appl
41	84	9.3	380	2	US-09-227-420-4	Sequence 4, Appl
42	83	9.2	16	1	US-08-333-565-26	Sequence 26, Appl
43	83	9.2	16	2	US-08-661-479-26	Sequence 26, Appl
44	83	9.2	591	3	US-09-082-737-2	Sequence 2, Appl
45	83	9.2	696	3	US-08-906-865-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1  
US-08-717-123-2  
; Sequence 2, Application US/08717123  
; Patent No. 5965703  
; GENERAL INFORMATION:  
; APPLICANT: Horne, William A.  
; APPLICANT: Oltersdorf, Tilman  
; TITLE OF INVENTION: Human BAD Polypeptides, Encoding Nucleic  
; TITLE OF INVENTION: Acids and Methods of Use  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Campbell and Flores  
; STREET: 4370 La Jolla Village Drive, Suite 700  
; CITY: San Diego  
; STATE: California  
; COUNTRY: United States  
; ZIP: 92122  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/717,123  
; FILING DATE: 20-SEP-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Campbell, Cathryn A.  
; REGISTRATION NUMBER: 31,815  
; REFERENCE/DOCKET NUMBER: P-ID 1929  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 535-9001  
; TELEFAX: (619) 535-8949  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 168 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-717-123-2

Query Match 99.7%; Score 902; DB 2; Length 168;  
Best Local Similarity 99.4%; Pred. No. 2.1e-84;  
Matches 167; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MFQIPEPSEQEDSSAERGLGSPAGDPSGSGKHRRQAPGLLWDASHOOEQPTSSSH 60  
DB 1 MFQIPEPSEQEDSSAERGLGSPAGDPSGSGKHRRQAPGLLWDASHOOEQPTSSSH 60

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RESULT      4
US-08-985-335-7
: Sequence 7, Application US/08985335
: Patent No. 6080847
: GENERAL INFORMATION:
: APPLICANT: Hillman, Jennifer L.
: APPLICANT: Yue, Henry
: APPLICANT: Lal, Preeti
: APPLICANT: Shah, Purvi
: APPLICANT: Corley, Neil C.
: TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL PROLIFERATION
: TITLE OF INVENTION: PROLIFERATION

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## RESULT

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US-09-410-372-1
; Sequence 1, Application US/09410372
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Yue, Henry
; APPLICANT: Lal, Preeti
; APPLICANT: Shah, Purvi
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
; TITLE OF INVENTION: PROLIFERATION
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304

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; APPLICANT: Yue, Henry  
; APPLICANT: Lal, Preeti  
; APPLICANT: Shah, Purvi  
; APPLICANT: Corlev, Neil C.

; TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL  
; PROLIFERATION;  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
;

STREET: 31/4 Porter Dr.  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304

STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/410,372  
FILING DATE:  
PRIOR APPLICATION DATA:

/ APPLICATION NUMBER: 08/985,335  
 / FILING DATE:  
 / ATTORNEY/AGENT INFORMATION:  
 / NAME: Billings, Lucy J.  
 / REGISTRATION NUMBER: 36,749

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-855-0555  
TELEFAX: 650-845-4166  
INFORMATION FOR SEO ID NO: 1:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 168 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
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LIBRARY: SYNORAB01  
CLONE: 358673  
US-09-410-372-1

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US-09-410-372-1

Query Match 100.0% Score 145; DB 18; Length 168;
Best Local Similarity 100.0%; Pred. No. 1.6e-11;
Matches 26; Conservative 0; Mismatches 0; Indels 0

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RESULT 6
US-09-410-372-7

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RESULT 6  
US-09-410-372-7

; Sequence 7, Application US/09410372  
; GENERAL INFORMATION:  
; APPLICANT: Hillman, Jennifer L.  
; APPLICANT: Yue, Henry  
; APPLICANT: Lal, Preeti  
; APPLICANT: Shah, Purvi  
; APPLICANT: Corley, Neil C.  
; TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL  
; TITLE OF INVENTION: PROLIFERATION  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Dr.  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA: US/09/410,372  
; APPLICATION NUMBER: US/09/410,372  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/985,335  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Billings, Lucy J.  
; REGISTRATION NUMBER: 36,749  
; REFERENCE/DOCKET NUMBER: PF-0421 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-855-0555  
; TELEFAX: 650-845-4166  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 168 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: GenBank  
; CLONE: 1683637  
; US-09-410-372-7

Query Match 100.0%; Score 145; DB 18; Length 168;  
Best Local Similarity 100.0%; Pred. No. 1.6e-11;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QSSWTRVFQSWWDRNLGRGSSAPSQ 26  
Db 143 QSSWTRVFQSWWDRNLGRGSSAPSQ 168  
|||||

RESULT 7  
US-09-456-357-32  
; Sequence 32, Application US/09456357  
; GENERAL INFORMATION:  
; APPLICANT: 3921-1-1-1  
; TITLE OF INVENTION: VIRAL VECTORS ENCODING APOPTOSIS-INDUCING PROTEINS AND  
; TITLE OF INVENTION: METHODS FOR MAKING AND USING THE SAME  
; FILE REFERENCE: 3921-1-1-1  
; CURRENT APPLICATION NUMBER: US/09/456,357  
; CURRENT FILING DATE: 1999-12-08  
; EARLIER APPLICATION NUMBER: 60/134,416  
; EARLIER FILING DATE: 1999-05-17  
; EARLIER APPLICATION NUMBER: 09/087,195  
; EARLIER FILING DATE: 1998-05-29  
; EARLIER APPLICATION NUMBER: 08/378,507  
; EARLIER FILING DATE: 1995-01-26  
; EARLIER APPLICATION NUMBER: 08/250,478

; EARLIER FILING DATE: 1994-05-27  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 32  
; LENGTH: 168  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-09-456-357-32

Query Match 100.0%; Score 145; DB 18; Length 168;  
Best Local Similarity 100.0%; Pred. No. 1.6e-11;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QSSWTRVFQSWWDRNLGRGSSAPSQ 26  
Db 143 QSSWTRVFQSWWDRNLGRGSSAPSQ 168  
|||||

RESULT 8  
US-09-580-523-1  
; Sequence 1, Application US/09580523  
; GENERAL INFORMATION:  
; APPLICANT: Zhou, Xiao-Mai  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR REGULATING APOPTOSIS,  
; TITLE OF INVENTION: AND METHODS OF MAKING AND SCREENING FOR COMPOUNDS  
; TITLE OF INVENTION: THAT REGULATE APOPTOSIS  
; FILE REFERENCE: A7483  
; CURRENT APPLICATION NUMBER: US/09/580,523  
; CURRENT FILING DATE: 2000-05-30  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 168  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-09-580-523-1

Query Match 100.0%; Score 145; DB 19; Length 168;  
Best Local Similarity 100.0%; Pred. No. 1.6e-11;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QSSWTRVFQSWWDRNLGRGSSAPSQ 26  
Db 143 QSSWTRVFQSWWDRNLGRGSSAPSQ 168  
|||||

RESULT 9  
US-09-587-473-21  
; Sequence 21, Application US/09587473  
; GENERAL INFORMATION:  
; APPLICANT: Zhang, Hui  
; APPLICANT: Tsvetkov, Lyuben  
; TITLE OF INVENTION: Protein Knockout Technology  
; FILE REFERENCE: 44574-5047-WO  
; CURRENT APPLICATION NUMBER: US/09/587,473  
; CURRENT FILING DATE: 2000-06-05  
; PRIOR APPLICATION NUMBER: US 60/137,494  
; PRIOR FILING DATE: 1999-06-04  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 21  
; LENGTH: 168  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-09-587-473-21

Query Match 100.0%; Score 145; DB 19; Length 168;  
Best Local Similarity 100.0%; Pred. No. 1.6e-11;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QSSSWTRVFQSWDRNLGRGSSAPSQ 26  
|||||  
Db 143 QSSSWTRVFQSWDRNLGRGSSAPSQ 168

## RESULT 10

PCT-US00-11864-3  
; Sequence 3, Application PC/TUS0011864  
; GENERAL INFORMATION:  
; APPLICANT: APOPTOSIS TECHNOLOGY, INC.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR REGULATING APOPTOSIS,  
; TITLE OF INVENTION: AND METHODS OF MAKING AND SCREENING FOR COMPOUNDS  
; TITLE OF INVENTION: THAT REGULATE APOPTOSIS  
; FILE REFERENCE: F137122  
; CURRENT APPLICATION NUMBER: PCT/US00/11864  
; CURRENT FILING DATE: 2000-05-30  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 162  
; TYPE: PRT  
; ORGANISM: Mus musculus  
PCT-US00-11864-3

Query Match 82.8%; Score 120; DB 1; Length 162;  
Best Local Similarity 73.1%; Pred. No. 3.8e-08;  
Matches 19; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 QSSSWTRVFQSWDRNLGRGSSAPSQ 26  
|||||  
Db 137 QSAGWTRIIQSWDRNLGRGSGTSPQ 162

## RESULT 11

US-09-580-523-3  
; Sequence 3, Application US/09580523  
; GENERAL INFORMATION:  
; APPLICANT: Zhou, Xiao-Mai  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR REGULATING APOPTOSIS,  
; TITLE OF INVENTION: AND METHODS OF MAKING AND SCREENING FOR COMPOUNDS  
; TITLE OF INVENTION: THAT REGULATE APOPTOSIS  
; FILE REFERENCE: A7483  
; CURRENT APPLICATION NUMBER: US/09/580,523  
; CURRENT FILING DATE: 2000-05-30  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 162  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-580-523-3

Query Match 82.8%; Score 120; DB 19; Length 162;  
Best Local Similarity 73.1%; Pred. No. 3.8e-08;  
Matches 19; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 QSSSWTRVFQSWDRNLGRGSSAPSQ 26  
|||||  
Db 137 QSAGWTRIIQSWDRNLGRGSGTSPQ 162

## RESULT 12

PCT-US00-11864-2  
; Sequence 2, Application PC/TUS0011864  
; GENERAL INFORMATION:  
; APPLICANT: APOPTOSIS TECHNOLOGY, INC.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR REGULATING APOPTOSIS,  
; TITLE OF INVENTION: AND METHODS OF MAKING AND SCREENING FOR COMPOUNDS  
; TITLE OF INVENTION: THAT REGULATE APOPTOSIS  
; FILE REFERENCE: F137122  
; CURRENT APPLICATION NUMBER: PCT/US00/11864

; CURRENT FILING DATE: 2000-05-30  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 204  
; TYPE: PRT  
; ORGANISM: Mus musculus  
PCT-US00-11864-2

Query Match 82.8%; Score 120; DB 1; Length 204;  
Best Local Similarity 73.1%; Pred. No. 4.7e-08;  
Matches 19; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 QSSSWTRVFQSWDRNLGRGSSAPSQ 26  
|||||  
Db 179 QSAGWTRIIQSWDRNLGRGSGTSPQ 204

## RESULT 13

PCT-US97-15871-1  
; Sequence 1, Application PC/TUS9715871  
; GENERAL INFORMATION:  
; APPLICANT: KORSMEYER, STANLEY J.  
; TITLE OF INVENTION: MODULATION OF APOPTOSIS BY SERINE  
; TITLE OF INVENTION: PHOSPHORYLATION OF BCL-X1/BCL-2 ASSOCIATED CELL DEATH  
; TITLE OF INVENTION: REGULATOR  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: HOWELL & HAERKAMP, L.C.  
; STREET: 7733 FORSYTH BLVD., SUITE 1400  
; CITY: ST. LOUIS  
; STATE: MISSOURI  
; COUNTRY: USA  
; ZIP: 63146  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US97/15871  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: HOLLAND, DONALD R.  
; REGISTRATION NUMBER: 35,197  
; REFERENCE/DOCKET NUMBER: 965018  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (314) 727-5188  
; TELEFAX: (314) 727-6092  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 204 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
PCT-US97-15871-1

Query Match 82.8%; Score 120; DB 1; Length 204;  
Best Local Similarity 73.1%; Pred. No. 4.7e-08;  
Matches 19; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 QSSSWTRVFQSWDRNLGRGSSAPSQ 26  
|||||  
Db 179 QSAGWTRIIQSWDRNLGRGSGTSPQ 204

## RESULT 14

PCT-US97-15871A-1  
; Sequence 1, Application PC/TUS9715871A

GENERAL INFORMATION:  
; APPLICANT: KORSMEYER, STANLEY J  
; TITLE OF INVENTION: MODULATION OF APOPTOSIS BY SERINE  
; TITLE OF INVENTION: PHOSPHORYLATION OF BCL-XL/BCL-2 ASSOCIATED CELL DEATH  
; TITLE OF INVENTION: REGULATOR  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: HOWELL & HAFERKAMP, L.C.  
; STREET: 7733 FORSYTH BLVD., SUITE 1400  
; CITY: ST. LOUIS  
; STATE: MISSOURI  
; COUNTRY: USA  
; ZIP: 63105  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US97/15871A  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: HOLLAND, DONALD R  
; REGISTRATION NUMBER: 35,197  
; REFERENCE/DOCKET NUMBER: 6029-1938  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (314) 727-5188  
; TELEFAX: (314) 727-6092  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 204 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
PCT-US97-15871A-1

Query Match 82.8%; Score 120; DB 1; Length 204;  
Best Local Similarity 73.1%; Pred. No. 4.7e-08;  
Matches 19; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 QSSSWTRVFQSWWDRNLGRGSSAPSQ 26  
||: ||: ||||| ||: |||||  
Db 179 QSAGWTRIIQSWWDRNLGKGSTPSQ 204

RESULT 15  
PCT-US98-19765-41  
; Sequence 41, Application PC/TUS9819765  
; GENERAL INFORMATION:  
; APPLICANT: WASHINGTON UNIVERSITY  
; TITLE OF INVENTION: CELL DEATH AGONISTS  
; NUMBER OF SEQUENCES: 55  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: HOWELL & HAFERKAMP, L.C.  
; STREET: 7733 FORSYTH BOULEVARD, SUITE 1400  
; CITY: ST. LOUIS  
; STATE: MO  
; COUNTRY: USA  
; ZIP: 63105  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US98/19765  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: HENDERSON, MELODIE W

REGISTRATION NUMBER: 37,848  
; REFERENCE/DOCKET NUMBER: 6029-6526  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 314-727-5188  
; TELEFAX: 314-727-6092  
; INFORMATION FOR SEQ ID NO: 41:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 204 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
PCT-US98-19765-41

Query Match 82.8%; Score 120; DB 1; Length 204;  
Best Local Similarity 73.1%; Pred. No. 4.7e-08;  
Matches 19; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 QSSSWTRVFQSWWDRNLGRGSSAPSQ 26  
||: ||: ||||| ||: |||||  
Db 179 QSAGWTRIIQSWWDRNLGKGSTPSQ 204

Search completed: October 9, 2001, 16:07:48  
Job time: 498 sec

